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OM protein - protein search, using sw model

Run on: January 26, 2006, 07:47:09 : Search time 44.1552 Seconds
(without alignments)
129.360 Million cell updates/sec

Title: US-09-662-293-7

Perfect score: 64

Sequence: 1 DKONYLALVRELK 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 897420

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	64	100.0	13	3	AAV52516 House dus
2	64	100.0	13	5	AAU96320 Der HMM-m
3	35	54.7	16	2	AAW45120 Human car
4	31	48.4	21	5	AD180376 Human leu
5	30	46.9	13	3	AAV98022 HLA class
6	30	46.9	13	7	ADM33519 HLA bindi
7	30	46.9	13	7	ADM34752 HLA bindi
8	30	46.9	13	7	ADM34752 HLA bindi
9	30	46.9	13	2	AAK60745 Lolium pe
10	30	46.9	16	7	ADM35806 HLA bindi
11	30	46.9	20	4	AAW97099 Peptide F
12	29	45.3	10	4	AAW42730 Mycoplasma
13	29	45.3	16	2	AAW45121 Human car
14	28	43.8	10	4	AAV95826 Human com
15	28	43.8	12	6	ABP68019 Bacillus
16	28	43.8	13	6	ABP68026 Bacillus
17	28	43.8	15	8	ADJ38607 HSV-4 BFL
18	28	43.8	15	8	ADJ38608 HSV-4 BFL
19	28	43.8	16	2	AAK41980 Human T C
20	28	43.8	16	3	AAV51484 Human TRF
21	28	43.8	16	3	AAK28946 Peptide C
22	28	43.8	16	3	AAV90112 Cat TRFP
23	28	43.8	16	3	AAV87687 Feline hu
24	28	43.8	17	7	ADD94191 Mouse HUT

25	28	43.8	17	8	ADT94021	Adt94021 rFel d 1 (
26	28	43.8	17	9	ADM77438	Adm77438 Human pla
27	28	43.8	19	2	AAR41978	Aar41978 Human T c
28	28	43.8	19	2	AAR36545	Aar36545 Peptide A
29	28	43.8	19	3	AAV51482	Aav51482 Human TRF
30	28	43.8	19	3	AAK28944	Aak28944 Peptide A
31	28	43.8	19	3	AAV90110	Aav90110 Cat TRFP
32	28	43.8	19	3	AAV87685	Aav87685 Feline hu
33	28	43.8	20	2	AAK41982	Aak41982 Human T c
34	28	43.8	20	2	AAK36547	Aak36547 Peptide C
35	28	43.8	20	9	ADZ65094	Adz65094 Haemophil
36	27	42.2	10	9	ADX39028	Adx39028 Amyloidosis
37	27	42.2	11	3	AAV51511	Aav51511 Human TRF
38	27	42.2	11	3	AAV28970	Aav28970 Peptide e
39	27	42.2	11	3	AAV90128	Aav90128 TRFP deri
40	27	42.2	11	3	AAV87714	Aav87714 Feline hu
41	27	42.2	11	8	ADV25368	Adv25368 Human ATI
42	27	42.2	13	2	AAK94334	Aak94334 Anti-thro
43	27	42.2	15	2	AAK60741	Aak60741 Lolium pe
44	27	42.2	15	2	AAK60742	Aak60742 Lolium pe
45	27	42.2	15	7	ADM35287	Adm35287 HLA bindi
46	27	42.2	15	7	ADM34054	Adm34054 HLA bindi
47	27	42.2	16	2	AAW40941	Aaw40941 Cryptic P
48	27	42.2	16	2	AAV25530	Aav25530 Human MHC
49	27	42.2	16	7	ADC34823	Adc34823 Cat aller
50	27	42.2	16	8	ADM12206	Adm12206 MHC class
51	27	42.2	16	8	ADO38424	Ado38424 Cat aller
52	27	42.2	16	8	ADQ26736	Adq26736 Topo V Hh
53	27	42.2	20	2	AAV15500	Aav15500 Human 5'
54	27	42.2	21	2	AAW35818	Aaw35818 Human Prb
55	27	42.2	21	5	AD180353	Ad180353 Human leu
56	27	42.2	21	5	AD180351	Ad180351 Human leu
57	27	42.2	21	5	AD180343	Ad180343 Human leu
58	27	42.2	21	5	AD180347	Ad180347 Human leu
59	27	42.2	21	5	AD180348	Ad180348 Human leu
60	27	42.2	21	5	AD180345	Ad180345 Human leu
61	27	42.2	21	5	AD180326	Ad180326 Human leu
62	27	42.2	21	5	AD180355	Ad180355 Human leu
63	27	42.2	21	5	AD180371	Ad180371 Human leu
64	27	42.2	21	5	AD180354	Ad180354 Human leu
65	26	40.6	10	4	AAK87550	Aak87550 Saccharom
66	26	40.6	10	4	AAK87551	Aak87551 Saccharom
67	26	40.6	11	8	ADV25385	Adv25385 Human som
68	26	40.6	11	8	ADV25369	Adv25369 Human bra
69	26	40.6	11	9	AEA45034	Aea45034 Apolipop
70	26	40.6	12	7	ADG85031	Adg85031 Phage dis
71	26	40.6	13	3	AAV99111	Aav99111 HLA class
72	26	40.6	13	6	ABP68022	Abp68022 Bacillus
73	26	40.6	14	9	ADV57875	Adv57875 G protein
74	26	40.6	14	9	ADV58630	Adv58630 G protein
75	26	40.6	14	9	ADV59434	Adv59434 G protein
76	26	40.6	15	4	AAW98979	Aaw98979 Vaccine r
77	26	40.6	15	4	AAK45751	Aak45751 Human Zal
78	26	40.6	15	4	AAK89578	Aak89578 HIV gp120
79	26	40.6	15	4	AAK89577	Aak89577 HIV gp120
80	26	40.6	15	4	AAK89579	Aak89579 HIV gp120
81	26	40.6	15	8	ADG42415	Adg42415 Human Zal
82	26	40.6	16	6	ABP82426	Abp82426 G protein
83	26	40.6	17	2	AAK3583	Aak3583 G protein
84	26	40.6	17	2	AAK3663	Aak3663 HIV princ
85	26	40.6	17	8	ADM19017	Adm19017 HLA-DR bo
86	26	40.6	17	8	ADM19032	Adm19032 HLA-DR bo
87	26	40.6	18	4	AAK89626	Aak89626 HIV gp120
88	26	40.6	18	4	AAK89624	Aak89624 HIV gp120
89	26	40.6	18	4	AAK89625	Aak89625 HIV gp120
90	26	40.6	20	5	AAU85583	Aau85583 Lung tumo
91	26	40.6	20	5	AAU70993	Aau70993 M. tuberc
92	26	40.6	20	6	ABU65555	Abu65555 Human lun
93	26	40.6	20	6	ABU66458	Abu66458 Lung can
94	26	40.6	20	7	ADH47370	Adh47370 Human lun
95	26	40.6	20	8	ADJ21289	Adj21289 Human lun
96	26	40.6	20	9	AEBO7909	Aeb07909 Peptide b
97	26	40.6	21	4	AAK89492	Aak89492 HIV gp120

98	26	40.6	21	4	AAB89193	AAB89193	HIV	gp120
99	26	40.6	21	4	AAB89491	AAB89491	HIV	gp120
100	26	40.6	21	4	AAB89192	AAB89192	HIV	gp120

ALIGNMENTS

RESULT 1

AAV52516
ID AAV52516 standard; peptide; 13 AA.

AC AAV52516;

DT 22-FEB-2000 (first entry)

DE House dust mite allergen protein (map) A/B fragment map(6).

KW Mite allergen protein; map; high molecular weight; HMW-map; allergy;

KW house dust mite; IGE; immunoglobulin E; allergen; mapA; mapB;

KW hypersensitivity reaction; therapy; treatment; diagnosis; human; feline;

KW canine; veterinary; antibody; vaccine; immunisation.

OS Dermatophagoides farinae.

PN W09954349-A2.

PD 28-OCT-1999.

PF 16-APR-1999; 99WO-US008524.

PR 17-APR-1998; 98US-00062013.

PR 13-MAY-1998; 98US-0085295P.

PR 02-SEP-1998; 98US-0089303P.

PA (HESK-) HESKA CORP.

PI Mccall CA, Hunter SM, Weber ER;

PT WPI; 2000-052700/04.

PS Claim 3; Page 69; 154pp; English.

XX Sequences AAV52510-V52522 represent proteolytic fragments of

CC Dermatophagoides farinae high molecular weight mite allergen protein (HM

CC -map) composition. The HMW-map composition was isolated from a D. farinae

CC homogenate by gel filtration, with each fraction being analysed for the

CC presence of proteins that bound to IGE present in mite-allergic dog

CC antisera. The HMW-map composition comprises mapA (a 109 kD protein) and

CC mapB (98 kD). Mite allergenic proteins and peptides, and nucleic acids

CC encoding them, may be used in therapeutic compositions to modify an

CC animal's hypersensitivity reaction to mite allergens. Animals that may be

CC treated include mammals and birds, especially felines, canines, equines,

CC humans, other pets, and work or domestic animals. The proteins or

CC fragments may also be used to diagnose allergies via a skin test. The

CC proteins and peptides can also be used to raise antibodies, which have a

CC variety of potential uses. For example, they can be used as vaccines to

CC passively immunise animals against dust mite hypersensitivity, as

CC positive controls in test kits and as tools to recover desired dust mite

CC allergens from a mixture of proteins

XX Sequence 13 AA;

SO Query Match 100.0%; Score 64; DB 3; Length 13;

Best Local Similarity 100.0%; Pred. No. 0.00013;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DKONYLALVRELK 13

DB 1 DKONYLALVRELK 13

RESULT 2
AAU96320
ID AAU96320 standard; peptide; 13 AA.

AC AAU96320;

DT 15-JUL-2002 (first entry)

DE Der HMW-map polypeptide #7.

KW Der HMW-map; American house dust mite; antiallergic; mite; IGE;

KW mite allergenic protein; immunoglobulin E; hypersensitivity;

KW immunocomplex formation.

OS Dermatophagoides farinae.

PN W0200222807-A2.

PD 21-MAR-2002.

PF 14-SEP-2001; 2001WO-US028730.

PR 14-SEP-2000; 2000US-00662293.

PA (HESK-) HESKA CORP.

PI Mccall CA, Hunter SM, Weber ER;

PT WPI; 2002-351888/38.

PS New mite allergenic protein isolated from Dermatophagoides, designated

CC Der HMW-map protein, useful as a vaccine for treating mite allergy.

XX Claim 12; Page 70; 161pp; English.

XX The invention relates to an isolated mite allergenic protein of

CC Dermatophagoides, designated Der HMW-map protein, and its related nucleic

CC acid. The Der HMW-map protein is useful for eliciting an immune response

CC against Der HMW-map protein. The protein or a reagent comprising a non-

CC proteinaceous epitope is useful for identifying an animal (e.g., dog,

CC cat) susceptible to or having an allergic response to a mite. A

CC therapeutic composition is useful for desensitising a host animal to an

CC allergic response to a mite. The DNA and protein can be used in the

CC detection of anti-Der HMW-map antibodies in animal fluids, and inhibition

CC of immunoglobulin (Ig) E or Der HMW-map protein activity associated with a

CC disease. Antibodies that bind to Der HMW-map are useful for inhibiting

CC binding of proteins to IGE, to prevent immunocomplex formation, thus

CC reducing hypersensitivity responses to mite allergens, and as vaccines

CC against mite allergen hypersensitivity. Sequences AAU96314-AAU96342

CC represent Der HMW-map polypeptides of the invention

XX Sequence 13 AA;

SO Query Match 100.0%; Score 64; DB 5; Length 13;

Best Local Similarity 100.0%; Pred. No. 0.00013;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DKONYLALVRELK 13

DB 1 DKONYLALVRELK 13

RESULT 3
AAW45120
ID AAW45120 standard; peptide; 16 AA.

AC AAW45120;

DT 28-APR-1998 (first entry)

DE Human cartilage glycoprotein 39 derived peptide #21.

XX Articular cartilage; immunosuppressive therapy; antigen; autoantigen;
 KW immunological tolerance; T-cell; human cartilage glycoprotein 39;
 KM HC gp-39; rheumatoid arthritis; epitope.
 XX Synthetic.
 OS Homo sapiens.
 XX MO9740068-A1.
 PN 30-OCT-1997.
 PD 22-APR-1997; 97WO-EP002051.
 PF 22-APR-1997; 96EP-00201106.
 PR 24-APR-1996; 96EP-00201106.
 XX (ALKU) AKZO NOBEL NV.
 PA Boots AMH, Verheijden GFM;
 PI WPI; 1997-535775/49.
 DR Peptide suitable for use in antigen specific immunosuppressive therapy -
 XX resembles or mimics epitope present on HC gp-39, so inducing systemic
 PT immunological tolerance to rheumatoid arthritis auto-antigen.
 PT Disclosure; Page 16; 82pp; English.
 XX The present sequence represents a peptide which resembles or mimics an
 CC epitope present on human cartilage glycoprotein 39 (HC gp-39), an
 CC autoantigen in rheumatoid arthritis. The invention relates to peptides
 CC consisting of 16-55 amino acid residues comprising at least one of the
 CC following 19 sequences: LVCYTSMS; FLCTHITS; IISFANIS; LKTLISVG;
 CC FIKSVPEF; EDGLDLAW; LYGERDQ; YDAKISQ; LDFISMT; FLSMTYDF;
 CC FKGQEDAS; YAVGYMLR; MLRGAPAS; LAYEIDCF; LRGATVHT; YLKROLNG;
 CC LAGAWMAL; VALDLDDF; or LDLDPOGS. They can be used medically in antigen
 CC specific immunosuppressive therapy, particularly the treatment of T-cell
 CC mediated destruction of articular cartilage in autoimmune diseases (e.g.
 CC rheumatoid arthritis). They can also be used to detect activated
 CC autoreactive T cells in an individual. The peptides have a specific
 CC effect on the autoreactive T cells, thus leaving the other components of
 CC the immune system intact, unlike the non-specific suppressive effect of
 CC immunosuppressive drugs, and do not cause toxic side effects. The
 CC peptides are predominantly recognised by autoreactive T cells from
 CC rheumatoid arthritis patients, but rarely by those from healthy donors
 CC
 SQ Sequence 16 AA;
 QY
 Db Query Match 54.7%; Score 35; DB 2; Length 16;
 Best Local Similarity 41.7%; Pred. No. 29;
 Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
 1 DKONYLALVREL 12
 |||:|:|:
 ADI80376
 ID ADI80376 standard; peptide; 21 AA.
 XX ADI80376;
 AC 22-APR-2004 (first entry)
 DE Human leukocyte antigen A sub-type peptide region 110-130 group 15.
 XX Major Histocompatibility Complex; MHC; CD8; CD4; immunosuppressive;
 KW antidiabetic; antirheumatic; antiarthritic; neuroprotective;
 KW antiinflammatory; gene therapy; T cell response; autoimmune disorder;
 KW graft-versus-host disease; graft rejection; rheumatoid arthritis;
 KW celiac disease; dermatitis herpeticiformis; diabetes; multiple sclerosis;
 KM Crohn's disease; Psoriasis; human leukocyte antigen.

XX Homo sapiens.
 OS Synthetic.
 XX MO200277030-A2.
 PN 03-OCT-2002.
 PD 27-MAR-2002; 2002WO-GB001499.
 PP 27-MAR-2001; 2001GB-00007628.
 PR (AVID-) AVIDEX LTD.
 PA Jakobsen BK, Cameron BJ;
 PI WPI; 2002-723521/78.
 DR New modified Major Histocompatibility Complex (MHC) molecule or nucleic
 XX acid encoding the MHC molecule, useful in medicine, particularly useful
 PT for treating autoimmune disorders, e.g. graft-versus-host disease or
 PT graft rejection.
 PT Disclosure; Fig 11; 107pp; English.
 XX The invention relates to a novel modified Major Histocompatibility
 CC Complex (MHC) molecule or a nucleic acid encoding the modified MHC
 CC molecule. The binding of the MHC molecule of a selected type to CD8 or
 CC CD4 is inhibited, but it can present the same peptide or peptides as
 CC unmodified molecules of the MHC type, which is for use in medicine. The
 CC invention further comprises: inhibiting the activity of T cells against a
 CC cell presenting molecules of a selected MHC type, by causing the cell to
 CC present modified molecules of the MHC type; a cell, which presents
 CC molecules of a selected MHC type and the modified molecules of the
 CC selected MHC subtype whose binding to CD8 or CD4 is inhibited, but which
 CC can present the same peptide or peptides as unmodified molecules of the
 CC MHC type; a nucleic acid molecule encoding the modified MHC molecules or
 CC its complementary sequence; a vector comprising the nucleic acid molecule
 CC ; and a host cell including the vector. The modified MHC molecule has the
 CC following activities: immunosuppressive, antidiabetic, antirheumatic,
 CC antiarthritic, neuroprotective, and antiinflammatory. The nucleic acid
 CC encoding the modified MHC molecule can be used in gene therapy to treat
 CC disorders. The modified MHC molecule, as well as the nucleic acid
 CC encoding the molecule, are useful in the manufacture of a medicament for
 CC inhibiting T cell response. The modified MHC molecule is particularly
 CC useful for treating an autoimmune disorder (which may be due to
 CC endogenous or exogenous etiology), graft-versus-host disease or graft
 CC rejection. These disorders also include rheumatoid arthritis, celiac
 CC disease, dermatitis herpeticiformis, diabetes, multiple sclerosis, Crohn's
 CC disease, or Psoriasis. This sequence represents a human leukocyte antigen
 CC polypeptide relating to the modified MHC molecule of the invention.
 CC
 SQ Sequence 21 AA;
 QY
 Db Query Match 48.4%; Score 31; DB 5; Length 21;
 Best Local Similarity 50.0%; Pred. No. 2; Indels 0; Gaps 0;
 Matches 6; Conservative 3; Mismatches 3;
 1 DKONYLALVREL 12
 |||:|:|:
 ADI80376
 ID ADI80376 standard; peptide; 13 AA.
 XX ADI80376;
 AC 07-AUG-2000 (first entry)
 DE HLA class II binding antigen epitope peptide #211.
 XX

KW Human leucocyte antigen: HLA class II; antigen epitope; pharmaceutical;
 KW immune response; chronic viral disease; cancer; autoimmune disease;
 KW rheumatoid arthritis; multiple sclerosis; myasthenia gravis; AIDS;
 KW allograft rejection; allergy; Lyme disease; hepatitis; prostate cancer;
 KW glomerulonephritis; food hypersensitivity; malaria.
 XX
 OS unidentified.
 XX
 PN MO9961916-A1.
 PD
 PD 02-DEC-1999.
 XX
 PF 28-MAY-1999; 99WO-US012066.
 XX
 PF 29-MAY-1998; 98US-0087192P.
 BR
 XX (EPIM-) EPIMMUNE INC.
 PA
 PI Sette A, Southwood S, Sidney J;
 XX
 PI WPI; 2000-097143/08.
 DR
 PT New compositions containing immunogenic peptide epitopes for various HLA
 PT class II DR molecules useful for inducing helper T cell response.
 XX
 PS Claim 1; Page 43; 60pp; English.
 XX
 CC The present invention relates to a new pharmaceutical composition
 CC comprising a unit dose form of a peptide, or analogue, comprising an
 CC epitope selected from those represented by peptides AAY9812-Y99339 which
 CC are derived from various antigens for various human leucocyte antigen
 CC class DR molecules, representative of the world wide population. The
 CC peptide/analogue binds to an HLA class II molecule at an IC-50 of less
 CC than or equal to 1,000 nM. The pharmaceutical focuses the immune response
 CC toward selected determinants and could therefore be used in cases of
 CC chronic viral diseases and cancer. Examples of diseases that can be
 CC treated using the peptide containing pharmaceutical include autoimmune
 CC diseases (rheumatoid arthritis, multiple sclerosis, and myasthenia
 CC gravis), allograft rejection, allergies, Lyme disease, hepatitis, post-
 CC streptococcal endocarditis or glomerulonephritis and food
 CC hypersensitivities. The peptide epitopes can be used to enhance immune
 CC responses against other immunogens administered with the peptides.
 CC Diseases which can be treated using immunogenic mixtures include prostate
 CC cancer, hepatitis B, hepatitis C, AIDS, renal carcinoma, cervical
 CC carcinoma, lymphoma, and condyloma acuminatum. The peptides may also be
 CC used to make monoclonal antibodies useful as potential diagnostic or
 CC therapeutic agents. The peptides may also be useful as diagnostic or
 CC reagents, for example, to determine the susceptibility of an individual
 CC to a treatment regimen. Also, the peptides may be used to predict which
 CC individuals will be at substantial risk of developing chronic infection.
 CC The selection of appropriate T and B cell epitopes should allow the
 CC development of epitope based vaccines particularly towards conserved
 CC epitopes of pathogens which are characterized by high sequence
 CC variability such as HIV, HCV and Malaria
 XX
 XX Sequence 13 AA;
 SQ
 Query Match 46.9%; Score 30; DB 3; Length 13;
 Best Local Similarity 85.7%; Pred. No. 1.9e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 KONYIAL 8
 DB 5 KONYLKL 11
 RESULT 6
 ADM33519
 ID ADM33519 standard; peptide; 13 AA.
 XX
 AC ADM33519;
 XX

DT 10-MAR-2005 (first entry)
 XX
 XX HLA binding epitope #4269.
 DE
 XX Virucide; cytostatic; gene therapy; vaccine; epitope; cytotoxic T cell;
 KW MHC class I; CTL; HTL; A2-restricted cytotoxic lymphocyte; HLA;
 KW viral disease; cancer.
 XX
 OS unidentified.
 XX
 PN WO2003040165-A2.
 PD
 PD 15-MAY-2003.
 XX
 PF 18-OCT-2001; 2001WO-US051650.
 XX
 PF 19-OCT-2000; 2000US-0242350P.
 PR 20-APR-2001; 2001US-0285624P.
 PR
 XX (EPIM-) EPIMMUNE INC.
 PA
 PI Sette A, Sidney J, Southwood S;
 XX
 PI WPI; 2003-441519/41.
 DR
 PT New composition comprising at least one peptide having allele-specific
 PT binding motifs for HLA, useful for preventing, treating or diagnosing
 PT viral diseases and cancer.
 XX
 PS Claim 1; Page 52-379; 382pp; English.
 XX
 CC The invention relates to a composition comprising at least one peptide
 CC having an isolated, prepared epitope selected from any of the sequences
 CC from 30 lists given in the specification. Also disclosed is a method for
 CC inducing a cytotoxic T cell response against a pre-selected antigen in a
 CC patient expressing a specific MHC class I allele by contacting cytotoxic
 CC T cells from the patient with the composition cited above. The
 CC composition comprises an epitope that is joined by an amino acid linker.
 CC The epitope is admixed or joined to a CTL or HTL epitope. The epitope is
 CC bound to an HLA molecule on the antigen-presenting cell, where when an A2
 CC -restricted cytotoxic lymphocyte (CTL) is present, a receptor of the CTL
 CC binds to a complex of the HLA molecule and the epitope. Specifically
 CC claimed are peptides having allele-specific binding motifs for HLA. The
 CC compositions and methods are useful for preventing, treating or
 CC diagnosing viral diseases and cancer. The peptide epitopes are useful as
 CC diagnostic agents for evaluating immune responses, for making antibodies
 CC and for evaluating efficacy of a vaccine. Sequences given in ADM29251-
 CC ADM37745 represent epitopes of the invention as given in Tables 2-31.
 XX
 XX Sequence 13 AA;
 SQ
 Query Match 46.9%; Score 30; DB 7; Length 13;
 Best Local Similarity 85.7%; Pred. No. 1.9e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 KONYIAL 8
 DB 5 KONYLKL 11
 RESULT 7
 ADM34752
 ID ADM34752 standard; peptide; 13 AA.
 XX
 AC ADM34752;
 XX
 DT 10-MAR-2005 (first entry)
 XX
 DE HLA binding epitope #5502.
 XX
 XX Virucide; cytostatic; gene therapy; vaccine; epitope; cytotoxic T cell;
 KW MHC class I; CTL; HTL; A2-restricted cytotoxic lymphocyte; HLA;
 KW viral disease; cancer.

XX OS Unidentified.
 XX PN WO2003040165-A2.
 XX PD 15-MAY-2003.
 XX PF 18-OCT-2001; 2001WO-US051650.
 XX PR 19-OCT-2000; 2000US-0242350P.
 XX PR 20-APR-2001; 2001US-0285624P.
 XX PA (EPIM-) EPIMMUNE INC.
 XX PI Sette A, Sidney J, Southwood S;
 XX DR WPI; 2003-441519/41.
 XX PT New composition comprising at least one peptide having allele-specific
 PT binding motifs for HLA, useful for preventing, treating or diagnosing
 PT viral diseases and cancer.
 XX PS Claim 1; Page 52-379; 382pp; English.
 XX SQ The invention relates to a composition comprising at least one peptide
 CC having an isolated, prepared epitope selected from any of the sequences
 CC from 30 lists given in the specification. Also disclosed is a method for
 CC inducing a cytotoxic T cell response against a pre-selected antigen in a
 CC patient expressing a specific MHC class I allele by contacting cytotoxic
 CC T cells from the patient with the composition cited above. The
 CC composition comprises an epitope that is joined by an amino acid linker.
 CC The epitope is admitted or joined to a CTL or HTL epitope. The epitope is
 CC bound to an HLA molecule on the antigen-presenting cell, where when an A2
 CC -restricted cytotoxic lymphocyte (CTL) is present, a receptor of the CTL
 CC binds to a complex of the HLA molecule and the epitope. Specifically
 CC claimed are peptides having allele-specific binding motifs for HLA. The
 CC compositions and methods are useful for preventing, treating or
 CC diagnosing viral diseases and cancer. The peptide epitopes are useful as
 CC diagnostic agents for evaluating immune responses, for making antibodies
 CC and for evaluating efficacy of a vaccine. Sequences given in ADW3745-
 CC ADW37745 represent epitopes of the invention as given in Tables 2-31.
 XX SQ Sequence 13 AA;
 Query March 46.9%; Score 30; DB 7; Length 13;
 Best Local Similarity 85.7%; Pred. No. 1.9e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 2 KONTYAL 8
 Db 5 KONTYKL 11
 RESULT 8
 AAR60745
 ID AAR60745 standard; peptide: 15 AA.
 XX AC AAR60745;
 XX DT 25-MAR-2003 (revised)
 DT 01-JUN-1995 (first entry)
 XX DE Lolium perenne protein allergen internal sequence LPI-16-10.
 XX KM Lolium perenne protein allergen; Lol PI; ryegrass pollen allergen;
 KM Dac GI; Poa PI; Phl PI.
 XX OS Lolium perenne.
 XX PA WO9421675-A2.
 XX PN 29-SEP-1994.
 XX PD

PF 09-MAR-1994; 94WO-US002537.
 XX PR 12-MAR-1993; 93US-00031001.
 XX PA (IMMU-) IMMUNOLOGIC PHARM CORP.
 XX PI Griffith IJ, Kuo M, Lugman M, Powers S;
 XX DR WPI; 1994-316937/39.
 XX PT Isolated peptide(s) of Lol or P I, major protein allergen of species
 PT Lolium perenne. - useful for diagnosis and treatment of sensitivity to
 PT rye-grass pollen allergen.
 XX PS Claim 2; Fig 4; 125pp; English.
 XX CC AAQ73596 is the PCR generated full length clone c26j, which encodes Lol
 CC PI (AAR60703) a major protein allergen of Lolium perenne (ryegrass).
 CC Internal peptides isolated from Lol PI, which contain at least one T cell
 CC epitope are described in AAR60710-R60757. These peptides can be used in
 CC the treatment and diagnosis of sensitivity to ryegrass pollen protein, or
 CC pollen proteins that are immunologically related to Lol PI e.g. Dac GI,
 CC Phl PI and Poa PI. (updated on 25-MAR-2003 to correct PN field.)
 XX SQ Sequence 15 AA;
 Query March 46.9%; Score 30; DB 2; Length 15;
 Best Local Similarity 55.6%; Pred. No. 2.2e+02;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 OY 1 DKONTYALV 9
 Db 1 DEPNYLAIV 9
 RESULT 9
 ADW35806
 ID ADW35806 standard; peptide: 16 AA.
 XX AC ADW35806;
 XX DT 10-MAR-2005 (first entry)
 XX DE HLA binding epitope #6556.
 XX KM Vitruicide; cytostatic; gene therapy; vaccine; epitope; cytotoxic T cell;
 KM MHC class I; CTL; HTL; A2-restricted cytotoxic lymphocyte; HLA;
 KM viral disease; cancer.
 XX OS Unidentified.
 XX PN WO2003040165-A2.
 XX PD 15-MAY-2003.
 XX PF 18-OCT-2001; 2001WO-US051650.
 XX PR 19-OCT-2000; 2000US-0242350P.
 PR 20-APR-2001; 2001US-0285624P.
 XX PA (EPIM-) EPIMMUNE INC.
 XX PI Sette A, Sidney J, Southwood S;
 XX DR WPI; 2003-441519/41.
 XX PT New composition comprising at least one peptide having allele-specific
 PT binding motifs for HLA, useful for preventing, treating or diagnosing
 PT viral diseases and cancer.
 XX PS Claim 1; Page 52-379; 382pp; English.
 XX SQ The invention relates to a composition comprising at least one peptide

having an isolated, prepared epitope selected from any of the sequences from 30 lists given in the specification. Also disclosed is a method for inducing a cytotoxic T cell response against a pre-selected antigen in a patient expressing a specific MHC class I allele by contacting cytotoxic T cells from the patient with the composition cited above. The composition comprises an epitope that is joined by an amino acid linker. The epitope is admixed or joined to a CTL or HTL epitope. The epitope is bound to an HLA molecule on the antigen-presenting cell, where when an A2-restricted cytotoxic lymphocyte (CTL) is present, a receptor of the CTL binds to a complex of the HLA molecule and the epitope. Specifically claimed are peptides having allele-specific binding motifs for HLA. The compositions and methods are useful for preventing, treating or diagnosing viral diseases and cancer. The peptide epitopes are useful as diagnostic agents for evaluating immune responses, for making antibodies and for evaluating efficacy of a vaccine. Sequences given in ADW29251-ADW37745 represent epitopes of the invention as given in Tables 2-31.

Query Match	46.9%	Score 30;	DB 7;	Length 16;
Best Local Similarity	60.0%;	Pred.	No. 2.4e+02;	
Matches	6; Conservative	2;	Mismatches	2; Indels 0; Gaps 0;

Qy	2	KÖNYLALVRE	11
			::
Db	3	KÖNTLAFVKQ	12

RESULT 10	
ADW34573	
ID ADW34573	standard; peptide; 16 AA

DT	10-MAR-2005	(first entry)
XX		
DE	HLA binding epitope #5323.	

KW virucide; cytostatic; gene therapy; vaccine; epitope; cytotoxic T cell,
 KW MHC class I; CTL; HTL; A2-restricted cytotoxic lymphocyte; HLA;
 KW viral disease; cancer.

xx
os Unidentified.

AA WO2003040165-A2.
PN

AA PD 15-MAY-2003.

AA
PF 18-OCT-2001; 2001WO-US051650.

PR 19-OCT-2000; 2000US-0242350P.

PR 20-APR-2001; 2001US-0285624P.

PA (EPIM-) EPIMUNE INC.

Sette A, Sidney J, Southwood S;

DR WPI; 2003-441519/41.

PT New composition comprising at least one peptide having allele-specific PT binding motifs for HLA, useful for preventing, treating or diagnosing PT viral diseases and cancer.

PS Claim 1; Page 52-379; 382pp; English.

CC The invention relates to a composition comprising at least one peptide
CC having an isolated, prepared epitope selected from any of the sequences
CC from 30 lists given in the specification. Also disclosed is a method for
CC inducing a cytotoxic T cell response against a pre-selected antigen in a
CC patient expressing a specific MHC class I allele by contacting cytotoxic
CC T cells from the patient with the composition cited above. The
CC composition comprises an epitope that is joined by an amino acid linker.
CC The epitope is admixed or joined to a CTL or HTL epitope. The epitope is

CC bound to an HLA molecule on the antigen-presenting cell where when an A2
CC restricted cytotoxic lymphocyte (CTL) is present, a receptor of the CTL
CC binds to a complex of the HLA molecule and the epitope. Specifically
CC claimed are peptides having allele-specific binding motifs for HLA. The
CC compositions and methods are useful for preventing, treating or
CC diagnosing viral diseases and cancer. The peptide epitopes are useful as
CC diagnostic agents for evaluating immune responses, for making antibodies
CC and for evaluating efficacy of a vaccine. Sequences given in ADW29231-
CC ADW37745 represent epitopes of the invention as given in Tables 2-5.

Sequence 16 AA;

Query Match	45.9%	Score 30;	DB 7;	Length 16;
Best Local Similarity	60.0%;	Pred. No. 2.4e+02;		
Matches 6; Conservative	2;	Mismatches	0;	Gaps 0;

QY 2 KQNYLALVRE 1 1
||| | | : :
Db 3 KQNTLAFVKQ 1 2

RESULT 11	
AAW97099	
ID	AAW97099 standard; peptide; 20 AA

AC AA97099

DT 30-APR-1999 (first entry)

DE Peptide from cell fluid obtained after rupture of *P. furiosus*.

KW Thermostable polypeptide factor; DNA synthesis activity; DNA polymerase;

KW in vitro DNA synthesis.

05 *Pyrococcus furiosus*.

PN WO9900506-A1

PD 07-JAN-1999.

PF 24-JUN-1998; 98WO-JP002845.

PR 26-JUN-1997; 97JP-00187496.

[illegible]

E

[illegible]

XX
XX
Phonetic alphabet

PT - for improvement of DNA synt

PS Example 3; Page 34; 177pp; Japanese.

CC AAW97099-104 represent peptides isolated from the cell fluid obtained from cultures of *Drosophila* expressing DCM2329. The peptides are derived from the mature portion of the protein.

CC from thermostable polypeptide factors which bind to, and promote the DNA binding of, but not the polymerase related factors at

CC be used to provide more efficient *in vitro* DNA synthesis and

CC factors in conjunction with a DNA polymerase

SQ Sequence 20 AA;

Query Match	46.9%	Score 30;	DB 2;	Length 20;
Best Local	54.5%	Pred. No. 3.1e+02;		
Matches	6; conservative	2; Mismatches	3; Indels	0; Gaps

Qy	1 DKONYLALVRE 11
	: :
Db	2 DKEGFLNKVRE 12

XX	Articular cartilage; immunosuppressive therapy; antigen; autoantigen;
KM	immunological tolerance; T-cell; human cartilage glycoprotein 39;
KW	HC gp-39; rheumatoid arthritis; epitope.
XX	Synthetic.
OS	Homo sapiens.
XX	
PN	MO9740068-A1.
PD	
XX	30-OCT-1997.
XX	
PF	22-APR-1997; 97WO-EP002051.
XX	
PR	24-APR-1996; 96EP-00201106.
XX	
PA	(ALKU) AKZO NOBEL NV.
PI	Boots AMH, Verheijden GFM;
DR	WPI; 1997-535775/49.
PT	Pepitide suitable for use in antigen specific immunosuppressive therapy -
XX	resembles or mimics epitope present on HC gp-39, so inducing systemic
XX	immunological tolerance to rheumatoid arthritis auto:antigen.
PS	, Disclosure; Page 16; 82pp; English.
CC	The present sequence represents a peptide which resembles or mimics an
CC	epitope present on human cartilage glycoprotein 39 (HC gp-39), an
CC	autoantigen in rheumatoid arthritis. The invention relates to peptides
CC	consisting of 16-55 amino acid residues comprising at least one of the
CC	following 19 sequences: LVCYTSWS; FLCHTILYS; ILYSFANIS; LKTLDSVGQ;
CC	FKSVPSPF; EDGLDILAW; LYGRARDKO; YDIAKISOH; LDFTSIMTY; FSTIMTYDF;
CC	FRGOEASPP; YAVGYMLRL; MLRLGAPAS; LAYVEICDF; LRGAIVHRT; YLKDROLAG;
CC	LGMAMWAL; VWALDLDPF; or LDLDPOGS. They can be used medically in antigen
CC	specific immunosuppressive therapy, particularly the treatment of T-cell
CC	mediated destruction of articular cartilage in autoimmune diseases (e.g.
CC	rheumatoid arthritis). They can also be used to detect activated
CC	autoreactive T cells in an individual. The peptides have a specific
CC	effect on the autoreactive T cells, thus leaving the other components of
CC	the immune system intact, unlike the non-specific suppressive effect of
CC	immunosuppressive drugs, and do not cause toxic side effects. The
CC	peptides are predominantly recognised by autoreactive T cells from
CC	rheumatoid arthritis patients, but rarely by those from healthy donors
XX	
SQ	Sequence 16 AA:
Query Match	45.3%; Score 29; DB 2; Length 16;
Best Local Similarity	36.4%; Pred. NO. 3.6e+02;
Matches	4; Conservative 5; Mismatches 2; Indels 0; Gaps 0.
Qy	3 QNYIALVRELK 13 :: :: 1 QHFTLLIKEMK 11
Db	
RESULT 14	
ID	AAG95826 standard; peptide; 10 AA.
AC	AAG95826;
XX	
DT	18-SEP-2001 (first entry)
XX	
DE	Human complementary peptide, SEQ ID NO: 2020.
XX	
KM	Human; complementary peptide; ligand; drug discovery; drug design.
XX	
OS	Homo sapiens.
XX	
PN	WO200142277-A2.
XX	

PD 14-JUN-2001.
XX 13-DEC-2000; 2000WO-GB004776.
XX 13-DEC-1999; 99GB-00029464.
XX (PROT-) PROTEOM LTD.
XX
XX Robert G, Heal JR;
XX WPI; 2001-408419/43.
XX
XX A set of peptide ligands consisting of specific complementary peptides to
XX proteins encoded by genes of the human genome, useful in an assay for
XX screening and identifying of one or more novel peptides which are drug
XX candidates or pro-drugs.
XX
XX Example 4; Page 332; 646pp; English.
XX
XX The invention relates to a set of complementary peptide ligands generated
XX from the human genome. The complementary peptides interact with their
XX relevant target proteins encoded in the human genome. They can be used as
XX reagents in drug discovery and as lead ligands to facilitate drug design
XX and development. The present sequence is a complementary peptide provided
XX in the specification
XX
XX Sequence 10 AA;
SQ

Query Match 43.8%; Score 28; DB 4; Length 10;
Best Local Similarity 62.5%; Pred. No. 3.2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DKQNYLAL 8
|:|:|:|:
Db 2 DEERYLAL 9

RESULT 15
ABP68019
ID ABP68019 standard; peptide; 12 AA.
XX
XX ABP68019;
XX
XX 08-JAN-2003 (first entry)
XX
XX Bacillus thuringiensis toxin Cry related peptide #12.
XX
XX Bacillus thuringiensis; insecticide; toxin; Cry; pepsin cleavage site;
XX pepsin; PCS.
XX
XX Bacillus thuringiensis.
XX Synthetic.
XX
XX FR2822157-A1.
XX
XX 20-SEP-2002.
XX
XX 19-MAR-2001; 2001FR-00003691.
XX
XX 19-MAR-2001; 2001FR-00003691.
XX
XX (AVET) AVENTIS CROPS SCIENCE SA.
XX
XX Freysinet G, Rang C, Frutos R;
XX
XX WPI; 2003-002439/01.
XX
XX New modified Cry protein, useful as insecticide, comprises at least one
XX additional pepsin cleavage site to reduce persistence in mammalian gut.
XX
XX Example 2; Page 21; 134pp; French.
XX
XX The present invention describes a modified Cry protein (I) that is

CC sensitive to pepsin and comprises at least one additional pepsin cleavage
CC site (PCS). Also described: (a) increasing pepsin sensitivity of Cry
CC proteins by incorporating at least one extra PCS; (b) polynucleotides
CC (II) that encode (I); (c) chimeric genes (CG) that contain a promoter,
CC (II) and terminator; (d) expression or transformation vector (III) that
CC contains CG; (e) host organism (IV) transformed with (III), also, where
CC the organism is a plant, its parts and seeds; (f) production of (I) by
CC growing (IV); and (g) mono- or polyclonal antibodies (Ab) directed
CC against (I). (I) has insecticide activity. (I) can be used as
CC insecticides, particularly where expressed in transgenic plants. (I) are
CC sensitive to enzymes in the digestive tract of mammals, so do not persist
CC in the tract (lack of persistence is required by regulatory authorities
CC for use, in foods, of seeds containing Cry proteins). Extra PCS do not
CC increase degradation in the digestive tract of insects, so have no effect
CC on insecticidal activity. ABV93450 to ABV93909 and ABP67997 to ABP68308
CC represent sequences used in the exemplification of the present invention
XX
XX Sequence 12 AA;
SQ

Query Match 43.8%; Score 28; DB 6; Length 12;
Best Local Similarity 60.0%; Pred. No. 4e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 QNYLALVREL 12
|:|:|:|:|:
Db 1 QNYLALVREL 10

RESULT 16
ABP68026
ID ABP68026 standard; peptide; 13 AA.
XX
XX ABP68026;
XX
XX 08-JAN-2003 (first entry)
XX
XX Bacillus thuringiensis toxin Cry related peptide #19.
XX
XX Bacillus thuringiensis; insecticide; toxin; Cry; pepsin cleavage site;
XX pepsin; PCS.
XX
XX Bacillus thuringiensis.
XX Synthetic.
XX
XX FR2822157-A1.
XX
XX 20-SEP-2002.
XX
XX 19-MAR-2001; 2001FR-00003691.
XX
XX 19-MAR-2001; 2001FR-00003691.
XX
XX 19-MAR-2001; 2001FR-00003691.
XX
XX (AVET) AVENTIS CROPS SCIENCE SA.
XX
XX Freysinet G, Rang C, Frutos R;
XX
XX WPI; 2003-002439/01.
XX
XX New modified Cry protein, useful as insecticide, comprises at least one
XX additional pepsin cleavage site to reduce persistence in mammalian gut.
XX
XX Example 2; Page 21; 134pp; French.
XX
XX The present invention describes a modified Cry protein (I) that is
XX sensitive to pepsin and comprises at least one additional pepsin cleavage
XX site (PCS). Also described: (a) increasing pepsin sensitivity of Cry
XX proteins by incorporating at least one extra PCS; (b) polynucleotides
XX (II) that encode (I); (c) chimeric genes (CG) that contain a promoter,
XX (II) and terminator; (d) expression or transformation vector (III) that
XX contains CG; (e) host organism (IV) transformed with (III), also, where
XX the organism is a plant, its parts and seeds; (f) production of (I) by
XX growing (IV); and (g) mono- or polyclonal antibodies (Ab) directed
XX against (I). (I) has insecticide activity. (I) can be used as

insecticides, particularly where expressed in transgenic plants. (1) are sensitive to enzymes in the digestive tract of mammals, so do not persist in the tract (lack of persistence is required by regulatory authorities for use, in foods, of seeds containing Cry proteins). Extra PCS do not increase degradation in the digestive tract of insects, so have no effect on insecticidal activity. ABV93450 to ABV93909 and ABP67997 to ABP68308 represent sequences used in the exemplification of the present invention

Sequence 13 AA:

Query Match 43.8%; Score 28; DB 6; Length 13;
Best Local Similarity 60.0%; Pred. No. 4.3e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 NYTLALVREL 12
|||:|
Db 1 QNWLALEEL 10

RESULT 17
ADJ38607
ID ADJ38607 standard; peptide, 15 AA.
XX
AC ADJ38607;
XX
DT 06-MAY-2004 (first entry)
XX
DE HSV-4 BFLF2 protein late domain motif mutant peptide #6.
XX
KM Virucide; HSV infection; antiviral; late domain motif; mutein; mutant.
XX
OS Human herpesvirus 4.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 8 /note= "Wild-type residue replaced with Ala"
XX
PN WO2004009027-A2.
XX
PD 29-JAN-2004.
XX
PE 21-JUL-2003; 2003WO-US022828.
XX
PR 19-JUL-2002; 2002US-0397265P.
PR 19-JUL-2002; 2002US-0397477P.
PR 19-JUL-2002; 2002US-0397479P.
PR 03-MAR-2003; 2003US-0451903P.
XX
PA (MYRI-) MYRIAD GENETICS INC.
XX
PI Morham S, Zavitz K, Hobden A;
XX
DR WPI; 2004-123282/12.
XX
PT Use of cells displaying herpes simplex virus (HSV) altered budding phenotype for the manufacture of a medicament for treating HSV infection.
XX
PS Example 14; Page 68; 74pp; English.
XX
CC The present invention relates to cells displaying herpes simplex virus (HSV) altered budding phenotype which are useful for the manufacture of a medicament for treating HSV infection. The medicament further comprises an adjuvant capable of stimulating cellular immune response e.g. IL-2, IL-4, IL-12, IL-18 or gamma-interferon. The cells are human cells and contain a nucleic acid encoding a mutant HSV protein or a nucleic acid encoding the polypeptide sufficient for virus-like particle assembly but devoid of late-domain motifs. The nucleic acid is within an HSV genome. The genome is devoid of late domain motifs capable of effecting viral budding. The composition also comprises a compound capable of interfering with the protein-protein interaction between a host cell protein capable of binding a late domain motif and a HSV protein containing a late domain motif. The composition further comprises another HSV protein or its motif. The composition further comprises another HSV protein or its

immunogenic fragment, and/or a nucleic acid encoding the other HSV protein or the immunogenic fragment. The present sequence is a mutant HSV peptide, derived from the wild-type peptide ADJ38601, used to illustrate the invention.

Sequence 15 AA:

Query Match 43.8%; Score 28; DB 8; Length 15;
Best Local Similarity 60.0%; Pred. No. 5.1e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 4 NYTLALVRELK 13
|||:|
Db 5 NYTLALLENK 14

RESULT 18
ADJ38608
ID ADJ38608 standard; peptide, 15 AA.
XX
AC ADJ38608;
XX
DT 06-MAY-2004 (first entry)
XX
DE HSV-4 BFLF2 protein late domain motif mutant peptide #7.
XX
KM Virucide; HSV infection; antiviral; late domain motif; mutein; mutant.
XX
OS Human herpesvirus 4.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 7.8 /note= "Wild-type residues replaced with Ala Ala"
XX
PN WO2004009027-A2.
XX
PD 29-JAN-2004.
XX
PE 21-JUL-2003; 2003WO-US022828.
XX
PR 19-JUL-2002; 2002US-0397265P.
PR 19-JUL-2002; 2002US-0397477P.
PR 19-JUL-2002; 2002US-0397479P.
PR 03-MAR-2003; 2003US-0451903P.
XX
PA (MYRI-) MYRIAD GENETICS INC.
XX
PI Morham S, Zavitz K, Hobden A;
XX
DR WPI; 2004-123282/12.
XX
PT Use of cells displaying herpes simplex virus (HSV) altered budding phenotype for the manufacture of a medicament for treating HSV infection.
XX
PS Example 14; Page 68; 74pp; English.
XX
CC The present invention relates to cells displaying herpes simplex virus (HSV) altered budding phenotype which are useful for the manufacture of a medicament for treating HSV infection. The medicament further comprises an adjuvant capable of stimulating cellular immune response e.g. IL-2, IL-4, IL-12, IL-18 or gamma-interferon. The cells are human cells and contain a nucleic acid encoding a mutant HSV protein or a nucleic acid encoding the polypeptide sufficient for virus-like particle assembly but devoid of late-domain motifs. The nucleic acid is within an HSV genome. The genome is devoid of late domain motifs capable of effecting viral budding. The composition also comprises a compound capable of interfering with the protein-protein interaction between a host cell protein capable of binding a late domain motif and a HSV protein containing a late domain motif. The composition further comprises another HSV protein or its immunogenic fragment, and/or a nucleic acid encoding the other HSV protein or the immunogenic fragment. The present sequence is a mutant HSV peptide, derived from the wild-type peptide ADJ38601, used to illustrate

```

CC the invention.
XX
SQ Sequence 15 AA;

Query Match      43.8%; Score 28; DB 8; Length 15;
Best Local Similarity 60.0%; Pred. No. 5.1e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 NYLALVRELK 13
   |||:|:|
Db 5 NYAALILENK 14

RESULT 19
AA41980
ID AAR41980 standard; peptide; 16 AA.
XX
XX AAR41980;
XX
XX 25-MAR-2003 (revised)
DT 21-APR-1994 (first entry)
XX
DE Human T cell reactive feline protein fragment C.
XX
XX Human; T cell; reactive; feline; protein; immune response; antigen;
XX tolerance; mammal; Dermatophagoides; Felis; Ambrosia; Lolium; Canis;
XX Cryptomeria; Alternaria; Alder; Betula; Quercus; Olea; Artemesia;
XX Plantago; Parietaria; Biatella; Apis; Periplaneta; autcautigen; ss.
XX
XX Homo sapiens.
XX
XX MO9319178-A2.
XX
XX 30-SEP-1993.
XX
XX 25-MAR-1993; 93WO-US002462.
XX
XX 25-MAR-1992; 92US-00857311.
XX 15-MAY-1992; 92US-00884718.
XX 15-JAN-1993; 93US-00006116.
XX
XX (IMMU-) IMMUNOLOGIC PHARM CORP.
XX
XX Gelfer ML, Garman RD, Greenstein JL, Kuo M, Briner TJ,
XX Morville M;
XX
XX WPI; 1993-32074/40.
XX
XX New peptide(s) for inducing tolerance - comprise one or more epitope(s)
XX of an allergen administered subcutaneously, for treating sensitivity to
XX cats, bees, etc.
XX
XX Claim 1; Fig 3; 107pp; English.
XX
XX The sequences given in AAR41975-82 are peptides derived from a human T
XX cell reactive feline protein. These peptides are used in a therapeutic
XX composition which is useful in treating diseases which involve an immune
XX response to a protein antigen. This composition may be used to induce
XX tolerance in a mammal to Dermatophagoides, Felis, Ambrosia, Lolium,
XX Cryptomeria, Alternaria, Alder, Betula, Quercus, Olea, Artemesia,
XX Plantago, Parietaria, Canis, Biatella, Apis, Periplaneta and to
XX autcautigen in humans. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 16 AA;

Query Match      43.8%; Score 28; DB 2; Length 16;
Best Local Similarity 41.7%; Pred. No. 5.5e+02;
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 DKONYLALVREL 12
   ||:|:|:|:|
Db 3 DKENALSLDKI 14

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RESULT 20
AA51484
ID AA51484 standard; protein; 16 AA.
XX
XX AA51484;
XX
XX 22-MAY-2000 (first entry)
DT
XX
XX Human TRFP derived peptide C.
XX
XX T-cell reactive feline protein; TRFP; T cell epitope; T cell receptor;
XX down regulation; immune response; allergen; immunoglobulin E;
XX sensitivity; cat protein allergen; human.
XX
XX Homo sapiens.
XX
XX US6019972-A.
XX
XX 01-FEB-2000.
XX
XX 02-SEP-1994; 94US-00300928.
XX
XX 03-NOV-1989; 89US-00431565.
XX 28-FEB-1991; 91US-00662276.
XX 13-DEC-1991; 91US-00807529.
XX 25-MAR-1992; 92US-00857311.
XX 15-MAY-1992; 92US-00884718.
XX 15-JAN-1993; 93US-00006116.
XX
XX (IMMU-) IMMUNOLOGIC PHARM CORP.
XX
XX Garman RD, Greenstein JL, Kuo M, Briner TJ, Morville M;
XX Gelfer ML;
XX
XX WPI; 2000-146862/13.
XX
XX Peptides of human T cell reactive feline protein for treating sensitivity
XX to cat protein allergens comprise at least one T cell epitope recognized
XX by a T cell receptor specific for the human T cell reactive feline
XX protein.
XX
XX Claim 8; Col 89-90; 105pp; English.
XX
XX This invention describes a novel peptide (I) of human T cell reactive
XX feline protein (hTRFP) having at least one T cell epitope recognized by a
XX T cell receptor specific for the human T cell reactive feline protein.
XX the peptide consisting of at least 7-30 amino acids, and having an amino
XX acid sequence derived from an amino acid sequence comprising 94, 96, 97,
XX 109, or 111 residues, given in the specification. The peptides down
XX regulate the immune response to the allergen. The peptides have reduced
XX immunoglobulin E binding and reduce T cell responsiveness. The peptide
XX (I) is useful in compositions for treating sensitivity to a cat protein
XX allergen in a subject. This sequence represents the human TRFP derived
XX peptide used in the method of the invention
XX
XX Sequence 16 AA;

Query Match      43.8%; Score 28; DB 3; Length 16;
Best Local Similarity 41.7%; Pred. No. 5.5e+02;
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 DKONYLALVREL 12
   ||:|:|:|:|
Db 3 DKENALSLDKI 14

RESULT 21
AAB28946
ID AAB28946 standard; peptide; 16 AA.
XX
XX AAB28946;
XX

```

DT 29-JAN-2001 (first entry)
 XX Peptide C derived from T cell reactive feline protein.
 DE Cat; allergy; human T cell reactive feline protein; hTRFP; immunotherapy.
 KM
 XX Felis sp.
 OS
 XX US6120769-A.
 PN
 XX 19-SEP-2000.
 PD
 XX 28-APR-1995; 95US-00431184.
 PF
 XX 03-NOV-1989; 89US-00431565.
 PR 28-FEB-1991; 91US-00662276.
 PR 13-DEC-1991; 91US-00807529.
 PR 25-MAR-1992; 92US-00857311.
 PR 15-MAY-1992; 92US-00884718.
 PR 15-JAN-1993; 93US-00006116.
 PR 02-SEP-1994; 94US-00300928.
 PA (IMMU-) IMMUNOLOGIC PHARM CORP.
 XX
 PI Geffer ML, Garman RD, Greenstein JL, Bond JF;
 XX WPI: 2000-601477/57.
 DR
 XX Detecting, preventing and treating sensitivity to cat protein allergen
 PT comprising combining a biological sample with a human T cell reactive
 PT feline protein and determining the extent of binding that occurs.
 XX
 PS Claim 2; Fig 17; 106pp; English.
 XX
 CC The present invention relates to the detection of sensitivity to a cat
 CC protein allergen by combining a blood sample from a subject with a
 CC peptide of human T cell reactive feline protein (hTRFP). This method and
 CC the hTRFP peptides are useful for diagnosing, preventing and treating cat
 CC allergies by reducing or abolishing an individual's allergic response to
 CC a cat allergen. DNA encoding the TRFP may be used as probes to locate
 CC equivalent sequences present in other species. These may further be used
 CC to study the mechanism of immunotherapy of cat allergy, and to design
 CC modified derivatives, analogues or functional equivalents useful in
 CC immunotherapy. The present sequence was used in the invention
 CC
 XX
 SQ Sequence 16 AA;
 Query Match 43.8%; Score 28; DB 3; Length 16;
 Best Local Similarity 41.7%; Pred. NO. 5.5e+02;
 Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
 QY 1 DKONYALVREL 12
 ||:|:|:|:|:
 DB 3 DKENALSLDKI 14
 RESULT 22
 ID AAY90112 standard; peptide; 16 AA.
 XX
 AC AAY90112;
 XX
 DT 12-SEP-2003 (revised)
 DT 13-JUL-2000 (first entry)
 XX
 DE Cat TRFP derived peptide, peptide C.
 XX
 KM Cat; TRFP; human T-cell reactive feline protein; cat protein allergen;
 KM house dust; Fel d I; cat allergy; Felis domesticus sensitivity; therapy;
 KM diagnosis; goat; sheep; horse; rabbit; dog.
 XX
 OS Felis catus.
 XX

PN US6025162-A.
 XX
 XX 15-FEB-2000.
 PD
 XX
 PF 28-APR-1995; 95US-00430944.
 XX
 PR 03-NOV-1989; 89US-00431565.
 PR 28-FEB-1991; 91US-00662276.
 PR 13-DEC-1991; 91US-00807529.
 PR 25-MAR-1992; 92US-00857311.
 PR 15-MAY-1992; 92US-00884718.
 PR 15-JAN-1993; 93US-00006116.
 PR 02-SEP-1994; 94US-00300928.
 PA (IMMU-) IMMUNOLOGIC PHARM CORP.
 XX
 PI Morgenstern JP, Griffitht JI, Rogers BL;
 XX WPI: 2000-181812/16.
 DR
 XX New human T cell reactive feline protein, useful for desensitizing cat
 PT allergic individuals to cat allergens.
 XX
 PS Claim 9; Fig 17; 108pp; English.
 XX
 CC This sequence is a peptide derived from the human T cell reactive feline
 CC protein (TRFP) of the invention. The protein is a cat protein allergen,
 CC and was isolated from a vacuum bag extract obtained by affinity
 CC purification of house dust collected from several homes with cats. TRFP
 CC is composed of two covalently linked peptide chains, and is also referred
 CC to as Fel d I. TRFP and its peptides are useful for reducing or
 CC preventing the adverse effects that exposure to cat allergens normally
 CC has on cat allergic individuals (i.e. to desensitize individuals to cat
 CC allergens or block the effect of the allergens). TRFP is also used in
 CC methods of diagnosing sensitivity to Felis domesticus in an individual.
 CC DNA sequences encoding TRFP can be used as probes to locate equivalent
 CC sequences present in other species, e.g. goat, sheep, horse, rabbit and
 CC dog, that may be useful in diagnostic and/or therapeutic applications.
 CC (Updated on 12-SEP-2003 to standardise OS field)
 CC
 XX
 SQ Sequence 16 AA;
 Query Match 43.8%; Score 28; DB 3; Length 16;
 Best Local Similarity 41.7%; Pred. NO. 5.5e+02;
 Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
 QY 1 DKONYALVREL 12
 ||:|:|:|:|:
 DB 3 DKENALSLDKI 14
 RESULT 23
 ID AAY87687 standard; protein; 16 AA.
 XX
 AC AAY87687;
 XX
 DT 22-AUG-2000 (first entry)
 DT
 XX
 DE Feline human TRFP peptide C.
 XX
 KM T-cell reactive feline protein; TRFP; Fel d I; cat allergen;
 KM antiallergic; T cell stimulator; diagnostic; immunotherapy.
 XX
 OS Felis sp.
 XX
 PN US6048962-A.
 PD 11-APR-2000.
 XX
 PF 27-APR-1995; 95US-00430014.
 XX
 PR 03-NOV-1989; 89US-00431565.
 XX

PR 28-FEB-1991; 91US-00662276.
 PR 13-DEC-1991; 91US-00807529.
 PR 25-MAR-1992; 92US-00857311.
 PR 15-MAY-1992; 92US-00884718.
 PR 15-JAN-1993; 93US-00006116.
 PR 02-SEP-1994; 94US-00300928.
 XX
 PA (IMMU-) IMMUNOLOGIC PHARM CORP.
 XX
 PI Kuo M, Rogers BL, Gelfer ML, Morgenstern JP, Brauer AM;
 PI Greenstein JL, Griffith IU, Garman RD;
 XX
 DR WPI; 2000-316905/27.
 XX
 PT New human T cell reactive feline protein useful for reducing or
 PT abolishing individual's allergic response to cat allergen comprising two
 PT different covalently linked peptide chains.
 XX
 PS Example 5; Col 89-90; 106pp; English.
 XX
 CC This invention describes a novel naturally occurring cat protein allergen
 CC (I), human T cell reactive feline protein (TRFP), comprising two
 CC different covalently linked peptide chains with a molecular weight of 20
 CC kD, 40 kD or 130 kD under non-reducing conditions and 5 kD or 10-18 kD
 CC under reducing conditions. The products of the invention have
 CC antiallergic activity and act as human T cell stimulators. TRFP is useful
 CC for reducing or preventing the adverse effects of cat allergens on cat
 CC allergic individuals and in ex vivo diagnostic tests to determine which
 CC peptides cause sensitivity so as to selectively use them to desensitize a
 CC cat sensitive individual. Purified TRFP is also useful for studying the
 CC mechanism of immunotherapy of cat allergy and to design modified
 CC derivatives, analogs or functional equivalents that are more useful in
 CC immunotherapy against cat allergy. DNA sequences encoding TRFP are useful
 CC as probes to locate equivalent sequences present in other species (goats,
 CC sheep, dogs, rabbits or horses) that may be useful in diagnostics and/or
 CC therapeutics. Fully defined and characterized TRFP provides complete and
 CC a very simple desensitization therapy. This sequence represents a human T
 CC cell reactive feline protein (also known as Fel d I) derived peptide C
 CC which is described in the method of the invention
 XX
 SQ Sequence 16 AA:
 Query Match 43.8%; Score 28; DB 3; Length 16;
 Best Local Similarity 41.7%; Pred. No. 5.5e+02;
 Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
 QY 1 DKONYLALVREL 12
 DB 3 DKENALSLDKI 14
 ||:|:|:|:
 ||:|:|:|:
 RESULT 24
 ID ADD94191 standard; peptide; 17 AA.
 XX
 AC ADD94191;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Mouse HUIV26 antibody mutant light chain CDR amino acid sequence SeqID76.
 XX
 KW grafted antibody; complementarity determining region; CDR, light CDR;
 KW heavy CDR; cryptic collagen epitope; solid tumour;
 KW new blood vessel growth; angiogenesis; tumour growth; cyrostatic;
 KW collagen agonist; collagen antagonist; cancer metastasis;
 KW anti-cryptic collagen; HUIV26; variable region light chain; mouse;
 KW murine; mutant; mutein.
 XX
 OS Synthetic.
 OS Mus musculus.
 XX
 PN WO2003046204-A2.
 XX

PD 05-JUN-2003.
 XX
 PR 26-NOV-2002; 2002MO-US038147.
 XX
 PR 26-NOV-2001; 2001US-00995529.
 PR 06-DEC-2001; 2001US-00011250.
 XX
 PA (CELL-) CELL MATRIX INC.
 XX
 PI Waking JD, Huse WD, Tang Y, Broek D, Brooks PC;
 XX
 DR WPI; 2003-513649/48.
 XX
 PT New cryptic collagen antibody with one or more complementarity
 PT determining regions, useful for diagnosing and treating disorders
 PT associated with angiogenesis, tumor growth and/or cancer metastasis.
 XX
 PS Claim 2; SEQ ID NO 76; 232pp; English.
 XX
 CC This invention relates to a novel grafted antibody or its functional
 CC fragment comprising one or more complementarity determining regions
 CC (CDRs) of a defined light CDR and a heavy CDR with at least one amino
 CC acid (aa) substitution where the antibody has specific binding activity
 CC for a cryptic collagen epitope. The growth of all solid tumours requires
 CC new blood vessel growth, angiogenesis, inhibition of which is an approach
 CC to limiting tumor growth. The invention may allow development of
 CC therapeutics with a cyrostatic activity as a collagen agonist or
 CC antagonist. The invention is useful for diagnosing and treating disorders
 CC associated with angiogenesis, tumor growth and/or cancer metastasis. The
 CC present sequence is the amino acid sequence of a mutant mouse anti-
 CC cryptic collagen site antibody HUIV26 variable region light chain CDR
 CC which may be used during the creation of an antibody of the invention.
 XX
 SQ Sequence 17 AA:
 Query Match 43.8%; Score 28; DB 7; Length 17;
 Best Local Similarity 71.4%; Pred. No. 5.9e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DKONYLA 7
 DB 11 NKKNYLA 17
 |:|:|:|:
 |:|:|:|:
 RESULT 25
 ID ADT94021 standard; peptide; 17 AA.
 XX
 AC ADT94021;
 XX
 DT 27-JAN-2005 (first entry)
 XX
 DE rFel d 1(2+1) fusion product, tryptic fragment T16+T17.
 XX
 KW Recombinant Fel d 1; rFel d 1; Felis domesticus allergen 1;
 KW Fel d 1 chain 1; Fel d 1 chain 2; fusion product; cat allergy;
 KW antiallergic; domestic cat; mutant; mutein; tryptic fragment.
 XX
 OS Felis catus.
 OS Synthetic.
 XX
 PN WO2004094639-A2.
 XX
 PD 04-NOV-2004.
 XX
 PF 22-APR-2004; 2004WO-IB001583.
 PF 24-APR-2003; 2003GB-00009345.
 PR
 XX
 PA (CLIN-) CLINOVATION.
 XX
 PI Groenlund H, Van Hage- Hamsten M;
 XX

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OM protein - protein search, using sw model

Run on: January 26, 2006, 07:50:06 : Search time 12.2155 Seconds
(without alignments)
87.985 Million cell updates/sec

Title: US-09-662-293-7
Perfect score: 64
Sequence: 1 DKONYLALVRELK 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 229350

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Issued Patents AA: *
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2: /cgn2_6/ptodata/1/1aa/6_COMB.pep: *
3: /cgn2_6/ptodata/1/1aa/H_COMB.pep: *
4: /cgn2_6/ptodata/1/1aa/PTCOMB_COMB.pep: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	64	100.0	13	2	US-09-292-225-7
2	35	54.7	16	2	US-09-171-705-21
3	35	54.7	16	2	US-09-657-757-21
4	30	46.9	20	2	US-09-446-504-7
5	30	46.9	20	2	US-09-712-266-7
6	29	45.3	16	2	US-09-171-705-22
7	29	45.3	16	2	US-09-657-757-22
8	28	43.8	16	2	US-08-300-928C-22
9	28	43.8	16	2	US-08-430-944D-22
10	28	43.8	16	2	US-08-430-944D-22
11	28	43.8	16	2	US-08-431-184-22
12	28	43.8	16	4	PCT-US93-02462-12
13	28	43.8	19	1	US-07-807-529A-10
14	28	43.8	19	2	US-08-300-928C-20
15	28	43.8	19	2	US-08-430-944D-20
16	28	43.8	19	2	US-08-430-944D-20
17	28	43.8	19	2	US-08-430-944D-20
18	28	43.8	19	4	PCT-US93-02462-10
19	28	43.8	20	4	PCT-US93-02462-14
20	27	42.2	11	1	US-07-807-529A-27
21	27	42.2	11	2	US-08-300-928C-76
22	27	42.2	11	2	US-08-430-944D-76
23	27	42.2	11	2	US-08-430-944D-76
24	27	42.2	11	2	US-08-431-184-76
25	27	42.2	16	2	US-09-142-885C-9
26	27	42.2	21	1	US-08-832-877-3
27	26	40.6	10	2	US-08-441-507-52

28	26	40.6	10	2	US-09-106-568E-46	Sequence 46, Appl
29	26	40.6	11	2	US-08-974-549A-63	Sequence 63, Appl
30	26	40.6	11	2	US-08-912-951-63	Sequence 63, Appl
31	26	40.6	11	2	US-09-402-181B-63	Sequence 63, Appl
32	26	40.6	11	2	US-09-721-456-63	Sequence 63, Appl
33	26	40.6	18	2	US-09-386-962C-9	Sequence 9, Appl
34	26	40.6	20	2	US-09-736-457-1851	Sequence 1851, Ap
35	26	40.6	20	2	US-10-017-754-1851	Sequence 1851, Ap
36	25	39.1	7	2	US-08-620-840C-13	Sequence 13, Appl
37	25	39.1	15	1	US-08-311-611A-4	Sequence 4, Appl
38	25	39.1	15	1	US-08-372-783-4	Sequence 4, Appl
39	25	39.1	15	1	US-08-372-105-4	Sequence 4, Appl
40	25	39.1	15	1	US-08-306-473A-4	Sequence 4, Appl
41	25	39.1	15	1	US-08-473-344-4	Sequence 4, Appl
42	25	39.1	15	1	US-08-621-803-1	Sequence 1, Appl
43	25	39.1	15	1	US-08-485-445A-4	Sequence 4, Appl
44	25	39.1	15	2	US-09-119-263-91	Sequence 4, Appl
45	25	39.1	15	2	US-08-657-162-4	Sequence 4, Appl
46	25	39.1	15	2	US-09-224-480-4	Sequence 4, Appl
47	25	39.1	15	2	US-09-093-539-4	Sequence 4, Appl
48	25	39.1	15	2	US-09-217-352-1	Sequence 1, Appl
49	25	39.1	15	2	US-09-790-230-4	Sequence 4, Appl
50	25	39.1	15	2	US-09-689-097-6	Sequence 6, Appl
51	25	39.1	15	4	PCT-US94-02465-4	Sequence 4, Appl
52	25	39.1	15	4	PCT-US95-00498-4	Sequence 4, Appl
53	25	39.1	15	4	PCT-US95-00656-4	Sequence 4, Appl
54	25	39.1	16	2	US-09-459-749D-3	Sequence 3, Appl
55	25	39.1	17	2	US-09-627-896B-16	Sequence 16, Appl
56	25	39.1	17	2	US-09-339-596A-16	Sequence 16, Appl
57	25	39.1	18	2	US-09-101-146-42	Sequence 42, Appl
58	25	39.1	21	2	US-08-782-877-1	Sequence 1, Appl
59	25	39.1	9	1	US-08-747-137-103	Sequence 103, App
60	24	37.5	13	1	US-08-388-267C-14	Sequence 14, Appl
61	24	37.5	13	2	US-09-277-720-14	Sequence 14, Appl
62	24	37.5	14	1	US-08-390-156A-104	Sequence 104, App
63	24	37.5	14	1	US-08-439-817-94	Sequence 94, Appl
64	24	37.5	14	2	US-08-545-860D-61	Sequence 61, Appl
65	24	37.5	14	2	US-09-428-082B-159	Sequence 159, App
66	24	37.5	14	4	PCT-US94-04496-61	Sequence 61, Appl
67	24	37.5	15	2	US-10-198-053-508	Sequence 508, App
68	24	37.5	15	2	US-08-218-025A-25	Sequence 25, Appl
69	24	37.5	16	1	US-08-218-025A-26	Sequence 26, Appl
70	24	37.5	16	1	US-08-241-054-108	Sequence 108, App
71	24	37.5	16	1	US-08-390-156A-91	Sequence 91, Appl
72	24	37.5	16	1	US-08-439-817-88	Sequence 88, Appl
73	24	37.5	16	1	US-08-485-508-108	Sequence 108, App
74	24	37.5	17	1	US-08-353-400-30	Sequence 30, Appl
75	24	37.5	17	1	US-08-467-220A-10	Sequence 10, Appl
76	24	37.5	17	1	US-08-388-267C-17	Sequence 17, Appl
77	24	37.5	17	1	US-08-470-110A-10	Sequence 10, Appl
78	24	37.5	17	1	US-08-667-769A-10	Sequence 10, Appl
79	24	37.5	17	1	US-08-940-371-10	Sequence 10, Appl
80	24	37.5	17	2	US-08-637-647-10	Sequence 10, Appl
81	24	37.5	17	2	US-09-277-220-17	Sequence 17, Appl
82	24	37.5	17	2	US-09-563-222C-26	Sequence 26, Appl
83	24	37.5	17	2	US-09-630-748B-1	Sequence 1, Appl
84	24	37.5	17	2	US-10-700-740-10	Sequence 10, Appl
85	24	37.5	17	2	US-10-146-505-9	Sequence 9, Appl
86	24	37.5	17	2	PCT-US93-08435-22	Sequence 22, Appl
87	24	37.5	17	4	PCT-US93-08435-35	Sequence 35, Appl
88	24	37.5	17	4	PCT-US95-17082A-10	Sequence 10, Appl
89	24	37.5	17	4	US-08-940-095-200	Sequence 200, App
90	24	37.5	18	2	US-08-940-093-200	Sequence 200, App
91	24	37.5	18	2	US-08-940-096-200	Sequence 200, App
92	24	37.5	18	2	US-09-465-719-200	Sequence 200, App
93	24	37.5	18	2	US-09-453-838-200	Sequence 200, App
94	24	37.5	18	2	US-09-461-325-423	Sequence 423, App
95	24	37.5	18	2	US-08-940-136-200	Sequence 200, App
96	24	37.5	18	2	US-09-453-833-200	Sequence 200, App
97	24	37.5	18	2	US-10-012-542-423	Sequence 423, App
98	24	37.5	18	2		
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ALIGNMENTS

RESULT 1

US-09-292-225-7
; Sequence 7, Application US/09292225
; Patent No. 645566
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/09/292,225
; CURRENT FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: 60/098,909
; EARLIER FILING DATE: 1998-09-02
; EARLIER APPLICATION NUMBER: 60/085,295
; EARLIER FILING DATE: 1998-05-13
; EARLIER APPLICATION NUMBER: 60/098,565
; EARLIER FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: 09/062,013
; EARLIER FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-09-292-225-7

Query Match

Best Local Similarity 100.0%; Score 64; DB 2; Length 13;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DKONYLALVRELK 13
Db 1 DKONYLALVRELK 13

RESULT 2

US-09-171-705-21
; Sequence 21, Application US/09171705
; Patent No. 6184204
; GENERAL INFORMATION:
; APPLICANT: BOOTS, ANNA M.H.
; APPLICANT: VERHEIJDEN, GILBERTUS F.M.
; TITLE OF INVENTION: NOVEL PEPTIDES SUITABLE FOR USE IN ANTIGEN SPECIFIC
; TITLE OF INVENTION: IMMUNOSUPPRESSIVE THERAPY
; FILE REFERENCE: O/96198 US
; CURRENT APPLICATION NUMBER: US/09/171,705
; CURRENT FILING DATE: 1999-02-09
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DERIVED FROM
; OTHER INFORMATION: SEQUENCE OF HUMAN CARTILAGE (HC) -39 PROTEIN
US-09-171-705-21

Query Match

Best Local Similarity 54.7%; Score 35; DB 2; Length 16;
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 1 DKONYLALVREL 12
Db 5 DKOHTTLIKEM 16

RESULT 3

US-09-657-757-21
; Sequence 21, Application US/09657757
; Patent No. 6881824
; GENERAL INFORMATION:
; APPLICANT: BOOTS, ANNA M.H.
; APPLICANT: VERHEIJDEN, GILBERTUS F.M.
; TITLE OF INVENTION: NOVEL PEPTIDES SUITABLE FOR USE IN ANTIGEN SPECIFIC
; TITLE OF INVENTION: IMMUNOSUPPRESSIVE THERAPY
; FILE REFERENCE: O/96198 US
; CURRENT APPLICATION NUMBER: US/09/657,757
; CURRENT FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: US/09/171,705
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DERIVED FROM
; OTHER INFORMATION: SEQUENCE OF HUMAN CARTILAGE (HC) -39 PROTEIN
US-09-657-757-21

Query Match

Best Local Similarity 54.7%; Score 35; DB 2; Length 16;
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 1 DKONYLALVREL 12
Db 5 DKOHTTLIKEM 16

RESULT 4

US-09-446-504-7
; Sequence 7, Application US/09446504
; Patent No. 6218150
; GENERAL INFORMATION:
; APPLICANT: UEMORI, Takashi
; APPLICANT: SATO, Yoshimi
; APPLICANT: FUJITA, Tomoko
; APPLICANT: MIYAKE, Kazue
; APPLICANT: MIYAKI, Hiroyuki
; APPLICANT: ASADA, Kiyozo
; APPLICANT: KATO, Ikunoshin
; TITLE OF INVENTION: DNA POLYMERASE-RELATED FACTORS
; FILE REFERENCE: 1422-408PCT
; CURRENT APPLICATION NUMBER: US/09/446,504
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: PCT/JP98/02845
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: JP 9-187496
; PRIOR FILING DATE: 1997-06-26
; PRIOR APPLICATION NUMBER: JP 9-320692
; PRIOR FILING DATE: 1997-11-27
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Pyrococcus furiosus
US-09-446-504-7

Query Match

Best Local Similarity 46.9%; Score 30; DB 2; Length 20;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 DKONYLALVRE 11
Db 2 DKEGFLNKVRE 12

RESULT 5

US-09-712-266-7
Sequence 7, Application US/09712266
Patent No. 633158
GENERAL INFORMATION:
APPLICANT: UEMORI, Takashi
APPLICANT: SATO, Yoshimi
APPLICANT: FUJITA, Tomoko
APPLICANT: MIYAKE, Kazuo
APPLICANT: MUKAI, Hiroyuki
APPLICANT: ASADA, Kiyozo
APPLICANT: KATO, Kunoshin
TITLE OF INVENTION: DNA POLYMERASE-RELATED FACTORS
FILE REFERENCE: 1422-408PCT
CURRENT APPLICATION NUMBER: US/09/712,266
CURRENT FILING DATE: 2000-11-15
PRIOR APPLICATION NUMBER: US 09/446,504
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: PCT/JP98/02845
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: JP 9-187496
PRIOR FILING DATE: 1997-06-26
PRIOR APPLICATION NUMBER: JP 9-320692
PRIOR FILING DATE: 1997-11-27
NUMBER OF SEQ ID NOS: 92
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 7
LENGTH: 20
TYPE: PRT
ORGANISM: Pyrococcus furiosus
US-09-712-266-7

Query Match 46.9%; Score 30; DB 2; Length 20;
Best Local Similarity 54.5%; Pred. No. 97;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DKONYLALVRE 11
DB 2 DKSGFLNKVRE 12

RESULT 6

US-09-171-705-22
Sequence 22, Application US/09171705
Patent No. 6184204
GENERAL INFORMATION:
APPLICANT: BOOTS, ANNA M.H.
APPLICANT: VERHEIJDEN, GILBERTUS F.M.
TITLE OF INVENTION: NOVEL PEPTIDES SUITABLE FOR USE IN ANTIGEN SPECIFIC
FILE REFERENCE: O/96198 US
CURRENT APPLICATION NUMBER: US/09/171,705
CURRENT FILING DATE: 1999-02-09
NUMBER OF SEQ ID NOS: 78
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 22
LENGTH: 16
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: DERIVED FROM
OTHER INFORMATION: SEQUENCE OF HUMAN CARTILAGE (HC) -39 PROTEIN
US-09-171-705-22

Query Match 45.3%; Score 29; DB 2; Length 16;
Best Local Similarity 36.4%; Pred. No. 1.2e+02;
Matches 4; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 3 QNYLALVRELK 13
DB 1 QHFTTLIKEMK 11

RESULT 7

US-09-657-757-22
Sequence 22, Application US/09657757
Patent No. 6881824
GENERAL INFORMATION:
APPLICANT: BOOTS, ANNA M.H.
APPLICANT: VERHEIJDEN, GILBERTUS F.M.
TITLE OF INVENTION: NOVEL PEPTIDES SUITABLE FOR USE IN ANTIGEN SPECIFIC
FILE REFERENCE: O/96198 US
CURRENT APPLICATION NUMBER: US/09/657,757
CURRENT FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: US/09/171,705
PRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 78
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 22
LENGTH: 16
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: DERIVED FROM
OTHER INFORMATION: SEQUENCE OF HUMAN CARTILAGE (HC) -39 PROTEIN
US-09-657-757-22

Query Match 45.3%; Score 29; DB 2; Length 16;
Best Local Similarity 36.4%; Pred. No. 1.2e+02;
Matches 4; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 3 QNYLALVRELK 13
DB 1 QHFTTLIKEMK 11

RESULT 8

US-08-300-928C-22
Sequence 22, Application US/08300928C
Patent No. 6019972
GENERAL INFORMATION:
APPLICANT: GEFFER, Malcolm L. et al.
TITLE OF INVENTION: PEPTIDES FOR HUMAN T CELL REACTIVE FELINE
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNOLOGIC PHARMACEUTICAL CORPORATION
STREET: 610 LINCOLN STREET
CITY: WALTHAM
STATE: Massachusetts
COUNTRY: USA
ZIP: 02145
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/300,928C
FILING DATE: September 2, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/807,529
FILING DATE: December 13, 1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: AMY E. MANDRAGOURAS
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 002.6US (IMI-044)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-300-928C-22

Query Match 43.8%; Score 28; DB 2; Length 16;
Best Local Similarity 41.7%; Pred. No. 1.7e+02;
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DKONYLALVREL 12
Db 3 DKENALSLDKI 14

RESULT 9
US-08-430-944D-22
Sequence 22, Application US/08430944D
Patent No. 6025162
GENERAL INFORMATION:
APPLICANT: Bruce L. Rogers et al.
TITLE OF INVENTION: A HUMAN T CELL REACTIVE FELINE PROTEIN
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/430,944D
FILING DATE: 28-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/430,014
FILING DATE: 27-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,928
FILING DATE: 02-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-044DV2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-430-944D-22

Query Match 43.8%; Score 28; DB 2; Length 16;
Best Local Similarity 41.7%; Pred. No. 1.7e+02;
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DKONYLALVREL 12
Db 3 DKENALSLDKI 14

RESULT 10

US-08-430-014-22
Sequence 22, Application US/08430014
Patent No. 6048962
GENERAL INFORMATION:
APPLICANT: GERTER, Malcolm L. et al.
TITLE OF INVENTION: PEPTIDES FOR HUMAN T CELL REACTIVE FELINE
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNOLOGIC PHARMACEUTICAL CORPORATION
STREET: 610 LINCOLN STREET
CITY: WALTHAM
STATE: Massachusetts
COUNTRY: USA
ZIP: 02145

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/430,014
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/300,928
FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 002,6US (IMI-044)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-430-014-22

Query Match 43.8%; Score 28; DB 2; Length 16;
Best Local Similarity 41.7%; Pred. No. 1.7e+02;
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DKONYLALVREL 12
Db 3 DKENALSLDKI 14

RESULT 11
US-08-431-184-22
Sequence 22, Application US/08431184
Patent No. 6120769
GENERAL INFORMATION:
APPLICANT: Bruce L. Rogers et al.
TITLE OF INVENTION: A HUMAN T CELL REACTIVE FELINE PROTEIN
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/431,184
FILING DATE: 28-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/430,014
FILING DATE: 27-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,928
FILING DATE: 02-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-044DV3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-431-184-22

Query Match 43.8%; Score 28; DB 2; Length 16;
Best Local Similarity 41.7%; Pred. No. 1.7e+02;
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DKONYALVREL 12
||:|:|:|:|:
Db 3 DKENALSLDKI 14

RESULT 12
PCT-US93-02462-12
Sequence 12, Application PC/TUS9302462
GENERAL INFORMATION:
APPLICANT: Gelter, Malcolm L.
APPLICANT: Garman, Richard D.
APPLICANT: Greenstein, Julia L.
APPLICANT: Kuo, Mei-chang
APPLICANT: Briner, Thomas J.
APPLICANT: Morville, Malcolm
TITLE OF INVENTION: PEPTIDES USEFUL FOR TOLERIZATION
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/02462
FILING DATE: 19930325
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/006,116
FILING DATE: 15-JAN-1993
APPLICATION NUMBER: US 07/884,718
FILING DATE: 15-MAY-1992
APPLICATION NUMBER: 07/857,311
FILING DATE: 25-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: IPC-031PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
PCT-US93-02462-12

Query Match 43.8%; Score 28; DB 4; Length 16;
Best Local Similarity 41.7%; Pred. No. 1.7e+02;
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DKONYALVREL 12
||:|:|:|:|:
Db 3 DKENALSLDKI 14

RESULT 13
US-07-807-529A-10
Sequence 10, Application US/07807529A
Patent No. 5547669
GENERAL INFORMATION:
APPLICANT: Rogers, Bruce L.
APPLICANT: Morgenstern, Jay
APPLICANT: Bond, Julian F.
APPLICANT: Garman, Richard D.
APPLICANT: Greenstein, Julia L.
APPLICANT: Kuo, Mei-chang
APPLICANT: Morville, Malcolm
TITLE OF INVENTION: RECOMBOTOPE PEPTIDES
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNOLOGIC PHARMACEUTICAL CORPORATION
STREET: One Kendall Square, Building 600
CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02139
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/807,529A
FILING DATE: 19911213
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/662,276
FILING DATE: 28-FEB-1991
APPLICATION NUMBER: US 07/431,565
FILING DATE: 03-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Channing, Stacey L.
REGISTRATION NUMBER: 31,095
REFERENCE/DOCKET NUMBER: IPC-027/IMI-015
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 494-0060
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-07-807-529A-10

Query Match 43.8%; Score 28; DB 1; Length 19;
Best Local Similarity 41.7%; Pred. No. 2.1e+02;

Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
Qy 1 DKONYALVREL 12
Db 3 DKENALSLDKI 14

RESULT 14

US-08-300-928C-20
Sequence 20, Application US/08300928C
Patent No. 6019972
GENERAL INFORMATION:
APPLICANT: GEFTER, Malcolm L. et al.
TITLE OF INVENTION: PEPTIDES FOR HUMAN T CELL REACTIVE FELINE
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNOLOGIC PHARMACEUTICAL CORPORATION
STREET: 610 LINCOLN STREET
CITY: WALTHAM
STATE: Massachusetts
COUNTRY: USA
ZIP: 02145
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/300,928C
FILING DATE: September 2, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/807,529
FILING DATE: December 13, 1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: AMY E. MANDRAGOURAS
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 002.6US (IMI-044)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-300-928C-20

Query Match 43.8%; Score 28; DB 2; Length 19;
Best Local Similarity 41.7%; Pred. No. 2.1e+02;
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DKONYALVREL 12
Db 3 DKENALSLDKI 14

RESULT 15
US-08-430-944D-20
Sequence 20, Application US/08430944D
Patent No. 6025162
GENERAL INFORMATION:
APPLICANT: Bruce L. Rogers et al.
TITLE OF INVENTION: A HUMAN T CELL REACTIVE FELINE PROTEIN
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street

CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/430,944D
FILING DATE: 28-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/430,014
FILING DATE: 27-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,928
FILING DATE: 02-SEPT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-044DV2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-430-944D-20

Query Match 43.8%; Score 28; DB 2; Length 19;
Best Local Similarity 41.7%; Pred. No. 2.1e+02;
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DKONYALVREL 12
Db 3 DKENALSLDKI 14

RESULT 16
US-08-430-014-20
Sequence 20, Application US/08430014
Patent No. 6048962
GENERAL INFORMATION:
APPLICANT: GEFTER, Malcolm L. et al.
TITLE OF INVENTION: PEPTIDES FOR HUMAN T CELL REACTIVE FELINE
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNOLOGIC PHARMACEUTICAL CORPORATION
STREET: 610 LINCOLN STREET
CITY: WALTHAM
STATE: Massachusetts
COUNTRY: USA
ZIP: 02145
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/430,014
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/300,928
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:

NAME: AMY E. MANDRAGOURAS
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 002.6US (IMI-044)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-430-014-20

Query Match 43.8%; Score 28; DB 2; Length 19;
Best Local Similarity 41.7%; Pred. No. 2.1e+02;
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 1 DKONYLALVREL 12
Db 3 DKENALSILDKI 14

RESULT 17

US-08-431-184-20
Sequence 20, Application US/08431184
Patent No. 6120769
GENERAL INFORMATION:
APPLICANT: Bruce L. Rogers et al.
TITLE OF INVENTION: A HUMAN T CELL REACTIVE FELINE PROTEIN
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/431,184
FILING DATE: 28-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/430,014
FILING DATE: 27-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,928
FILING DATE: 02-SEPT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-044DV3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-431-184-20

Query Match 43.8%; Score 28; DB 2; Length 19;
Best Local Similarity 41.7%; Pred. No. 2.1e+02;
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 1 DKONYLALVREL 12
Db 3 DKENALSILDKI 14

RESULT 18

PCT-US93-02462-10
Sequence 10, Application PC/TUS9302462
GENERAL INFORMATION:
APPLICANT: Gelfer, Malcolm L.
APPLICANT: Garman, Richard D.
APPLICANT: Greenstein, Julia L.
APPLICANT: Kuo, Mei-chang
APPLICANT: Briner, Thomas J.
APPLICANT: Morville, Malcolm
TITLE OF INVENTION: PEPTIDES USEFUL FOR TOLERIZATION
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/02462
FILING DATE: 19930325
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/006,116
FILING DATE: 15-JAN-1993
APPLICATION NUMBER: US 07/884,718
FILING DATE: 15-MAY-1992
APPLICATION NUMBER: 07/857,311
FILING DATE: 25-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IPC-031PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
PCT-US93-02462-10

Query Match 43.8%; Score 28; DB 4; Length 19;
Best Local Similarity 41.7%; Pred. No. 2.1e+02;
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 1 DKONYLALVREL 12
Db 3 DKENALSILDKI 14

RESULT 19

PCT-US93-02462-14
Sequence 14, Application PC/TUS9302462
GENERAL INFORMATION:
APPLICANT: Gelfer, Malcolm L.
APPLICANT: Garman, Richard D.
APPLICANT: Greenstein, Julia L.
APPLICANT: Kuo, Mei-chang

APPLICANT: Briner, Thomas J.
APPLICANT: Morville, Malcolm
TITLE OF INVENTION: PEPTIDES USEFUL FOR TOLERIZATION
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/02462
FILING DATE: 19930325
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/006,116
FILING DATE: 15-JAN-1993
APPLICATION NUMBER: US 07/884,718
FILING DATE: 15-MAY-1992
APPLICATION NUMBER: 07/857,311
FILING DATE: 25-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IPC-031PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
PCT-US93-02462-14

Query Match 43.8%; Score 28; DB 4; Length 20;
Best Local Similarity 41.7%; Pred. 2.2e+02;
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DKONYALVREL 12
Db 4 DKENALSLDKI 15

RESULT 20
US-07-807-529A-27
Sequence 27, Application US/07807529A
Patent No. 5547669
GENERAL INFORMATION:
APPLICANT: Rogers, Bruce L.
APPLICANT: Morgenstern, Jay
APPLICANT: Bond, Julian F.
APPLICANT: Garman, Richard D.
APPLICANT: Greenstein, Julia L.
APPLICANT: Kuo, Mei-chang
APPLICANT: Morville, Malcolm
TITLE OF INVENTION: RECOMBITOPE PEPTIDES
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
STREET: One Kendall Square, Building 600
CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02139
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/807,529A
FILING DATE: 19911213
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/662,276
FILING DATE: 28-FEB-1991
APPLICATION NUMBER: US 07/431,565
FILING DATE: 03-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Channing, Stacey L.
REGISTRATION NUMBER: 31,095
REFERENCE/DOCKET NUMBER: IPC-027/im1-015
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 494-0060
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-807-529A-27

Query Match 42.2%; Score 27; DB 1; Length 11;
Best Local Similarity 55.6%; Pred. No. 1.7e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DKONYALV 9
Db 3 DKENALSL 11

RESULT 21
US-08-300-928C-76
Sequence 76, Application US/08300928C
Patent No. 6019972
GENERAL INFORMATION:
APPLICANT: GEFTER, Malcolm L. et al.
TITLE OF INVENTION: PEPTIDES FOR HUMAN T CELL REACTIVE FELINE
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
STREET: 610 LINCOLN STREET
CITY: WALTHAM
STATE: Massachusetts
COUNTRY: USA
ZIP: 02145
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/300,928C
FILING DATE: September 2, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/807,529
FILING DATE: December 13, 1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: AMY E. MANDRAGOURAS
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 002.6US(IM1-044)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 76:

SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-300-928C-76

Query Match 42.2%; Score 27; DB 2; Length 11;
Best local similarity 55.6%; Pred. No. 1.7e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 DKONYLALV 9
||:|:|:
Db 3 DKENALSL 11

RESULT 22
US-08-430-944D-76
Sequence 76, Application US/08430944D
Patent No. 6025162
GENERAL INFORMATION:
APPLICANT: Bruce L. Rogers et al.
TITLE OF INVENTION: A HUMAN T CELL REACTIVE FELINE PROTEIN
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/430.944D
FILING DATE: 28-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/430.014
FILING DATE: 27-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300.928
FILING DATE: 02-SEPT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-044DV2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 76:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-430-944D-76

Query Match 42.2%; Score 27; DB 2; Length 11;
Best local similarity 55.6%; Pred. No. 1.7e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 DKONYLALV 9
||:|:|:
Db 3 DKENALSL 11

RESULT 23
US-08-430-014-76
Sequence 76, Application US/08430014

Patent No. 6048962
GENERAL INFORMATION:
APPLICANT: GEFTER, Malcolm L. et al.
TITLE OF INVENTION: PEPTIDES FOR HUMAN T CELL REACTIVE FELINE
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNOLOGIC PHARMACEUTICAL CORPORATION
STREET: 610 LINCOLN STREET
CITY: WALTHAM
STATE: Massachusetts
COUNTRY: USA
ZIP: 02145
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/430.014
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/300,928
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: AMY E. MANDRAGOURAS
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 002.6US(IMI-044)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 76:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-430-014-76

Query Match 42.2%; Score 27; DB 2; Length 11;
Best local similarity 55.6%; Pred. No. 1.7e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 DKONYLALV 9
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Db 3 DKENALSL 11

RESULT 24
US-08-431-184-76
Sequence 76, Application US/08431184
Patent No. 6120769
GENERAL INFORMATION:
APPLICANT: Bruce L. Rogers et al.
TITLE OF INVENTION: A HUMAN T CELL REACTIVE FELINE PROTEIN
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/431.184

; FILING DATE: 28-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/430,014
; FILING DATE: 27-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/300,928
; FILING DATE: 02-SEPT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IMI-044DV3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 76:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-431-184-76

Query Match 42.2%; Score 27; DB 2; Length 11;
Best Local Similarity 55.6%; Pred. No. 1.7e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DKONYLALV 9
Db 3 DKENALSL 11

RESULT 25
US-09-142-885C-9
; Sequence 9, Application US/09142885C
; Patent No. 6737406
; GENERAL INFORMATION:
; APPLICANT: Kay, Anthony
; APPLICANT: Larche, Mark
; TITLE OF INVENTION: Cryptic Peptides and Method for Their Identification
; FILE REFERENCE: 4028/75652
; CURRENT APPLICATION NUMBER: US/09/142,885C
; CURRENT FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: PCT/GB97/00783
; PRIOR FILING DATE: 1997-03-20
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 9
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Felis domesticus
US-09-142-885C-9

Query Match 42.2%; Score 27; DB 2; Length 16;
Best Local Similarity 55.6%; Pred. No. 2.6e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DKONYLALV 9
Db 6 DKENALSL 14

Search completed: January 26, 2006, 08:06:59
Job time : 13.3822 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 26, 2006, 08:04:12 : Search time 42.25 Seconds
(without alignments)
128.563 Million cell updates/sec

Title: US-09-662-293-7

Perfect score: 64
Sequence: 1 DKONYLALVRELK 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 369445

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

Published Applications AA Main:*

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- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	64	100.0	13	4 US-10-218-743-7	Sequence 7, Appli
2	30	46.9	20	3 US-09-971-309-7	Sequence 7, Appli
3	29	45.3	10	3 US-09-573-822C-39	Sequence 39, Appli
4	28	43.8	10	3 US-09-572-404B-2020	Sequence 2020, Ap
5	28	43.8	17	3 US-09-995-529-76	Sequence 76, Appli
6	28	43.8	17	3 US-09-995-529-76	Sequence 76, Appli
7	28	43.8	19	2 US-08-464-363-10	Sequence 10, Appli
8	28	43.8	19	4 US-10-463-113-10	Sequence 10, Appli
9	27	42.2	11	2 US-08-464-363-37	Sequence 27, Appli
10	27	42.2	11	4 US-10-463-113-27	Sequence 27, Appli
11	27	42.2	16	4 US-10-245-871-163	Sequence 163, App
12	27	42.2	16	4 US-10-253-286-163	Sequence 163, App
13	27	42.2	16	4 US-10-702-400-104	Sequence 104, App
14	27	42.2	16	5 US-10-809-689-8	Sequence 8, Appli
15	27	42.2	16	5 US-10-805-650-104	Sequence 104, App
16	26	40.6	10	3 US-09-994-595-46	Sequence 46, Appli
17	26	40.6	11	4 US-10-044-632-63	Sequence 63, Appli
18	26	40.6	11	4 US-10-044-632-63	Sequence 63, Appli
19	26	40.6	11	4 US-10-325-810-63	Sequence 63, Appli
20	26	40.6	11	5 US-10-877-124-63	Sequence 63, Appli
21	26	40.6	11	5 US-10-877-022-63	Sequence 63, Appli
22	26	40.6	11	5 US-10-877-146-63	Sequence 63, Appli
23	26	40.6	14	2 US-08-908-884-23	Sequence 23, Appli
24	26	40.6	14	3 US-09-908-323-23	Sequence 23, Appli
25	26	40.6	15	4 US-10-084-813-684	Sequence 684, App
26	26	40.6	15	4 US-10-084-813-685	Sequence 685, App
27	26	40.6	15	4 US-10-084-813-686	Sequence 686, App

28	26	40.6	15	4 US-10-239-313A-82	Sequence 82, Appli
29	26	40.6	15	4 US-10-461-093-6	Sequence 6, Appli
30	26	40.6	16	4 US-10-225-567A-1099	Sequence 1099, Ap
31	26	40.6	16	4 US-10-225-567A-2256	Sequence 2256, Ap
32	26	40.6	17	4 US-10-676-909-52	Sequence 52, Appli
33	26	40.6	17	4 US-10-676-909-52	Sequence 67, Appli
34	26	40.6	18	4 US-10-084-813-731	Sequence 731, App
35	26	40.6	18	4 US-10-084-813-732	Sequence 732, App
36	26	40.6	18	4 US-10-084-813-733	Sequence 733, App
37	26	40.6	18	4 US-10-615-383-9	Sequence 9, Appli
38	26	40.6	18	4 US-10-690-184-9	Sequence 9, Appli
39	26	40.6	18	4 US-10-689-082-9	Sequence 9, Appli
40	26	40.6	20	3 US-09-736-457-1851	Sequence 1851, Ap
41	26	40.6	20	3 US-09-902-941-1851	Sequence 1851, Ap
42	26	40.6	20	3 US-08-849-626-1851	Sequence 1851, Ap
43	26	40.6	20	4 US-10-017-754-1851	Sequence 1851, Ap
44	26	40.6	20	4 US-10-113-872-1851	Sequence 1851, Ap
45	26	40.6	20	4 US-10-283-017-1851	Sequence 1851, Ap
46	26	40.6	20	5 US-10-451-304-14	Sequence 14, Appli
47	26	40.6	20	6 US-11-021-928A-301	Sequence 301, App
48	26	40.6	21	4 US-10-084-813-299	Sequence 299, App
49	26	40.6	21	4 US-10-084-813-300	Sequence 300, App
50	26	40.6	21	4 US-10-084-813-597	Sequence 597, App
51	26	40.6	21	4 US-10-084-813-598	Sequence 598, App
52	26	40.6	21	4 US-10-084-813-599	Sequence 599, App
53	25	39.1	7	3 US-09-910-346C-13	Sequence 13, Appli
54	25	39.1	7	4 US-10-163-106B-7	Sequence 7, Appli
55	25	39.1	7	5 US-10-757-077-7	Sequence 7, Appli
56	25	39.1	11	5 US-10-783-311-176	Sequence 176, App
57	25	39.1	13	4 US-10-428-408A-12	Sequence 12, Appli
58	25	39.1	13	4 US-10-428-694-12	Sequence 12, Appli
59	25	39.1	13	4 US-10-699-874-12	Sequence 12, Appli
60	25	39.1	15	3 US-09-765-527-1	Sequence 1, Appli
61	25	39.1	15	4 US-10-446-828-4	Sequence 4, Appli
62	25	39.1	15	4 US-10-319-786-4	Sequence 4, Appli
63	25	39.1	16	3 US-09-459-749D-3	Sequence 3, Appli
64	25	39.1	16	4 US-10-270-871-3	Sequence 3, Appli
65	25	39.1	17	3 US-09-249-011A-16	Sequence 16, Appli
66	25	39.1	17	4 US-10-225-567A-2179	Sequence 2179, Ap
67	25	39.1	17	5 US-10-986-089A-16	Sequence 16, Appli
68	25	39.1	18	5 US-10-953-901-838	Sequence 838, App
69	25	39.1	20	5 US-10-690-276-583	Sequence 583, App
70	25	39.1	21	3 US-09-782-977-1	Sequence 1, Appli
71	25	39.1	21	3 US-09-974-879-555	Sequence 555, App
72	25	39.1	21	3 US-09-305-736-561	Sequence 561, App
73	25	39.1	21	3 US-09-818-683-561	Sequence 561, App
74	25	39.1	21	3 US-09-818-683-561	Sequence 561, App
75	25	39.1	21	3 US-10-621-401-555	Sequence 555, App
76	24	37.5	9	4 US-10-158-596A-33	Sequence 33, Appli
77	24	37.5	9	4 US-10-157-775B-33	Sequence 33, Appli
78	24	37.5	9	4 US-10-254-446A-33	Sequence 33, Appli
79	24	37.5	9	4 US-10-155-683B-33	Sequence 33, Appli
80	24	37.5	9	4 US-10-057-475B-10908	Sequence 10908, A
81	24	37.5	9	4 US-10-057-475B-10959	Sequence 10959, A
82	24	37.5	9	4 US-10-154-884B-10908	Sequence 10908, A
83	24	37.5	9	4 US-10-154-884B-10959	Sequence 10959, A
84	24	37.5	9	4 US-10-668-600-33	Sequence 33, Appli
85	24	37.5	10	4 US-10-158-596A-33	Sequence 33, Appli
86	24	37.5	10	4 US-10-117-337-546	Sequence 546, App
87	24	37.5	10	4 US-10-657-022-554	Sequence 554, App
88	24	37.5	10	5 US-10-734-049A-169	Sequence 169, App
89	24	37.5	10	6 US-11-067-064-546	Sequence 546, App
90	24	37.5	11	6 US-11-067-159-546	Sequence 546, App
91	24	37.5	11	5 US-10-783-311-152	Sequence 152, App
92	24	37.5	12	5 US-10-858-706-19	Sequence 19, Appli
93	24	37.5	13	4 US-10-302-447-111	Sequence 111, App
94	24	37.5	13	4 US-10-702-400-85	Sequence 85, Appli
95	24	37.5	13	5 US-10-805-650-85	Sequence 85, Appli
96	24	37.5	13	5 US-10-948-707-978	Sequence 978, App
97	24	37.5	14	3 US-09-840-577-7	Sequence 77, Appli
98	24	37.5	14	4 US-10-609-217-159	Sequence 159, App
99	24	37.5	14	4 US-10-632-188-159	Sequence 159, App
100	24	37.5	14	4 US-10-651-723-159	Sequence 159, App

ALIGNMENTS

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RESULT 1
US-10-218-743-7
; Sequence 7, Application US/10218743
; Publication No. US20030096779A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/10/218,743
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/292,225
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: 60/098,909
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/085,295
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/098,565
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: 09/062,013
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 7
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-10-218-743-7

Query Match      100.0%; Score 64; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DKONYLALVRELK 13
      |||||
DB      1 DKONYLALVRELK 13

RESULT 2
US-09-971-309-7
; Sequence 7, Application US/09971309
; Patent No. US2002010675A1
; GENERAL INFORMATION:
; APPLICANT: UEMORI, Takashi
; APPLICANT: SATO, Yoshimi
; APPLICANT: FUJITA, Tomoko
; APPLICANT: MIYAKE, Kazuo
; APPLICANT: MUKAI, Hiroyuki
; APPLICANT: ASADA, Kiyozo
; APPLICANT: KATO, Ikumoshin
; TITLE OF INVENTION: DNA POLYMERASE-RELATED FACTORS
; FILE REFERENCE: 1422-0494P
; CURRENT APPLICATION NUMBER: US/09/971,309
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 09/446,504
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: PCT/J998/02845
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: JP 9-187496
; PRIOR FILING DATE: 1997-06-26
; PRIOR APPLICATION NUMBER: JP 9-320692
; PRIOR FILING DATE: 1997-11-27
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 7
; LENGTH: 20
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; TYPE: PRT
; ORGANISM: Pyrococcus furiosus
US-09-971-309-7

Query Match      46.9%; Score 30; DB 3; Length 20;
Best Local Similarity 54.5%; Pred. No. 3.2e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 DKONYLALVRE 11
      ||:|
DB      2 DKSGFLNKVRE 12

RESULT 3
US-09-573-822C-39
; Sequence 39, Application US/09573822C
; Publication No. US20030199011A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands generated from microbial genome sequ
; FILE REFERENCE: Microbe patent
; CURRENT APPLICATION NUMBER: US/09/573,822C
; CURRENT FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 804
; SOFTWARE: ProPatent version 1.0
; SEQ ID NO 39
; LENGTH: 10
; TYPE: PRT
; ORGANISM: mycoplasma genitalium
; FEATURE:
; OTHER INFORMATION: Sequence located in MG017 at 15-24 and may interact with Sequence
US-09-573-822C-39

Query Match      45.3%; Score 29; DB 3; Length 10;
Best Local Similarity 55.6%; Pred. No. 2.3e+02;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      5 YLALVRELK 13
      |:|:|:|
DB      1 FLSLVKEYK 9

RESULT 4
US-09-572-404B-2020
; Sequence 2020, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProPatent version 1.0
; SEQ ID NO 2020
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in SFRS8 OR SWAP at 110-119 and may interact with
US-09-572-404B-2020

Query Match      43.8%; Score 28; DB 3; Length 10;
Best Local Similarity 62.5%; Pred. No. 3.4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 DKONYLAL 8
      |:|
DB      2 DEERYLAL 9
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RESULT 5
US-09-995-529-76
; Sequence 76, Application US/09995529
; Publication No. US2003009655A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Tang, Ying
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 76
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic antibody mutation
US-09-995-529-76
Query Match 43.8%; Score 28; DB 3; Length 17;
Best Local Similarity 71.4%; Pred. No. 6.1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKONYLA 7
: : : : :
Db 11 NKNKYLA 17

RESULT 6
US-09-995-529-76
; Sequence 76, Application US/09995529
; Publication No. US20040091482A9
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Tang, Ying
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 76
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic antibody mutation
US-09-995-529-76
Query Match 43.8%; Score 28; DB 3; Length 17;
Best Local Similarity 71.4%; Pred. No. 6.1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKONYLA 7
: : : : :
Db 11 NKNKYLA 17

RESULT 7
US-08-464-363-10
; Sequence 10, Application US/08464363
; Publication No. US20030035815A1
; GENERAL INFORMATION:
; APPLICANT: Rogers, Bruce L.
; APPLICANT: Morgenshtern, Jay
; APPLICANT: Bond, Julian F.
; APPLICANT: Garman, Richard D.

```

```

; APPLICANT: Greenstein, Julia L.
; APPLICANT: Kuo, Mei-chang
; APPLICANT: Morville, Malcolm
; TITLE OF INVENTION: RECOMBINOPE PEPTIDES
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lahive & Cockfield
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII TEXT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,363
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/807,529
; FILING DATE: 13-DEC-1991
; APPLICATION NUMBER: US 07/662,276
; FILING DATE: 28-FEB-1991
; APPLICATION NUMBER: US 07/431,565
; FILING DATE: 03-NOV-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IMI-015CN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-464-363-10
Query Match 43.8%; Score 28; DB 2; Length 19;
Best Local Similarity 41.7%; Pred. No. 6.9e+02;
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 DKONYLALVREL 12
: : : : :
Db 3 DKENALSLLDKI 14

RESULT 8
US-10-463-113-10
; Sequence 10, Application US/10463113
; Publication No. US20040057959A1
; GENERAL INFORMATION:
; APPLICANT: Rogers, Bruce L.
; APPLICANT: Morgenshtern, Jay
; APPLICANT: Bond, Julian F.
; APPLICANT: Garman, Richard D.
; APPLICANT: Greenstein, Julia L.
; APPLICANT: Kuo, Mei-chang
; APPLICANT: Morville, Malcolm
; TITLE OF INVENTION: RECOMBINOPE PEPTIDES
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lahive & Cockfield, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:

```

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/463,113
FILING DATE: 16-Jun-2003
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/807,529
FILING DATE: 13-DEC-1991
APPLICATION NUMBER: US 07/662,276
FILING DATE: 28-FEB-1991
APPLICATION NUMBER: US 07/431,565
FILING DATE: 03-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-015CN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-463-113-10

Query Match 43.8%; Score 28; DB 4; Length 19;
Best Local Similarity 41.7%; Pred. No. 6.9e+02;
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DKONYLALVREL 12
||:|:|:|:
Db 3 DKENALSLDKT 14

RESULT 9
US-08-464-363-27
Sequence 27, Application US/08464363
Publication No. US20030035815A1
GENERAL INFORMATION:
APPLICANT: Rogers, Bruce L.
APPLICANT: Morgensstern, Jay
APPLICANT: Bond, Julian F.
APPLICANT: Garman, Richard D.
APPLICANT: Greenstein, Julia L.
APPLICANT: Kuo, Mei-chang
APPLICANT: Morville, Malcolm
TITLE OF INVENTION: RECOMBITOPE PEPTIDES
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lahive & Cockfield
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,363
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/807,529
FILING DATE: 13-DEC-1991
APPLICATION NUMBER: US 07/662,276

FILING DATE: 28-FEB-1991
APPLICATION NUMBER: US 07/431,565
FILING DATE: 03-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-015CN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-363-27

Query Match 42.2%; Score 27; DB 2; Length 11;
Best Local Similarity 55.6%; Pred. No. 5.7e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DKONYLALV 9
||:|:|:|:
Db 3 DKENALSL 11

RESULT 10
US-10-463-113-27

Sequence 27, Application US/10463113
Publication No. US20040057959A1

GENERAL INFORMATION:

APPLICANT: Rogers, Bruce L.

APPLICANT: Morgensstern, Jay

APPLICANT: Bond, Julian F.

APPLICANT: Garman, Richard D.

APPLICANT: Greenstein, Julia L.

APPLICANT: Kuo, Mei-chang

APPLICANT: Morville, Malcolm

TITLE OF INVENTION: RECOMBITOPE PEPTIDES

NUMBER OF SEQUENCES: 76

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lahive & Cockfield, LLP

STREET: 28 State Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII TEXT

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/463,113

FILING DATE: 16-Jun-2003

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/807,529

FILING DATE: 13-DEC-1991

APPLICATION NUMBER: US 07/662,276

FILING DATE: 28-FEB-1991

APPLICATION NUMBER: US 07/431,565

FILING DATE: 03-NOV-1989

ATTORNEY/AGENT INFORMATION:

NAME: Amy E. Mandragouras

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: IMI-015CN

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400

TELEFAX: (617) 742-4214

INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:

LENGTH: 11 amino acids

TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-10-463-113-27

Query Match 42.2%; Score 27; DB 4; Length 11;
Best Local Similarity 55.6%; Pred. No. 5.7e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DKONYALV 9
Db 3 DKENALSL 11

RESULT 11
US-10-245-871-163

; Sequence 163, Application US/10245871
; Publication No. US20030235594A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: 11-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2013
; CURRENT APPLICATION NUMBER: US/10/245,871
; CURRENT FILING DATE: 2003-01-09
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 905
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 163
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Felis domesticus
US-10-245-871-163

Query Match 42.2%; Score 27; DB 4; Length 16;
Best Local Similarity 55.6%; Pred. No. 8.6e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DKONYALV 9
Db 6 DKENALSL 14

RESULT 12
US-10-253-286-163

; Sequence 163, Application US/10253286
; Publication No. US20040058881A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: 11-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2015
; CURRENT APPLICATION NUMBER: US/10/253,286
; CURRENT FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 905
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 163
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Felis domesticus
US-10-253-286-163

Query Match 42.2%; Score 27; DB 4; Length 16;
Best Local Similarity 55.6%; Pred. No. 8.6e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DKONYALV 9
Db 6 DKENALSL 14

RESULT 13
US-10-702-400-104

; Sequence 104, Application US/10702400
; Publication No. US20040197800A1
; GENERAL INFORMATION:
; APPLICANT: Borns, Michael
; TITLE OF INVENTION: DNA Polymerase Blends and Uses Thereof
; FILE REFERENCE: 25436/2364
; CURRENT APPLICATION NUMBER: US/10/702,400
; CURRENT FILING DATE: 2003-11-05
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 104
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Methanopyrus kandleri
US-10-702-400-104

Query Match 42.2%; Score 27; DB 4; Length 16;
Best Local Similarity 62.5%; Pred. No. 8.6e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 6 LALVRELK 13
Db 6 LSLVKEIK 13

RESULT 14
US-10-809-689-8

; Sequence 8, Application US/10809689
; Publication No. US20040265342A1
; GENERAL INFORMATION:
; APPLICANT: Eric Potter Clarkson
; TITLE OF INVENTION: Methods and compositions for desensitisation
; FILE REFERENCE: 5538/1010
; CURRENT APPLICATION NUMBER: US/10/809,689
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: PCT/GB99/00080
; PRIOR FILING DATE: 1999-01-11
; PRIOR APPLICATION NUMBER: GB/9800445.0
; PRIOR FILING DATE: 1998-01-09
; PRIOR APPLICATION NUMBER: GB/9820474.6
; PRIOR FILING DATE: 1998-09-21
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Felis catus
US-10-809-689-8

Query Match 42.2%; Score 27; DB 5; Length 16;
Best Local Similarity 55.6%; Pred. No. 8.6e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DKONYALV 9
Db 6 DKENALSL 14

RESULT 15
US-10-805-650-104

; Sequence 104, Application US/10805650
; Publication No. US20050048530A1
; GENERAL INFORMATION:
; APPLICANT: Borns, Michael
; TITLE OF INVENTION: DNA Polymerase Fusions and Uses Thereof
; FILE REFERENCE: 25436/2382

CURRENT APPLICATION NUMBER: US/10/805,650
CURRENT FILING DATE: 2004-03-19
PRIOR APPLICATION NUMBER: US 60/457,426
PRIOR FILING DATE: 2003-03-25
NUMBER OF SEQ ID NOS: 148
SOFTWARE: PatentIn version 3.1
SEQ ID NO 104
LENGTH: 16
TYPE: PRT
ORGANISM: Methanopyrus kandleri
US-10-805-650-104

Query Match 42.2%; Score 27; DB 5; Length 16;
Best Local Similarity 62.5%; Pred. No. 8.6e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 6 LALVRELK 13
DB 6 LSLVLEIK 13

RESULT 16
US-09-994-595-46
Sequence 46, Application US/09994595
Publication No. US20030039981A1
GENERAL INFORMATION:
APPLICANT: Bhattacharjee, J
APPLICANT: Suvarna, Kalavati
APPLICANT: Bhattacharjee, Vasker
TITLE OF INVENTION: METHODS AND REAGENTS FOR DETECTING FUNGAL PATHOGENS IN
FILE REFERENCE: 96,247-A
CURRENT APPLICATION NUMBER: US/09/994,595
CURRENT FILING DATE: 2001-11-27
PRIOR APPLICATION NUMBER: 08/650,809
PRIOR FILING DATE: 1997-05-20
NUMBER OF SEQ ID NOS: 160
SOFTWARE: Microsoft Word 97
SEQ ID NO 46
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Polypeptide segment of ACVS_EMENT shown in Figure 4.
US-09-994-595-46

Query Match 40.6%; Score 26; DB 3; Length 10;
Best Local Similarity 66.7%; Pred. No. 7.7e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 YLALVRELK 13
DB 2 YLALRRHFK 10

RESULT 17
US-10-044-692-63
Sequence 63, Application US/10044692
Publication No. US20030096344A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
THERAPEUTIC METHODS
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/044,692
FILING DATE: 11-Jan-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/912,951
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-00260005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..11
OTHER INFORMATION: /note= "motif E peptide from
Drosophila melanogaster TART non-LTR
retrotransposible element reverse
transcriptase"

US-10-044-692-63
SEQUENCE DESCRIPTION: SEQ ID NO: 63:

Query Match 40.6%; Score 26; DB 4; Length 11;
Best Local Similarity 50.0%; Pred. No. 8.6e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 KQNTYALV 9
DB 3 KQSYLGVI 10

RESULT 18
US-10-044-539-63
Sequence 63, Application US/10044539
Publication No. US20030100093A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
THERAPEUTIC METHODS

```

NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/044,539
FILING DATE: 11-Jan-2002
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/912,951
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..11
OTHER INFORMATION: /note="motif E peptide from
Drosophila melanogaster TART non-LTR
retrotransposable element reverse
transcriptase"
SEQUENCE DESCRIPTION: SEQ ID NO: 63:
US-10-044-539-63
Query Match 40.6%; Score 26; DB 4; Length 11;
Best Local Similarity 50.0%; Pred. No. 8.6e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 2 KONYLALV 9
Db 3 KOSYLGVI 10
RESULT 19
US-10-325-810-63
; Sequence 63, Application US/10325810
; Publication No. US20030204069A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.

```

```

Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/325,810
FILING DATE: 20-Dec-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/402,181
FILING DATE: 29-Sep-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ausubius, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..11
OTHER INFORMATION: /note="motif E peptide from
Drosophila melanogaster TART non-LTR
retrotransposable element reverse
transcriptase"
SEQUENCE DESCRIPTION: SEQ ID NO: 63:
US-10-325-810-63
Query Match 40.6%; Score 26; DB 4; Length 11;
Best Local Similarity 50.0%; Pred. No. 8.6e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 2 KONYLALV 9
Db 3 KOSYLGVI 10

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RESULT 20
US-10-877-124-63
Sequence 63, Application US/10877124
Publication No. US20040242529A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/877,124
FILING DATE: 24-Jun-2004
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/432,503
FILING DATE: 02-Nov-1999
APPLICATION NUMBER: 08/974,549
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-Apr-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-Apr-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-May-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-May-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-Oct-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-Oct-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..11
OTHER INFORMATION: /notes= "motif E peptide from
Drosophila melanogaster TART non-LTR

retrotransposable element reverse
transcriptase"
SEQUENCE DESCRIPTION: SEQ ID NO: 63:
US-10-877-124-63
Query Match 40.6%; Score 26; DB 5; Length 11;
Best Local Similarity 50.0%; Pred. No. 8.6e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 2 KONTALV 9
DB 3 KQSYLGI 10
RESULT 21
US-10-877-022-63
Sequence 63, Application US/10877022
Publication No. US20040247613A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/877,022
FILING DATE: 24-Jun-2004
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/432,503
FILING DATE: 02-Nov-1999
APPLICATION NUMBER: 08/974,549
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-Apr-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-Apr-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-May-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-May-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-Oct-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-Oct-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200

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? TELEFAX: (415) 576-0300
? INFORMATION FOR SEQ ID NO: 63:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 11 amino acids
? TYPE: amino acid
? STRANDEDNESS: <Unknown>
? TOPOLOGY: linear
? MOLECULE TYPE: peptide
? FEATURE:
? NAME/KEY: Peptide
? LOCATION: 1..11
? OTHER INFORMATION: /note="motif E peptide from
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? retrotransposable element reverse
? transcriptase"
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? SEQUENCE DESCRIPTION: SEQ ID NO: 63:
? US-10-877-022-63
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? Best Local Similarity 50.0%; Pred. No. 8,6e+02;
? Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0
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? QY 2 KONYLALV 9
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? Db 3 KOSYLGVI 10
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? RESULT 22
? US-10-877-146-63
? Sequence 63, Application US/10877146
? Publication No. US20050013825A1
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? GENERAL INFORMATION:
? APPLICANT: Cecch, Thomas R.
? Lingner, Joachim
? Nakamura, Toru
? Chapman, Karen B.
? Morin, Gregg B.
? Harley, Calvin B.
? Andrews, William H.
?
? TITLE OF INVENTION: Human Telomerase Catalytic Subunit
? NUMBER OF SEQUENCES: 727
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Townsend and Townsend and Crew LLP
? STREET: Two Embarcadero Center, Eighth Floor
? CITY: San Francisco
? STATE: California
? COUNTRY: USA
? ZIP: 94111-3834
?
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.30
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? CURRENT APPLICATION DATA:
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? FILING DATE: 24-Jun-2004
? CLASSIFICATION: <Unknown>
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? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US/09/432,503
? FILING DATE: 02-Nov-1999
? APPLICATION NUMBER: 08/974,549
? FILING DATE: <Unknown>
? APPLICATION NUMBER: US 08/844,419
? FILING DATE: 18-APR-1997
? APPLICATION NUMBER: US 08/846,017
? FILING DATE: 25-APR-1997
? APPLICATION NUMBER: US 08/851,843
? FILING DATE: 06-MAY-1997
? APPLICATION NUMBER: US 08/854,050
? FILING DATE: 09-MAY-1997
? APPLICATION NUMBER: US 08/911,312
? FILING DATE: 14-AUG-1997
? APPLICATION NUMBER: US 08/912,951
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1      FILING DATE: 14-AUG-1997
2      APPLICATION NUMBER: US 08/915,503
3      FILING DATE: 14-AUG-1997
4      APPLICATION NUMBER: WO PCT/US97/17618
5      FILING DATE: 01-OCT-1997
6      APPLICATION NUMBER: WO PCT/US97/17885
7      FILING DATE: 01-OCT-1997
8      ATTORNEY/AGENT INFORMATION:
9      NAME: Apple, Randolph Ted
10     REGISTRATION NUMBER: 36,429
11     REFERENCE/DOCKET NUMBER: 015389-002610US
12     TELECOMMUNICATION INFORMATION:
13     TELEPHONE: (415) 576-0200
14     TELEFAX: (415) 576-0300
15     INFORMATION FOR SEQ ID NO: 63:
16     SEQUENCE CHARACTERISTICS:
17     LENGTH: 11 amino acids
18     TYPE: amino acid
19     STRANDEDNESS: <Unknown>
20     TOPOLOGY: linear
21     MOLECULE TYPE: peptide
22     FEATURE:
23     NAME/KEY: Peptide
24     LOCATION: 1..11
25     OTHER INFORMATION: /note="motif E peptide from
26     Drosophila melanogaster TART non-LTR
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32     Query Match      40.6%; Score 26; DB 5; Length 11;
33     Best Local Similarity 50.0%; Pred.No. 8.6e+02;
34     Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0.
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36     QY      2 KONTIAY 9      |||::
37     Db      3 KSYIYGI 10
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39     RESULT 23
40     US-08-908-884-23
41     Sequence 23, Application US/08908884
42     Publication No. US20020138872A1
43     GENERAL INFORMATION:
44     APPLICANT: Dong et al.
45     TITLE OF INVENTION: ACQUIRED RESISTANCE GENES AND USES THEREOF
46     NUMBER OF SEQUENCES: 28
47     CORRESPONDENCE ADDRESSES:
48     ADDRESSEE: Clark & Biling LLP
49     STREET: 176 Federal Street
50     CITY: Boston
51     STATE: MA
52     COUNTRY: USA
53     ZIP: 02110
54     COMPUTER READABLE FORM:
55     MEDIUM TYPE: Diskette
56     COMPUTER: IBM Compatible
57     OPERATING SYSTEM: DOS
58     SOFTWARE: FAR2SE0 for Windows Version 2.0
59     CURRENT APPLICATION DATA:
60     APPLICATION NUMBER: US/08/908,884
61     FILING DATE:
62     CLASSIFICATION: 800
63     PRIOR APPLICATION DATA:
64     APPLICATION NUMBER: 60/023,851
65     FILING DATE: August 9, 1996
66     APPLICATION NUMBER: 60/035,166
67     FILING DATE: January 10, 1997
68     APPLICATION NUMBER: 60/046,769
69     FILING DATE: May 16, 1997
70     ATTORNEY/AGENT INFORMATION:
71     NAME: Elbing, Karen L

```

REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00786/339004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEFAX: 617-428-7045
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-908-884-23

Query Match 40.6%; Score 26; DB 2; Length 14;
Best Local Similarity 41.7%; Pred. No. 1.1e+03;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 KONYLALVRELK 13
Db 2 KORYMEIOETLK 13

RESULT 24
US-09-908-323-23
Sequence 23, Application US/09908323
Patent No. US20020073447A1

GENERAL INFORMATION:
APPLICANT: Dong et al.
TITLE OF INVENTION: ACQUIRED RESISTANCE GENES AND USES THEREOF
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:

ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
CITY: Boston
STATE: MA
COUNTRY: USA

ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/908,323
FILING DATE: 17-Jul-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/908,884
FILING DATE: <Unknown>
APPLICATION NUMBER: 60/035,166
FILING DATE: January 10, 1997
APPLICATION NUMBER: 60/046,769
FILING DATE: May 16, 1997

ATTORNEY/AGENT INFORMATION:
NAME: Elbing, Karen L.
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00786/339004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEFAX: 617-428-7045

INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-908-323-23

Query Match 40.6%; Score 26; DB 3; Length 14;
Best Local Similarity 41.7%; Pred. No. 1.1e+03;

Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
Qy 2 KONYLALVRELK 13
Db 2 KORYMEIOETLK 13

RESULT 25
US-10-084-813-684
Sequence 684, Application US/10084813
Publication No. US20030066615A1
GENERAL INFORMATION:
APPLICANT: SAXINGER, CARL
TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
FILE REFERENCE: 215875
CURRENT APPLICATION NUMBER: US/10/084,813
PRIOR FILING DATE: 2002-02-27
PRIOR APPLICATION NUMBER: PCT/US00/23505
PRIOR FILING DATE: 2000-08-25
PRIOR APPLICATION NUMBER: US 60/151,270
PRIOR FILING DATE: 1999-08-27
NUMBER OF SEQ ID NOS: 1242
SOFTWARE: PatentIn version 3.1
SEQ ID NO 684
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-684

Query Match 40.6%; Score 26; DB 4; Length 15;
Best Local Similarity 30.8%; Pred. No. 1.2e+03;
Matches 4; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
Qy 1 DKONYLALVRELK 13
Db 3 DQGNFPLIKNLK 15

Search completed: January 26, 2006, 08:38:34
Job time : 44.25 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 26, 2006, 08:05:12 : Search time 2.46552 Seconds
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Title: US-09-662-293-7

Perfect score: 64

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Scoring table:

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Searched: 75621 seqs, 10829074 residues

Total number of hits satisfying chosen parameters: 37628

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries,

Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	42.2	16	7	US-11-033-039-163	Sequence 163, App
2	40.6	19	7	US-11-166-412-150	Sequence 150, App
3	39.1	7	6	US-10-753-537-13	Sequence 13, App1
4	39.1	7	7	US-11-039-268-13	Sequence 13, App1
5	37.5	17	6	US-10-981-356A-18	Sequence 18, App1
6	37.5	17	6	US-10-981-356A-24	Sequence 24, App1
7	37.5	17	7	US-11-096-046-18	Sequence 18, App1
8	37.5	17	7	US-11-096-046-24	Sequence 24, App1
9	37.5	17	7	US-11-105-708-23	Sequence 23, App1
10	37.5	17	7	US-11-136-559-27	Sequence 27, App1
11	35.9	12	7	US-11-021-305-31	Sequence 31, App1
12	35.9	20	7	US-11-041-693-201	Sequence 201, App1
13	34.4	7	6	US-10-494-781-6	Sequence 6, App1
14	34.4	9	7	US-11-045-024-3529	Sequence 3529, App
15	34.4	9	7	US-11-045-024-3575	Sequence 3575, App
16	34.4	9	7	US-11-045-024-3576	Sequence 3576, App
17	34.4	9	7	US-11-045-024-10581	Sequence 10581, A
18	34.4	9	7	US-11-045-024-10652	Sequence 10652, A
19	34.4	9	7	US-11-045-024-10720	Sequence 10720, A
20	34.4	9	7	US-11-045-024-12381	Sequence 12381, A
21	34.4	9	7	US-11-045-024-12445	Sequence 12445, A
22	34.4	9	7	US-11-045-024-12456	Sequence 12456, A
23	34.4	9	7	US-11-045-024-13980	Sequence 13980, A
24	34.4	10	7	US-11-045-024-3581	Sequence 3581, App
25	34.4	10	7	US-11-045-024-3582	Sequence 3582, App

26	34.4	10	7	US-11-045-024-10647	Sequence 10647, A
27	34.4	10	7	US-11-045-024-10716	Sequence 10716, A
28	34.4	10	7	US-11-045-024-12440	Sequence 12440, A
29	34.4	10	7	US-11-045-024-12452	Sequence 12452, A
30	34.4	11	7	US-11-045-024-3558	Sequence 3558, App
31	34.4	11	7	US-11-045-024-10541	Sequence 10541, A
32	34.4	11	7	US-11-045-024-12349	Sequence 12349, A
33	34.4	11	7	US-11-104-117-7	Sequence 7, App1
34	34.4	12	6	US-10-501-111A-100	Sequence 100, App
35	34.4	12	6	US-10-501-111A-137	Sequence 137, App
36	34.4	12	6	US-11-021-305-29	Sequence 29, App1
37	34.4	14	6	US-10-494-781-27	Sequence 27, App1
38	34.4	15	6	US-10-494-781-28	Sequence 28, App1
39	34.4	15	6	US-10-984-376-18	Sequence 18, App1
40	34.4	15	7	US-11-045-024-13314	Sequence 13314, A
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44	34.4	15	7	US-11-045-024-13351	Sequence 13351, A
45	34.4	15	7	US-11-045-024-13359	Sequence 13359, A
46	34.4	15	7	US-11-045-024-13515	Sequence 13515, A
47	34.4	15	7	US-11-045-024-13516	Sequence 13516, A
48	34.4	15	7	US-11-045-024-14259	Sequence 14259, A
49	34.4	15	7	US-11-045-024-14521	Sequence 14521, A
50	34.4	19	6	US-10-503-575-296	Sequence 296, App
51	34.4	20	7	US-11-127-877-574	Sequence 574, App
52	34.4	20	7	US-11-166-412-90	Sequence 90, App1
53	34.4	21	7	US-11-041-693-205	Sequence 205, App
54	33.6	18	7	US-11-010-748A-673	Sequence 673, App
55	32.8	7	6	US-10-485-788A-253	Sequence 253, App
56	32.8	7	6	US-10-485-788A-254	Sequence 254, App
57	32.8	8	6	US-10-485-788A-255	Sequence 255, App
58	32.8	8	7	US-11-045-024-1239	Sequence 4239, App
59	32.8	8	7	US-11-045-024-4240	Sequence 4240, App
60	32.8	8	7	US-11-045-024-9440	Sequence 9440, App
61	32.8	8	7	US-11-045-024-9481	Sequence 9481, App
62	32.8	8	7	US-11-045-024-11503	Sequence 11503, A
63	32.8	8	7	US-11-045-024-11535	Sequence 11535, A
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65	32.8	9	7	US-11-045-024-4266	Sequence 4266, App
66	32.8	9	7	US-11-045-024-9443	Sequence 9443, App
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72	32.8	10	7	US-11-045-024-11508	Sequence 11508, A
73	32.8	10	7	US-11-045-024-11536	Sequence 11536, A
74	32.8	11	7	US-11-045-024-4301	Sequence 4301, App
75	32.8	11	7	US-11-045-024-7450	Sequence 7450, App
76	32.8	11	7	US-11-045-024-7469	Sequence 7469, App
77	32.8	11	7	US-11-045-024-12664	Sequence 12664, A
78	32.8	12	6	US-10-973-977-4	Sequence 4, App1
79	32.8	12	6	US-10-501-111A-49	Sequence 49, App1
80	32.8	12	6	US-10-501-111A-64	Sequence 64, App1
81	32.8	12	6	US-10-501-111A-133	Sequence 133, App
82	32.8	12	6	US-10-501-111A-143	Sequence 143, App
83	32.8	12	6	US-10-501-111A-144	Sequence 144, App
84	32.8	12	7	US-11-021-305-36	Sequence 36, App1
85	32.8	13	6	US-10-511-559-1147	Sequence 1147, App
86	32.8	13	6	US-11-045-024-14262	Sequence 14262, A
87	32.8	13	7	US-11-045-024-14511	Sequence 14511, A
88	32.8	13	7	US-11-045-024-14513	Sequence 14513, A
89	32.8	14	6	US-11-045-024-14513	Sequence 27, App1
90	32.8	15	7	US-11-054-197-27	Sequence 27, App1
91	32.8	15	7	US-11-054-197-27	Sequence 27, App1
92	32.8	15	7	US-11-045-024-13097	Sequence 13097, A
93	32.8	15	7	US-11-045-024-13404	Sequence 13404, A
94	32.8	15	7	US-11-045-024-13407	Sequence 13407, A
95	32.8	17	6	US-10-834-197-201	Sequence 201, App
96	32.8	17	6	US-10-834-197-229	Sequence 229, App
97	32.8	17	6	US-10-973-977-74	Sequence 74, App1
98	32.8	18	6	US-10-467-657-3550	Sequence 3550, App
99	32.8	18	6	US-10-467-657-3550	Sequence 3550, App
100	32.8	18	6	US-11-033-039-1237	Sequence 1237, App

99 21 32.8 18 7 US-11-220-439-4 Sequence 4, Appli
100 21 32.8 18 7 US-11-220-439-22 Sequence 22, Appli

ALIGNMENTS

RESULT 1

US-11-033-039-163
; Sequence 163, Application US/11033039
; Publication No. US20060002947A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: LT-KEY/ANTIGENIC EPIOTOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REF-20170501
; CURRENT APPLICATION NUMBER: US/11/033,039
; CURRENT FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 10/245,871
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 1452
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 163
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Felis catus
US-11-033-039-163

Query Match 42.2%; Score 27; DB 7; Length 16;
Best Local Similarity 55.6%; Pred. No. 19;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 DKONYLALV 9
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DB 6 DKENALSL 14

RESULT 2

US-11-166-412-150
; Sequence 150, Application US/11166412
; Publication No. US20060014231A1
; GENERAL INFORMATION:
; APPLICANT: Van Kompaey, Luc
; APPLICANT: Tomme, Peter H. M.
; TITLE OF INVENTION: Methods and Compositions To Promote Bone Homeostasis
; FILE REFERENCE: P27,927-D USA
; CURRENT APPLICATION NUMBER: US/11/166,412
; CURRENT FILING DATE: 2005-06-24
; PRIOR APPLICATION NUMBER: 60/582,704
; PRIOR FILING DATE: 2004-06-24
; PRIOR APPLICATION NUMBER: 60/630,449
; PRIOR FILING DATE: 2004-11-23
; PRIOR APPLICATION NUMBER: 60/673,206
; PRIOR FILING DATE: 2005-04-20
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 150
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Protein domain fragment
US-11-166-412-150

Query Match 40.6%; Score 26; DB 7; Length 19;
Best Local Similarity 66.7%; Pred. No. 35;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 YLALVRELLK 13

DB 3 YLAVVYPLK 11
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RESULT 3

US-10-753-537-13
; Sequence 13, Application US/10753537
; Publication No. US20050260230A1
; GENERAL INFORMATION:
; APPLICANT: STEWARD, LANCE E
; APPLICANT: FERNANDEZ-SALAS, ESTER
; APPLICANT: HERRINGTON, TODD M
; APPLICANT: AOKI, KEI R
; TITLE OF INVENTION: Leucine-based motif and clostridial neurotoxins
; FILE REFERENCE: D-2885CIP
; CURRENT APPLICATION NUMBER: US/10/753,537
; CURRENT FILING DATE: 2004-01-08
; PRIOR APPLICATION NUMBER: US/09/910,346C
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 09/620,840
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 7
; TYPE: PRT
; ORGANISM: frog
US-10-753-537-13

Query Match 39.1%; Score 25; DB 6; Length 7;
Best Local Similarity 83.3%; Pred. No. 5.8e+04;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DKONYL 6
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DB 2 DKONLL 7

RESULT 4

US-11-039-268-13
; Sequence 13, Application US/11039268
; Publication No. US20050276820A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance
; APPLICANT: HERRINGTON, Todd
; APPLICANT: Aoki, Kei
; TITLE OF INVENTION: LEUCINE-BASED MOTIF AND CLOSTRIDIAL NEUROTOXINS
; FILE REFERENCE: ALLE0014-106 (17355DIV1)
; CURRENT APPLICATION NUMBER: US/11/039,268
; CURRENT FILING DATE: 2005-01-19
; PRIOR APPLICATION NUMBER: 09/620,840
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: DIV of 09/620,840
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fragment having properties substantially similar to that of
US-11-039-268-13

Query Match 39.1%; Score 25; DB 7; Length 7;
Best Local Similarity 83.3%; Pred. No. 5.8e+04;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DKONYL 6
|||:|:|
DB 2 DKONLL 7

RESULT 5
US-10-981-356A-18
; Sequence 18, Application US/10981356A
; Publication No. US20060015952A1
; GENERAL INFORMATION:
; APPLICANT: FILVAROFF, ELLEN H.
; TITLE OF INVENTION: SCREENING ASSAYS AND METHODS OF TUMOR TREATMENT
; FILE REFERENCE: P2068R1
; CURRENT APPLICATION NUMBER: US/10/981,356A
; PRIOR FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: US 60/520,398
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/557,951
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 45
; SEQ ID NO 18
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-10-981-356A-18

Query Match 37.5%; Score 24; DB 6; Length 17;
Best Local Similarity 57.1%; Pred. No. 73;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKONYLA 7
:::|||||
Db 11 NOKNYLA 17

RESULT 6
US-10-981-356A-24
; Sequence 24, Application US/10981356A
; Publication No. US20060015952A1
; GENERAL INFORMATION:
; APPLICANT: FILVAROFF, ELLEN H.
; TITLE OF INVENTION: SCREENING ASSAYS AND METHODS OF TUMOR TREATMENT
; FILE REFERENCE: P2068R1
; CURRENT APPLICATION NUMBER: US/10/981,356A
; PRIOR FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: US 60/520,398
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/557,951
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 45
; SEQ ID NO 24
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-981-356A-24

Query Match 37.5%; Score 24; DB 6; Length 17;
Best Local Similarity 57.1%; Pred. No. 73;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKONYLA 7
:::|||||
Db 11 NOKNYLA 17

RESULT 7
US-11-096-046-18
; Sequence 18, Application US/11096046
; Publication No. US20050276802A1
; GENERAL INFORMATION:
; APPLICANT: ADAMS, CAMELIA W.
; APPLICANT: FERRARA, NAPOLEONE
; APPLICANT: FILVAROFF, ELLEN H.
; APPLICANT: MAO, WEIGUANG
; APPLICANT: PRESTA, LEONARD G.

APPLICANT: TEJADA, MAX L.
; TITLE OF INVENTION: Humanized Anti-TGF-Beta Antibodies
; FILE REFERENCE: P1954R1US
; CURRENT APPLICATION NUMBER: US/11/096,046
; PRIOR FILING DATE: 2005-03-31
; PRIOR APPLICATION NUMBER: US 60/558,290
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 18
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-096-046-18

Query Match 37.5%; Score 24; DB 7; Length 17;
Best Local Similarity 57.1%; Pred. No. 73;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKONYLA 7
:::|||||
Db 11 NOKNYLA 17

RESULT 8
US-11-096-046-24
; Sequence 24, Application US/11096046
; Publication No. US20050276802A1
; GENERAL INFORMATION:
; APPLICANT: ADAMS, CAMELIA W.
; APPLICANT: FERRARA, NAPOLEONE
; APPLICANT: FILVAROFF, ELLEN H.
; APPLICANT: MAO, WEIGUANG
; APPLICANT: PRESTA, LEONARD G.
; TITLE OF INVENTION: Humanized Anti-TGF-Beta Antibodies
; FILE REFERENCE: P1954R1US
; CURRENT APPLICATION NUMBER: US/11/096,046
; PRIOR FILING DATE: 2005-03-31
; PRIOR APPLICATION NUMBER: US 60/558,290
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 24
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-096-046-24

Query Match 37.5%; Score 24; DB 7; Length 17;
Best Local Similarity 57.1%; Pred. No. 73;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKONYLA 7
:::|||||
Db 11 NOKNYLA 17

RESULT 9
US-11-105-708-23
; Sequence 23, Application US/11105708
; Publication No. US20050281821A1
; GENERAL INFORMATION:
; APPLICANT: Pernasetti, Flavia
; APPLICANT: Freimark, Bruce
; APPLICANT: Van Bopp, Dennis
; APPLICANT: Brooks, Peter C
; TITLE OF INVENTION: Method and Composition for Angiogenesis Inhibition
; FILE REFERENCE: 30797-704.501
; CURRENT APPLICATION NUMBER: US/11/105,708
; PRIOR FILING DATE: 2005-04-13
; PRIOR APPLICATION NUMBER: 09/478,977
; PRIOR FILING DATE: 2000-01-06

; PRIOR APPLICATION NUMBER: 60/152,496
; PRIOR FILING DATE: 1999-09-02
; PRIOR APPLICATION NUMBER: 60/143,534
; PRIOR FILING DATE: 1999-09-02
; PRIOR APPLICATION NUMBER: 60/114,878
; PRIOR FILING DATE: 1999-01-06
; PRIOR APPLICATION NUMBER: 60/114,877
; PRIOR FILING DATE: 1999-01-06
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-105-708-23

Query Match 37.5% Score 24; DB 7; Length 17;
Best Local Similarity 57.1% Pred. No. 73;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DKONYLA 7
Db 11 NOKNYLA 17

RESULT 10
US-11-136-559-27
; Sequence 27, Application US/11136559
; Publication No. US20050287164A1
; GENERAL INFORMATION:
; APPLICANT: PATTI, Joseph M
; APPLICANT: HUTCHINS, Jeff T
; APPLICANT: DOMANSKI, Paul
; APPLICANT: PATEL, Pratiksha
; APPLICANT: HALL, Andrea
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLPA PROTEIN . . .
; FILE REFERENCE: P07069US04/BAS
; CURRENT APPLICATION NUMBER: US/11/136,559
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US/10/056,052
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: 60/308,116
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/298,413
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/274,611
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/264,072
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-11-136-559-27

Query Match 37.5% Score 24; DB 7; Length 17;
Best Local Similarity 57.1% Pred. No. 73;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DKONYLA 7
Db 11 NOKNYLA 17

RESULT 11
US-11-021-305-31
; Sequence 31, Application US/11021305
; Publication No. US20050282733A1
; GENERAL INFORMATION:

; APPLICANT: Prins, Johannes B
; APPLICANT: Hutley, Louise J
; TITLE OF INVENTION: Differentiation-modulating agents and uses therefor
; FILE REFERENCE: DAV1169.001CPI
; CURRENT APPLICATION NUMBER: US/11/021,305
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: USSN 60/392,130
; PRIOR FILING DATE: 2002-06-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31
; LENGTH: 12
; TYPE: PRT
; ORGANISM: mammalian
US-11-021-305-31

Query Match 35.9% Score 23; DB 7; Length 12;
Best Local Similarity 62.5% Pred. No. 75;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 4 NYLALVRE 11
Db 2 SYLALYTE 9

RESULT 12
US-11-041-893-201
; Sequence 201, Application US/11041893
; Publication No. US2006002941A1
; GENERAL INFORMATION:
; APPLICANT: Mahairas, Gregory G.
; TITLE OF INVENTION: COMPOSITIONS COMPRISING IMMUNE RESPONSE
; FILE REFERENCE: 100123.401
; CURRENT APPLICATION NUMBER: US/11/041,893
; CURRENT FILING DATE: 2005-01-24
; PRIOR APPLICATION NUMBER: US 60/616,855
; PRIOR FILING DATE: 2004-10-06
; PRIOR APPLICATION NUMBER: US 60/538,713
; PRIOR FILING DATE: 2004-01-23
; NUMBER OF SEQ ID NOS: 295
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 201
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-11-041-893-201

Query Match 35.9% Score 23; DB 7; Length 20;
Best Local Similarity 36.4% Pred. No. 1,4e+02;
Matches 4; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Oy 3 QNYLALVREIK 13
Db 4 ESYQELVKLE 14

RESULT 13
US-10-494-781-6
; Sequence 6, Application US/10494781
; Publication No. US20050244895A1
; GENERAL INFORMATION:
; APPLICANT: King's College London
; TITLE OF INVENTION: Diagnosis of Demyelinating or Spongiform Disease
; FILE REFERENCE: IT/KE/N13246
; CURRENT APPLICATION NUMBER: US/10/494,781
; CURRENT FILING DATE: 2004-05-06
; PRIOR APPLICATION NUMBER: GB 0127000.8
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: GB 0202562.5
; PRIOR FILING DATE: 2002-02-04
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1

SEQ ID NO 6
LENGTH: 7
TYPE: PRT
ORGANISM: Bovine
US-10-494-781-6

Query Match 34.4%; Score 22; DB 6; Length 7;
Best Local Similarity 100.0%; Pred. No. 5.8e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKON 4
DB 4 DKON 7

RESULT 14
US-11-045-024-3529
Sequence 3529, Application US/11045024
Publication No. US20050271676A1
GENERAL INFORMATION:

APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Livingston, Brian
APPLICANT: Chesnut, Robert
APPLICANT: Baker, Denise Marie
APPLICANT: Celis, Esteban
APPLICANT: Kubo, Ralph
APPLICANT: Grey, Howard M.
APPLICANT: EpiImmune Inc.
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2060.0040007
CURRENT APPLICATION NUMBER: US/11/045.024
CURRENT FILING DATE: 2005-01-28
PRIOR APPLICATION NUMBER: US 09/412,863
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: US 08/027,146
PRIOR FILING DATE: 1993-03-05
PRIOR APPLICATION NUMBER: US 08/073,205
PRIOR FILING DATE: 1993-06-04
PRIOR APPLICATION NUMBER: US 08/103,396
PRIOR FILING DATE: 1993-08-06
PRIOR APPLICATION NUMBER: US 08/159,184
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/159,339
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/347,610
PRIOR FILING DATE: 1994-12-01
NUMBER OF SEQ ID NOS: 14528
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3529

LENGTH: 9
TYPE: PRT
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-3529

Query Match 34.4%; Score 22; DB 7; Length 9;
Best Local Similarity 55.6%; Pred. No. 5.8e+04;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 YLALVRELK 13
DB 1 YLALITALIK 9

RESULT 15
US-11-045-024-3575
Sequence 3575, Application US/11045024
Publication No. US20050271676A1
GENERAL INFORMATION:

APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Livingston, Brian
APPLICANT: Chesnut, Robert
APPLICANT: Baker, Denise Marie
APPLICANT: Celis, Esteban
APPLICANT: Kubo, Ralph
APPLICANT: Grey, Howard M.
APPLICANT: EpiImmune Inc.
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2060.0040007
CURRENT APPLICATION NUMBER: US/11/045.024
CURRENT FILING DATE: 2005-01-28
PRIOR APPLICATION NUMBER: US 09/412,863
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: US 08/027,146
PRIOR FILING DATE: 1993-03-05
PRIOR APPLICATION NUMBER: US 08/073,205
PRIOR FILING DATE: 1993-06-04
PRIOR APPLICATION NUMBER: US 08/103,396
PRIOR FILING DATE: 1993-08-06
PRIOR APPLICATION NUMBER: US 08/159,184
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/159,339
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/347,610
PRIOR FILING DATE: 1994-12-01
NUMBER OF SEQ ID NOS: 14528
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3575

LENGTH: 9
TYPE: PRT
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-3575

Query Match 34.4%; Score 22; DB 7; Length 9;
Best Local Similarity 62.5%; Pred. No. 5.8e+04;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 LALVRELK 13
DB 2 LELLELRLK 9

RESULT 16
US-11-045-024-3576
Sequence 3576, Application US/11045024
Publication No. US20050271676A1
GENERAL INFORMATION:

APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Livingston, Brian
APPLICANT: Chesnut, Robert
APPLICANT: Baker, Denise Marie
APPLICANT: Celis, Esteban
APPLICANT: Kubo, Ralph
APPLICANT: Grey, Howard M.
APPLICANT: EpiImmune Inc.
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2060.0040007
CURRENT APPLICATION NUMBER: US/11/045.024
CURRENT FILING DATE: 2005-01-28
PRIOR APPLICATION NUMBER: US 09/412,863
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: US 08/027,146
PRIOR FILING DATE: 1993-03-05
PRIOR APPLICATION NUMBER: US 08/073,205

```
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3576
; LENGTH: 9
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-3576
```

```
Query Match          34.4%; Score 22; DB 7; Length 9;
Best Local Similarity 62.5%; Pred. No. 5.8e+04;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY          6 LALVRELK 13
           |||: |||
Db          2 LELLELKK 9
```

RESULT 17

```
US-11-045-024-10581
; Sequence 10581, Application US/11045024
; Publication No. US20050271676A1
```

GENERAL INFORMATION:

```
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Livingston, Brian
APPLICANT: Chesnut, Robert
APPLICANT: Baker, Denise Marie
APPLICANT: Celis, Esteban
APPLICANT: Kubo, Ralph
APPLICANT: Grey, Howard M.
```

APPLICANT: EpiImmune Inc.

TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency

TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions

FILE REFERENCE: 2060.004007

CURRENT APPLICATION NUMBER: US/11/045,024

PRIOR FILING DATE: 2005-01-28

PRIOR APPLICATION NUMBER: US 09/412,863

PRIOR FILING DATE: 1999-10-05

PRIOR APPLICATION NUMBER: US 08/027,146

PRIOR FILING DATE: 1993-03-05

PRIOR APPLICATION NUMBER: US 08/073,205

PRIOR FILING DATE: 1993-06-04

PRIOR APPLICATION NUMBER: US 08/103,396

PRIOR FILING DATE: 1993-08-06

PRIOR APPLICATION NUMBER: US 08/159,184

PRIOR FILING DATE: 1993-11-29

PRIOR APPLICATION NUMBER: US 08/159,339

PRIOR FILING DATE: 1993-11-29

PRIOR APPLICATION NUMBER: US 08/205,713

PRIOR FILING DATE: 1994-03-04

PRIOR APPLICATION NUMBER: US 08/347,610

PRIOR FILING DATE: 1994-12-01

NUMBER OF SEQ ID NOS: 14528

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 10581

LENGTH: 9

TYPE: PRT

ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS

US-11-045-024-10581

```
Query Match          34.4%; Score 22; DB 7; Length 9;
```

```
Best Local Similarity 55.6%; Pred. No. 5.8e+04;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY          5 YLALVRELK 13
           |||: |||
Db          1 YLALTRALIK 9
```

RESULT 18

US-11-045-024-10652

```
; Sequence 10652, Application US/11045024
; Publication No. US20050271676A1
```

GENERAL INFORMATION:

```
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Livingston, Brian
APPLICANT: Chesnut, Robert
APPLICANT: Baker, Denise Marie
APPLICANT: Celis, Esteban
APPLICANT: Kubo, Ralph
APPLICANT: Grey, Howard M.
```

APPLICANT: EpiImmune Inc.

TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency

TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions

FILE REFERENCE: 2060.004007

CURRENT APPLICATION NUMBER: US/11/045,024

PRIOR FILING DATE: 2005-01-28

PRIOR APPLICATION NUMBER: US 09/412,863

PRIOR FILING DATE: 1999-10-05

PRIOR APPLICATION NUMBER: US 08/027,146

PRIOR FILING DATE: 1993-03-05

PRIOR APPLICATION NUMBER: US 08/073,205

PRIOR FILING DATE: 1993-06-04

PRIOR APPLICATION NUMBER: US 08/103,396

PRIOR FILING DATE: 1993-08-06

PRIOR APPLICATION NUMBER: US 08/159,184

PRIOR FILING DATE: 1993-11-29

PRIOR APPLICATION NUMBER: US 08/159,339

PRIOR FILING DATE: 1993-11-29

PRIOR APPLICATION NUMBER: US 08/205,713

PRIOR FILING DATE: 1994-03-04

PRIOR APPLICATION NUMBER: US 08/347,610

PRIOR FILING DATE: 1994-12-01

NUMBER OF SEQ ID NOS: 14528

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 10652

LENGTH: 9

TYPE: PRT

ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS

US-11-045-024-10652

```
Query Match          34.4%; Score 22; DB 7; Length 9;
Best Local Similarity 62.5%; Pred. No. 5.8e+04;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY          6 LALVRELK 13
           |||: |||
Db          2 LELLELKK 9
```

RESULT 19

US-11-045-024-10720

```
; Sequence 10720, Application US/11045024
; Publication No. US20050271676A1
```

GENERAL INFORMATION:

```
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Livingston, Brian
APPLICANT: Chesnut, Robert
APPLICANT: Baker, Denise Marie
APPLICANT: Celis, Esteban
```



```
RESULT 22
US-11-045-024-12496
; Sequence 12496, Application US/11045024
; Publication NO. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Estebean
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epiimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12496
; LENGTH: 9
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-12496

Query Match      34.4%; Score 22; DB 7; Length 9;
Best Local Similarity 62.5%; Pred. No. 5.8e+04;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
RESULT 23
US-11-045-024-13980
; Sequence 13980, Application US/11045024
; Publication NO. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Estebean
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epiimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13980

CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13980

US-11-045-024-13980
; Sequence 13981, Application US/11045024
; Publication NO. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Estebean
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epiimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13981

Query Match      34.4%; Score 22; DB 7; Length 9;
Best Local Similarity 55.6%; Pred. No. 5.8e+04;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
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LENGTH: 10
 TYPE: PRT
 ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
 US-11-045-024-3581

Query Match 34.4%; Score 22; DB 7; Length 10;
 Best Local Similarity 62.5%; Pred. No. 94;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 LALVRELK 13
 Db 3 LELLEELK 10

RESULT 25
 US-11-045-024-3582
 Sequence 3582, Application US/11045024
 Publication No. US20050271676A1
 GENERAL INFORMATION:
 APPLICANT: Sette, Alessandro
 APPLICANT: Sidney, John
 APPLICANT: Southwood, Scott
 APPLICANT: Livingston, Brian
 APPLICANT: Chesnut, Robert
 APPLICANT: Baker, Denise Marie
 APPLICANT: Celis, Eserben
 APPLICANT: Kubo, Ralph
 APPLICANT: Grey, Howard M.
 APPLICANT: Epimmune Inc.
 TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
 TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
 FILE REFERENCE: 2060.0040007
 CURRENT APPLICATION NUMBER: US/11/045,024
 CURRENT FILING DATE: 2005-01-28
 PRIOR APPLICATION NUMBER: US 09/412,863
 PRIOR FILING DATE: 1999-10-05
 PRIOR APPLICATION NUMBER: US 08/027,146
 PRIOR FILING DATE: 1993-03-05
 PRIOR APPLICATION NUMBER: US 08/073,205
 PRIOR FILING DATE: 1993-06-04
 PRIOR APPLICATION NUMBER: US 08/103,396
 PRIOR FILING DATE: 1993-08-06
 PRIOR APPLICATION NUMBER: US 08/159,184
 PRIOR FILING DATE: 1993-11-29
 PRIOR APPLICATION NUMBER: US 08/159,339
 PRIOR FILING DATE: 1993-11-29
 PRIOR APPLICATION NUMBER: US 08/205,713
 PRIOR FILING DATE: 1994-03-04
 PRIOR APPLICATION NUMBER: US 08/347,610
 PRIOR FILING DATE: 1994-12-01
 NUMBER OF SEQ ID NOS: 14528
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 3582
 LENGTH: 10
 TYPE: PRT
 ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
 US-11-045-024-3582

Query Match 34.4%; Score 22; DB 7; Length 10;
 Best Local Similarity 62.5%; Pred. No. 94;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 LALVRELK 13
 Db 3 LELLEELK 10

Search completed: January 26, 2006, 08:39:06
 Job time : 2.46552 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 26, 2006, 07:48:50 ; Search time 6.5 Seconds
(without alignments)
192.434 Million cell updates/sec

Title: US-09-662-293-7

Perfect score: 64

Sequence: 1 DKONYLALVRELK 13

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 4071

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database :

1: PIR.80:*
2: p1r1:*
3: p1r2:*
4: p1r3:*
5: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	39.1	15	2 A41338	isocitrate lyase (
2	25	39.1	20	2 S19615	globin - polychaet
3	24	37.5	18	2 A20923	light meromyosin -
4	24	37.5	20	2 S35970	ribosomal protein
5	24	37.5	21	2 S35978	ribosomal protein
6	23	35.9	20	2 A44921	hydroxypyruvate re
7	22	34.4	14	2 PA0015	seed storage prote
8	21	32.8	18	2 S49026	ribosomal protein
9	21	32.8	20	2 S71017	hypothetical prote
10	21	32.8	20	2 S4465	pyrithocorcin - Py
11	20	31.2	11	2 PU0034	dextranucrase (EC
12	20	31.2	17	2 I55226	myosin heavy chain
13	20	31.2	17	2 E29501	fibritopeptide A -
14	20	31.2	17	2 A35550	adrenocortical cel
15	20	31.2	20	2 B53875	creatinase kinase (E
16	20	31.2	20	2 A61150	2-oxoglutarate dec
17	20	31.2	21	2 PD0015	actin-binding prot
18	19	29.7	7	2 S71867	glutathione transf
19	19	29.7	11	2 I52960	glucose-6-phosphat
20	19	29.7	14	2 S29486	GTP-binding protei
21	19	29.7	15	2 PQ0193	T-cell receptor al
22	19	29.7	15	2 PQ0193	T-cell receptor al
23	19	29.7	16	2 S10809	protein kinase C i
24	19	29.7	16	2 PH1778	T cell receptor al
25	19	29.7	16	2 PH1781	T cell receptor al
26	19	29.7	17	2 PC2196	zymogen granule me
27	19	29.7	17	2 PH0769	T-cell receptor be
28	19	29.7	18	2 B44995	alkanal monooxygen
29	19	29.7	18	2 PH1792	T cell receptor al

30	19	29.7	19	2 JP0054	ribosomal protein
31	19	29.7	20	2 CA9164	chromogranin-B - r
32	19	29.7	20	2 JP0053	ribosomal protein
33	19	29.7	20	2 JP0055	ribosomal protein
34	19	29.7	20	2 H49034	nuclear antigen EB
35	19	29.7	20	2 PH1783	T cell receptor al
36	19	29.7	20	2 T01691	hypothetical prote
37	19	29.7	20	2 AE0120	insertion element
38	19	29.7	21	2 PH1369	ig heavy chain DJ
39	18	28.1	9	2 PT0270	ig heavy chain CRD
40	18	28.1	13	4 I70075	glycophorin B (mis
41	18	28.1	14	2 PH1705	ig heavy chain V r
42	18	28.1	14	2 D61308	hemocyanin chain 5
43	18	28.1	15	2 PQ0195	Sfil-glycoprotein
44	18	28.1	15	2 PA0046	protein QAI00044 -
45	18	28.1	15	2 PQ0192	scylar glycoprotei
46	18	28.1	15	2 PH1616	ig H chain V-D-J r
47	18	28.1	15	2 S29175	D-galactose-bindin
48	18	28.1	16	2 S10807	protein kinase C i
49	18	28.1	17	2 S09607	phenylalanine-tRNA
50	18	28.1	17	2 UQ2320	hypothetical 2.1K
51	18	28.1	18	2 C56211	progesterone recep
52	18	28.1	18	2 A60118	22K protein - Lyme
53	18	28.1	18	2 A45138	arsenite oxidase I
54	18	28.1	19	2 S59717	hypothetical prote
55	18	28.1	20	2 S46205	comosain (EC 3.4.2
56	18	28.1	20	2 A20999	fructose-bisphosph
57	18	28.1	20	2 I67551	monocyte chemotact
58	18	28.1	20	2 C56385	nitrophenol 3 - Rh
59	18	28.1	20	2 A05310	apolipoprotein E -
60	18	28.1	21	2 PH1731	ig heavy chain V r
61	18	28.1	21	2 PH1731	ig heavy chain V r
62	17	26.6	7	2 PS0254	18K protein 5507 -
63	17	26.6	9	2 A33527	fructose-2,6-bisph
64	17	26.6	10	2 PN0136	pepsin (EC 3.4.23.
65	17	26.6	10	2 PT0243	ig heavy chain CRD
66	17	26.6	11	2 S66606	quinoline 2-oxidor
67	17	26.6	12	2 A40763	sucrose-6-phosphat
68	17	26.6	12	2 S10624	lipovitelin - Afr
69	17	26.6	12	2 F84132	hypothetical prote
70	17	26.6	13	2 S09733	photosystem I prot
71	17	26.6	15	2 I46512	photosystem I prot
72	17	26.6	15	2 PQ0194	tropomn - rabbit
73	17	26.6	15	2 A41436	Sz-glycoprotein -
74	17	26.6	16	2 S10808	alpha-macroglobuli
75	17	26.6	16	2 B60566	protein kinase C i
76	17	26.6	16	2 S09732	cytochrome P450m51
77	17	26.6	17	1 A05168	photosystem I prot
78	17	26.6	17	2 I46511	conantokin G [vali
79	17	26.6	17	2 A46592	tropomn - rabbit
80	17	26.6	17	2 UQ2310	lactase-phlorizin
81	17	26.6	19	2 PQ0409	hypothetical 2.1K
82	17	26.6	20	2 PN0133	RNA-directed RNA P
83	17	26.6	20	2 S68028	pepsin (EC 3.4.23.
84	17	26.6	20	2 S18582	iodochronine 5'-mo
85	17	26.6	20	2 I54189	hypothetical prote
86	17	26.6	20	2 S35921	galactose-1-phosph
87	17	26.6	20	2 S03954	T-cell receptor ga
88	17	26.6	20	2 AC0269	acidic fibroblast
89	17	26.6	21	2 PQ0749	probable trp opero
90	16	25.0	2	2 S70727	self-incompatibili
91	16	25.0	8	2 I54379	lpgf protein - Shi
92	16	25.0	9	2 PH1675	gene NP2 protein -
93	16	25.0	12	2 A34858	ig heavy chain V r
94	16	25.0	12	2 PH1676	protease E - bla
95	16	25.0	13	2 E60396	ig heavy chain V r
96	16	25.0	13	2 JN0389	antigen 7H8/2 - ma
97	16	25.0	14	2 PH1677	histamine-releasin
98	16	25.0	14	2 PH1677	ig heavy chain V r
99	16	25.0	14	2 PC1215	homeotic protein E
100	16	25.0	15	2 A44920	2-halo benzotrate 1,2
			2	2 PQ0174	scylar glycoprotei

ALIGNMENTS

RESULT 1

A4138
 Iisocitrate lyase (EC 4.1.3.1) - Acinetobacter calcoaceticus (fragment)
 C:Species: Acinetobacter calcoaceticus
 C>Date: 28-May-1992 #sequence_revision 28-May-1992 #text_change 09-Jul-2004
 C:Accession: A4138
 R:Hoyt, J.C.; Johnson, K.E.; Reeves, H.C.
 J. Bacteriol. 173, 6844-6848, 1991
 A:Title: Purification and characterization of Acinetobacter calcoaceticus isocitrate lyase
 A:Reference number: A4138; MUID:92041568; PMID:1938889
 A:Accession: A4138
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-15 <HOY>
 A:Cross-references: UNIPROT:P28467; UNIPARC:UPI00001251F5
 C:Keywords: carbon-carbon lyase; oxo-acid-lyase

Query Match 39.1%; Score 25; DB 2; Length 15;
 Best Local Similarity 54.5%; Pred. No. 3.8e+02;
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 KONYLALVRELK 13
 DB 4 QTAIDAVRELK 14

RESULT 2

S19615
 globin - polychaete (Eudistylia vancouveri) (fragment)
 N:Alternate names: chlorochuorin
 C:Species: Eudistylia vancouveri
 C>Date: 19-Mar-1997 #sequence_revision 10-Oct-1997 #text_change 09-Jul-2004
 C:Accession: S19615
 R:Qabar, A.N.; Stern, M.S.; Walz, D.A.; Chiu, J.T.; Tinkovich, R.; Wall, J.S.; Kapp, O.H.
 J. Mol. Biol. 222, 1109-1129, 1991
 A:Title: Hierarchy of globin complexes. The quaternary structure of the extracellular chain
 A:Reference number: S19532; MUID:92106333; PMID:1762147
 A:Accession: S19615
 A:Molecule type: protein
 A:Residues: 1-20 <QAB>
 A:Cross-references: UNIPROT:Q7M3Q5; UNIPARC:UPI000017BD6C
 A:Experimental source: plume
 C:Keywords: calcium; dodecamer; heme; homotetramer; oxygen carrier

Query Match 39.1%; Score 25; DB 2; Length 20;
 Best Local Similarity 50.0%; Pred. No. 5.1e+02;
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 DKONYLAL 8
 DB 12 DRQNLMSW 19

RESULT 3

A20923
 light meromyosin - chicken (fragment)
 C:Species: Gallus gallus (chicken)
 C>Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 31-Dec-2004
 C:Accession: A20923
 R:Nyitrai, L.; Mocz, G.; Szilagyi, L.; Balint, M.; Lu, R.C.; Wong, A.; Gergely, J.
 J. Biol. Chem. 258, 13213-13220, 1983
 A:Title: The proteolytic substructure of light meromyosin.
 A:Reference number: A92403; MUID:84032553; PMID:6355107
 A:Accession: A20923
 A:Molecule type: protein
 A:Residues: 1-18 <NYT>
 A:Cross-references: UNIPROT:Q8J572; UNIPARC:UPI00001775EC
 C:Superfamily: myosin motor domain homology
 C:Keywords: ATP; muscle

Query Match 37.5%; Score 24; DB 2; Length 18;
 Best Local Similarity 41.7%; Pred. No. 6.9e+02;
 Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 KONYLALVRELK 13
 DB 2 KOAFTQOIRELK 13

RESULT 4

S35970
 ribosomal protein L10 - Citrobacter freundii (fragment)
 C:Species: Citrobacter freundii
 C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
 C:Accession: S35970
 R:Zhyvoloup, A.
 submitted to the EMBL Data Library, August 1993
 A:Reference number: S35970
 A:Accession: S35970
 A:Molecule type: DNA
 A:Residues: 1-20 <ZHY>
 A:Cross-references: UNIPROT:P43448; UNIPARC:UPI0000177309; EMBL:X74448
 C:Genetics:
 A:Gene: rplJ
 C:Superfamily: Escherichia coli ribosomal protein L10
 C:Keywords: protein biosynthesis; ribosome

Query Match 37.5%; Score 24; DB 2; Length 20;
 Best Local Similarity 50.0%; Pred. No. 7.7e+02;
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DKONYLALVREL 12
 DB 7 DKQALVAVSEV 18

RESULT 5

S35978
 ribosomal protein L10 - Proteus vulgaris (fragment)
 C:Species: Proteus vulgaris
 C>Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 09-Jul-2004
 C:Accession: S35978
 R:Zhyvoloup, A.
 submitted to the EMBL Data Library, August 1993
 A:Reference number: S35970
 A:Accession: S35978
 A:Molecule type: DNA
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-21 <ZHY>
 A:Cross-references: UNIPROT:P51411; UNIPARC:UPI000016EADB; EMBL:X74446; NID:G396471; PID:
 C:Genetics:
 A:Gene: rplJ
 C:Superfamily: Escherichia coli ribosomal protein L10
 C:Keywords: protein biosynthesis; ribosome

Query Match 37.5%; Score 24; DB 2; Length 21;
 Best Local Similarity 50.0%; Pred. No. 8.1e+02;
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DKONYLALVREL 12
 DB 7 DKQALVAVSEV 18

RESULT 6

A44921
 hydroxyphenylacetate reductase (EC 1.1.1.81) - Methylobacterium extorquens (fragment)
 C:Species: Methylobacterium extorquens
 C>Date: 01-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
 C:Accession: A44921
 R:Chistoserdova, L.V.; Lidstrom, M.E.
 J. Bacteriol. 174, 71-77, 1992

A>Title: Cloning, mutagenesis, and physiological effect of a hydroxypyruvate reductase g
 A/Reference number: A44921; MUID:92104992; PMID:1729225
 A/Accession: A44921
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-20 <CH1>
 A/Cross-references: UNIPARC:UPI000016P931; GB:M81443; NID:G150010; PIDN:AAA25378.1; PID:
 A/Note: sequence extracted from NCBI backbone (NCBIN:75202, NCBI:75203)
 A/Keywords: oxidoreductase

Query Match 35.9%; Score 23; DB 2; Length 20;
 Best Local Similarity 45.5%; Pred. No. 1.2e+03;
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 DKONYLALVRE 11
 ||: |||
 Db 9 DRESLDAPVRE 19

RESULT 7

PA0015
 seed storage protein 12S 2 - Arabidopsis thaliana (fragment)
 C/Species: Arabidopsis thaliana (mouse-ear cress)
 C/Date: 30-Jan-1992 #sequence_revision 06-Jan-1995 #text_change 11-Jul-1997
 C/Accession: PA0015
 R/Kmo, M.; Kawakami, T.; Miyake, N.; Tsugita, A.
 Submitted to JIPID, July 1994
 A/Description: Separation and characterization of Arabidopsis proteins by two-dimensions
 A/Reference number: PA0001
 A/Accession: PA0015
 A/Molecule type: protein
 A/Residues: 1-14 <KAM>
 A/Cross-references: UNIPARC:UPI000017B010
 A/Experimental source: seed
 A/Keywords: pyrogutamic acid; seed; storage protein
 F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 34.4%; Score 22; DB 2; Length 14;
 Best Local Similarity 36.4%; Pred. No. 1.3e+03;
 Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 3 QNYLALVRELK 13
 ||: |||
 Db 1 QNYLGVPEQLQ 11

RESULT 8

S49026
 ribosomal protein H525 [validated] - Haloarcula marismortui (fragment)
 C/Species: Haloarcula marismortui
 C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
 C/Accession: S49026; S63967
 R/Engemann, S.; Herfurth, E.; Briesemeister, U.; Grelle, G.; Wittmann-Liebold, B.
 Submitted to the Protein Sequence Database, November 1994
 A/Description: Cartography of ribosomal proteins of the 30S subunit from the halophilic
 A/Reference number: S49023
 A/Accession: S49026
 A/Molecule type: protein
 A/Residues: 1-18 <ENG>
 A/Cross-references: UNIPROT:Q7M532; UNIPARC:UPI000017AE43

R/Engemann, S.; Noelle, R.; Herfurth, E.; Briesemeister, U.; Grelle, G.; Wittmann-Liebold,
 B.; Blochem. 234, 24-31, 1995
 A/Title: Cartography of ribosomal proteins of the 30S subunit from the halophilic Haloar
 A/Reference number: S63964; MUID:96096717; PMID:8529646
 A/Accession: S63967
 A/Molecule type: protein
 A/Residues: 1-18 <ENW>
 A/Cross-references: UNIPARC:UPI000017AE43

C/Keywords: blocked amino end; protein biosynthesis; ribosome
 Query Match 32.8%; Score 21; DB 2; Length 18;
 Best Local Similarity 55.6%; Pred. No. 2.5e+03;

Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 QNYLALVRE 11
 ||: |||
 Db 10 RNVLGAPVRE 18

RESULT 9

S71017
 hypothetical protein - Streptococcus pneumoniae (fragment)
 C/Species: Streptococcus pneumoniae
 C/Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 31-Dec-2004
 C/Accession: S71017
 R/Martin, B.; Sharples, G.J.; Humbert, O.; Lloyd, R.G.; Claverly, J.P.
 Mol. Microbiol. 19, 1035-1045, 1996
 A/Title: The mmsA locus of Streptococcus pneumoniae encodes a RecG-like protein involve
 A/Reference number: S71015; MUID:96249697; PMID:8830261
 A/Accession: S71017
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-20 <MAR>
 A/Cross-references: UNIPROT:Q97PE0; UNIPROT:Q8DNU1; UNIPARC:UPI000017AC6F; EMBL:Z49988
 A/Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1995
 C/Superfamily: cephalosporin-C deacetylase

Query Match 32.8%; Score 21; DB 2; Length 20;
 Best Local Similarity 57.1%; Pred. No. 2.7e+03;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 ALVRELK 13
 ||: |||
 Db 5 ALLEELK 11

RESULT 10

S44465
 pyrrhocoricin - Pyrrhocoris apterus
 C/Species: Pyrrhocoris apterus
 C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
 C/Accession: S44465
 R/Cociancich, S.; Dupont, A.; Hegy, G.; Lanot, R.; Holder, F.; Hetru, C.; Hoffmann, J.A.
 Biochem. J. 300, 567-575, 1994
 A/Title: Novel inducible antibacterial peptides from a hemipteran insect, the sap-suckl
 A/Reference number: S44463; MUID:94271176; PMID:8002963
 A/Accession: S44465
 A/Molecule type: protein
 A/Residues: 1-20 <COC>
 A/Cross-references: UNIPROT:P37362; UNIPARC:UPI0000132E13

C/Function:
 A/Description: antibacterial protein
 A/Note: active against Gram-negative bacteria
 C/Keywords: antibacterial; hemolymph; immune response

Query Match 32.8%; Score 21; DB 2; Length 20;
 Best Local Similarity 66.7%; Pred. No. 2.7e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DKONYL 6
 ||: |||
 Db 2 DKGSYL 7

RESULT 11

P00034
 dextransucrase (EC 2.4.1.5) - Streptococcus bovis (fragment)
 C/Species: Streptococcus bovis
 C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
 C/Accession: P00034
 R/Dezono, Y.; Tsumori, H.; Mukasa, H.
 Submitted to JIPID, October 1993
 A/Description: Purification and properties of glucosyltransferase synthesizing 1,6-alpha
 A/Reference number: P00034
 A/Accession: P00034

A/Molecule type: protein
 A/Residues: 1-11 <UEZ>
 A/Cross-references: UNIPROT:Q7M102; UNIPARC:UPI000017CA7D
 A/Experimental source: ATCC 9809
 A/Keywords: glycosyltransferase; hexosyltransferase

Query Match 31.2% Score 20; DB 2; Length 11;
 Best Local Similarity 36.4%; Pred. No. 2.3e+03;
 Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DKONYLALVRE 11
 ||:|:|
 Db 1 DETAVALTIRE 11

RESULT 12
 155226
 myosin heavy chain - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
 C/Accession: I55226
 R/Weydert, A.; Daudas, P.; Caravatti, M.; Minty, A.; Bugalsky, G.; Cohen, A.; Robert, B.
 J. Biol. Chem. 259, 13867-13874, 1983
 A/Title: Sequential accumulation of mRNAs encoding different myosin heavy chain isoforms
 in fast myosin heavy chain from mouse skeletal muscle.
 A/Reference number: I55226; MUID:84061805; PMID:6196357
 A/Accession: I55226
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-17 <RES>
 A/Cross-references: UNIPROT:Q61932; UNIPARC:UPI00000E7F83; GB:K00986; NID:9199975; PIDN:
 A/Superfamily: myosin heavy chain; myosin motor domain homology

Query Match 31.2% Score 20; DB 2; Length 17;
 Best Local Similarity 27.3%; Pred. No. 3.5e+03;
 Matches 3; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 3 ONYLALVRELK 13
 |:|:|:|
 Db 1 RNHLRVESMQ 11

RESULT 13
 E29501
 fibrinopeptide A - pig
 C/Species: Sus scrofa domestica (domestic pig)
 C/Date: 21-Nov-1987 #sequence_revision 21-Nov-1987 #text_change 09-Jul-2004
 C/Accession: E29501
 R/Blomback, B.; Blomback, M.; Hann, C.
 unpublished results, cited by Blomback, B., and Blomback, M., in *Chemotaxonomy and Ser*
 A/Reference number: A29501
 A/Accession: E29501
 A/Molecule type: protein
 A/Residues: 1-17 <BLO>
 A/Cross-references: UNIPROT:P14460; UNIPARC:UPI000012A764
 R/Blomback, B.; Blomback, M.; Groendahl, N.J.
 Acta Chem. Scand. 19, 1789-1791, 1965
 A/Title: Studies on fibrinopeptides from mammals.
 A/Reference number: A03118
 A/Contents: annotation; confirmation of species assignment
 C/Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfid

Query Match 31.2% Score 20; DB 2; Length 17;
 Best Local Similarity 57.1%; Pred. No. 3.5e+03;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DKONYLA 7
 ||:|:|
 Db 5 DKGERLA 11

RESULT 14
 A35550

adrenocortical cell major secreted protein - bovine (fragment)
 C/Species: Bos primigenius taurus (cattle)
 C/Date: 21-Sep-1990 #sequence_revision 21-Sep-1990 #text_change 09-Jul-2004
 C/Accession: A35550
 R/Shi, D.L.; Savona, C.; Gagnon, J.; Cochet, C.; Chambaz, E.M.; Feige, J.J.
 J. Biol. Chem. 265, 2881-2887, 1990
 A/Title: Transforming growth factor-beta stimulates the expression of alpha-2-macroglobu
 A/Reference number: A35550; MUID:90153919; PMID:1689294
 A/Accession: A35550
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-17 <SHI>
 A/Cross-references: UNIPROT:Q7M2N4; UNIPARC:UPI000017C495

Query Match 31.2% Score 20; DB 2; Length 17;
 Best Local Similarity 45.5%; Pred. No. 3.5e+03;
 Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 KONYLALVREL 12
 ||:|:|
 Db 5 KPLYMVLVPSL 15

RESULT 15
 B53875
 creatine kinase (EC 2.7.3.2) CK-I - coho salmon (fragment)
 C/Species: Oncorhynchus kisutch (coho salmon)
 C/Date: 26-Sep-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
 C/Accession: B53875
 R/White, K.C.; Buechter, D.D.; Kenyon, G.L.
 J. Protein Chem. 11, 489-494, 1992
 A/Title: The principal islet of the Coho salmon (*Oncorhynchus kisutch*) contains the BB is
 A/Reference number: A53875; MUID:93080727; PMID:1449598
 A/Accession: B53875
 A/Status: preliminary; not compared with conceptual translation
 A/Molecule type: nucleic acid
 A/Residues: 1-20 <MHI>
 A/Cross-references: UNIPROT:Q9PSI4; UNIPARC:UPI00000PBF09
 A/Experimental source: Brockmann body, principal islet
 A/Note: sequence extracted from NCBI backbone (NCBI:P:120600)
 C/Superfamily: creatine kinase; creatine kinase repeat homology
 C/Keywords: phosphotransferase

Query Match 31.2% Score 20; DB 2; Length 20;
 Best Local Similarity 66.7%; Pred. No. 4.1e+03;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 KONYLA 7
 ||:|:|
 Db 10 KMNYSA 15

RESULT 16
 A61150
 2-oxoglutarate decarboxylase (EC 4.1.1.71) - *Euglena gracilis* (fragment)
 C/Species: *Euglena gracilis*
 C/Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 09-Jul-2004
 C/Accession: A61150
 R/Shigekia, S.; Nakano, Y.
 Arch. Biochem. Biophys. 288, 22-28, 1991
 A/Title: Characterization and molecular properties of 2-oxoglutarate decarboxylase from
 A/Reference number: A61150; MUID:91378443; PMID:1910306
 A/Accession: A61150
 A/Molecule type: protein
 A/Residues: 1-20 <SHI>
 A/Cross-references: UNIPROT:Q7M266; UNIPARC:UPI000017AED8
 C/Keywords: carbon-carbon lyase; carboxy-lyase; homotetramer; mitochondrion

Query Match 31.2% Score 20; DB 2; Length 20;
 Best Local Similarity 44.4%; Pred. No. 4.1e+03;
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 5 YLALVRELK 13

Db 3 YKAPVKDVK 11

RESULT 17

PD0015
 A:Title: actin-binding protein - Tetrahymena pyriformis (fragment)
 C:Species: Tetrahymena pyriformis
 C:Date: 13-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 09-Jul-2004
 C:Accession: PD0015
 R:Watanabe, A.; Kurasawa, Y.; Watanabe, Y.; Numata, O.
 J. Biochem. 123, 607-613, 1998
 A:Title: A new Tetrahymena actin-binding protein is localized in the division furrow.
 A:Reference number: PD0015; MUID:98207047; PMID:9538250
 A:Accession: PD0015
 A:Molecule type: protein
 A:Residues: 1-21 <MAT>
 A:Cross-references: UNIPROT:P81424; UNIPARC:UPI000012A412
 C:Genetics:
 A:Genetic code: SGCS
 C:Superfamily: plastin; alpha-actinin actin-binding domain homology; calmodulin repeat h
 C:Keywords: EF hand

Query Match 31.2%; Score 20; DB 2; Length 21;
 Best Local Similarity 40.0%; Pred. No. 4.3e+03;
 Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 DKONYLALVR 10
 |||:
 Db 6 DLKHPYLIR 15

RESULT 18

S7167
 A:Title: glutathione transferase (EC 2.5.1.18) class alpha 5 - pig (fragment)
 N:Alternate names: glutathione S-transferase class alpha 5
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-May-1999
 C:Accession: S7167
 R:Roimim, P.; Anglade, P.; Debrauwer, L.; Tulliez, J.
 Biochem. J. 317, 879-884, 1996
 A:Title: Characterization of pig liver glutathione S-transferases using HPLC-electrospira
 A:Reference number: S71674; MUID:96332484; PMID:8760377
 A:Accession: S7167
 A:Molecule type: protein
 A:Residues: 1-7 <ROU>
 A:Cross-references: UNIPARC:UPI00001754D3
 C:Comment: At least five species-independent classes of cytosolic glutathion transferase
 s mitochondrial form are known.
 C:Complex: dimer
 C:Function:
 A:Description: catalyzes the nucleophilic conjugation of intracellular glutathione to a
 A:Pathway: detoxification; xenobiotics metabolism
 A:Note: increased hydrophilicity of GSH-conjugates facilitates their further metabolism
 C:Superfamily: glutathione transferase
 C:Keywords: dimer; transferase

Query Match 29.7%; Score 19; DB 2; Length 7;
 Best Local Similarity 75.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 4 NYLA 7
 |||:
 Db 4 NYIA 7

RESULT 19

I52980
 A:Title: glucocerebrosidase - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
 C:Accession: I52980; I65971

R:Reiner, O.; Wiggerson, M.; Horowitz, M.
 DNA 7, 107-116, 1988

A:Title: Structural analysis of the human glucocerebrosidase genes.
 A:Reference number: I52980; MUID:88195776; PMID:3359914
 A:Accession: I52980
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-11 <RES>
 A:Cross-references: UNIPARC:UPI000016A981; GB:M18916; NID:G183023; PIDN:AAA35878.1; PID
 A:Accession: I65971
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-11 <RE2>
 A:Cross-references: UNIPARC:UPI000016A981; GB:M18917; NID:G183025; PIDN:AAA35879.1; PID

Query Match 29.7%; Score 19; DB 2; Length 11;
 Best Local Similarity 80.0%; Pred. No. 3.5e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 9 VRELK 13
 |||:
 Db 7 VRELE 11

RESULT 20

S29486
 A:Title: GTP-binding protein o-rab3 - electric ray (Discopyge ommata) (fragment)
 C:Species: Discopyge ommata
 C:Date: 22-Nov-1993 #sequence_revision 27-Feb-1997 #text_change 13-Mar-1997
 C:Accession: S29486
 R:Volkmann, W.; Pevaner, J.; Elferink, L.A.; Scheller, R.H.
 FEBS Lett. 317, 53-56, 1993
 A:Title: Association of three small GTP-binding proteins with cholinergic synaptic vesic
 A:Reference number: S29485; MUID:93154521; PMID:8428634
 A:Accession: S29486
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-14 <VOL>
 A:Cross-references: UNIPARC:UPI000017BF30

Query Match 29.7%; Score 19; DB 2; Length 14;
 Best Local Similarity 42.9%; Pred. No. 4.4e+03;
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 3 QNYLALV 9
 |||:
 Db 7 QNFNAVI 13

RESULT 21

PQ0193
 A:Title: stylar glycoprotein 3 - Peruvian tomato (fragment)
 N:Alternate names: S3-glycoprotein
 C:Species: Lycopersicon peruvianum (Peruvian tomato)
 C:Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 23-Aug-1997
 C:Accession: PQ0193; A28819
 R:Ma, S.L.; Williams, E.G.; Atkinson, A.; Anderson, M.A.; Cornish, E.C.; Grego, B.; Si
 Planta 169, 184-191, 1986
 A:Title: Style proteins of a wild tomato (Lycopersicon peruvianum) associated with expr
 A:Reference number: PQ0192
 A:Accession: PQ0193
 A:Molecule type: protein
 A:Residues: 1-15 <MAU>
 A:Cross-references: UNIPARC:UPI00001427C8
 A:Experimental source: style, strain Mill
 R:Anderson, M.A.; Cornish, E.C.; Ma, S.L.; Williams, E.G.; Hoggart, R.; Atkinson, A.;
 J.P.; Crawford, R.J.; Clarke, A.E.
 Nature 321, 38-44, 1986
 A:Title: Cloning of cDNA for a stylar glycoprotein associated with expression of self-i
 A:Reference number: A28819
 A:Accession: A28819
 A:Status: preliminary
 A:Molecule type: protein

A:Residues: 1-15 <AND>
A:Cross-references: UNIPARC:UPI00001427C8
C:Keywords: glycoprotein

Query Match 29.7%; Score 19; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 4.7e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 NYLALV 9
|:|:|
Db 3 DYQLQV 8

RESULT 22

PH0784
T-cell receptor alpha chain (F1) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C/Accession: PH0784
R:Caranova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A/Title: T cell receptor genes in a series of class I major histocompatibility complex-II allelic exclusion and antigen-specific repertoire.
A/Reference number: PH0746; MUID:92078846; PMID:1836010
A:Accession: PH0784
A:Molecule type: mRNA
A:Residues: 1-15 <CAS>
A:Cross-references: UNIPARC:UPI000017C76B; EMBL:X60885
A:Experimental source: T lymphocyte
C:Keywords: T-cell receptor

Query Match 29.7%; Score 19; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 4.7e+03;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 DKONYLAL 8
|:|:|
Db 5 DPSNNVL 12

RESULT 23

S10809
protein kinase C inhibitor KCIP-1 isoform f - sheep (fragment)
N/Alternate names: probable lipocortin
C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C/Date: 19-Mar-1997 #sequence_revision 13-Sep-1998 #text_change 13-Sep-1998
C/Accession: S10809
R:Tokery, A.; Ellis, C.A.; Sellers, L.A.; Aitken, A.
Eur. J. Biochem. 191, 421-429, 1990
A/Title: Protein kinase C inhibitor proteins. Purification from sheep brain and sequence
A/Reference number: S10804; MUID:90345949; PMID:2143472
A:Accession: S10809
A:Molecule type: protein
A:Residues: 1-16 <PRO>
A:Cross-references: UNIPARC:UPI00001758AA
A:Experimental source: brain
C:Superfamily: 14-3-3 protein

Query Match 29.7%; Score 19; DB 2; Length 16;
Best Local Similarity 55.6%; Pred. No. 5e+03;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 DKONYLALV 9
|:|:|
Db 3 DYRYLAEV 11

RESULT 24

PH1778
T cell receptor alpha chain V region (clone 1PBL V alpha 24-5) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C/Accession: PH1778

R:Porcelli, S.; Yockey, C.E.; Brenner, M.B.; Bal, S.P.
J. Exp. Med. 178, 1-16, 1993
A/Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood

A/Reference number: PH1754; MUID:93301585; PMID:8391057
A:Accession: PH1778
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-16 <FOR>
A:Cross-references: UNIPARC:UPI000017C36C

Query Match 29.7%; Score 19; DB 2; Length 16;
Best Local Similarity 50.0%; Pred. No. 5e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 YLALVR 10
|:|:|
Db 1 YICVVR 6

RESULT 25

PH1781
T cell receptor alpha chain V region (clone 2DN V alpha 24-2) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C/Accession: PH1781
R:Porcelli, S.; Yockey, C.E.; Brenner, M.B.; Bal, S.P.
J. Exp. Med. 178, 1-16, 1993
A/Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood
A/Reference number: PH1754; MUID:93301585; PMID:8391057
A:Accession: PH1781
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-16 <FOR>
A:Cross-references: UNIPARC:UPI000017C374

Query Match 29.7%; Score 19; DB 2; Length 16;
Best Local Similarity 50.0%; Pred. No. 5e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 YLALVR 10
|:|:|
Db 1 YICVVR 6

Search completed: January 26, 2006, 08:05:00
Job time : 9.5 secs

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OM protein - protein search, using sw model

Run on: January 26, 2006, 07:47:56 ; Search time 38.6638 Seconds
(without alignments)
237.221 Million cell updates/sec

Title: US-09-662-293-7
Perfect score: 64
Sequence: 1 DKONYLALVRELK 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 15779

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Uniprot_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	27	42.2	20 2 Q9R5T5_PROMI	Q9R5T5 proteus mix
2	27	42.2	20 2 Q9R595_9SYNE	Q9R595 synechococ
3	26	40.6	16 2 Q4KN88_MUSSP	Q4KN88 mus spretus
4	25	39.1	15 1 ACEA_ACICA	P28467 actinobact
5	25	39.1	20 2 Q7M3Q5_EUDVA	Q7M3Q5 eudistyllia
6	24	37.5	15 2 Q76UT2_9CAUD	Q76UT2 lactococcus
7	24	37.5	18 1 LYS_ESTAC	P82175 estigmena a
8	24	37.5	18 2 Q9D5S9_ADE04	Q9D5S9 human adeno
9	24	37.5	19 1 RL10_CITFR	P43448 citrobacter
10	24	37.5	19 2 Q4XBH7_PLACH	Q4XBH7 plasmodium
11	24	37.5	20 1 RL10_PROVU	P51411 proteus vul
12	24	37.5	20 2 Q4YD10_PLABE	Q4YD10 plasmodium
13	24	37.5	21 2 Q7W1L5_ADE04	Q7W1L5 human adeno
14	23	35.9	9 2 Q5D4Q6_SALTY	Q5D4Q6 bacillus sc
15	23	35.9	16 2 Q9UC18_SALTY	Q9UC18 homo sapien
16	23	35.9	17 2 Q9ZXC4_9EUC4	Q9ZXC4 discorospag
17	23	35.9	17 2 Q92X12_BPARI	Q92X12 bacteriophag
18	23	35.9	18 2 Q7W1L5_ADE04	Q7W1L5 human adeno
19	23	35.9	18 2 Q9W9C1_ADE04	Q9W9C1 human adeno
20	23	35.9	19 2 Q6L8F5_HUMAN	Q6L8F5 homo sapien
21	23	35.9	19 2 Q667U6_LITRO	Q667U6 lithobius f
22	23	35.9	19 2 Q9GPK3_9MYRI	Q9GPK3 actinobact
23	23	35.9	19 2 Q4X122_PLACH	Q4X122 plasmodium
24	23	35.9	19 2 Q4X122_PLACH	Q4X122 plasmodium
25	23	35.9	20 2 Q8WGC5_9EUC4	Q8WGC5 blepharipod
26	23	35.9	20 2 Q49132_METEX	Q49132 methylobact
27	22	34.4	9 2 Q5RBL7_PONRY	Q5RBL7 pongo pygma
28	22	34.4	15 2 Q7TN03_HUMAN	Q7TN03 homo sapien
29	22	34.4	15 2 Q7R6W8_PLAYO	Q7R6W8 plasmodium
30	22	34.4	15 2 Q6Q0R4_HELPY	Q6Q0R4 helicobacte
31	22	34.4	19 2 Q905E3_9HIV1	Q905E3 human immun

32	22	34.4	20 2 Q8WU51_HUMAN	Q8WU51 homo sapien
33	22	34.4	20 2 Q9TWM9_OCTVU	Q9TWM9 octopus vul
34	22	34.4	20 2 Q4XG46_PLACH	Q4XG46 plasmodium
35	22	34.4	21 2 Q7RPH5_PLAYO	Q7RPH5 plasmodium
36	21	32.8	16 2 Q9R4K7_GALTE	Q9R4K7 alteromonas
37	21	32.8	16 2 Q9QY10_RAT	Q9QY10 rattus norv
38	21	32.8	17 2 Q9L8K0_ENTFA	Q9L8K0 enterococcu
39	21	32.8	17 2 Q9QVH7_9MUT1	Q9QVH7 rattus sp.
40	21	32.8	18 2 Q7M532_HALMA	Q7M532 haloarcula
41	21	32.8	18 2 Q9B2M7_HUMAN	Q9B2M7 homo sapien
42	21	32.8	18 2 Q37852_BPARI	Q37852 bacteriophag
43	21	32.8	19 2 Q4XGK3_PLACH	Q4XGK3 plasmodium
44	21	32.8	19 2 Q90R12_9HIV1	Q90R12 human immun
45	21	32.8	20 1 PYRRH_PYPAP	PYRRH pyrrhocoris
46	21	32.8	20 2 P82258_ASPEL	P82258 aspergillus
47	21	32.8	20 2 Q4XN21_PLACH	Q4XN21 plasmodium
48	21	32.8	20 2 P82940_HORVU	P82940 hordeum vul
49	21	32.8	21 2 Q4XL35_PLACH	Q4XL35 plasmodium
50	21	32.8	21 2 Q5VAV3_9MARC	Q5VAV3 plagiocchila
51	21	32.8	21 2 Q5VAV5_9MARC	Q5VAV5 nipponoleje
52	21	32.8	21 2 Q5VAV7_9MARC	Q5VAV7 myricocolea
53	21	32.8	21 2 Q5VAV9_9MARC	Q5VAV9 jubaia bogo
54	21	32.8	21 2 Q5VAV1_9MARC	Q5VAV1 cyclolejeun
55	21	32.8	21 2 Q5VAV3_9MARC	Q5VAV3 ceratolejeun
56	21	31.2	8 2 Q8WGC9_9EUC4	Q8WGC9 upogobia af
57	20	31.2	11 2 Q7M102_STRBO	Q7M102 streptococc
58	20	31.2	12 2 Q9XNR6_PYLTI	Q9XNR6 pylaetella 1
59	20	31.2	13 2 P97622_RAT	P97622 rattus norv
60	20	31.2	14 1 PA2T2_BUNCA	PA2T2 bungarus hir
61	20	31.2	14 2 Q94TW5_9EUC4	Q94TW5 proteus mix
62	20	31.2	14 2 Q863R0_PROLO	Q863R0 procyon lot
63	20	31.2	14 2 Q863R1_BASAS	Q863R1 bassariscus
64	20	31.2	14 2 Q863R2_MELUS	Q863R2 melogale mo
65	20	31.2	14 2 Q863R3_ARCCL	Q863R3 arctonox co
66	20	31.2	14 2 Q863R4_TAXTA	Q863R4 taxidea tax
67	20	31.2	14 2 Q863R5_MELME	Q863R5 melos meles
68	20	31.2	14 2 Q863R6_ICTST	Q863R6 ictonyx str
69	20	31.2	14 2 Q863R7_GALVI	Q863R7 galictis vi
70	20	31.2	14 2 Q863R8_EIRBA	Q863R8 eira barbat
71	20	31.2	14 2 Q863R9_GULU	Q863R9 guilo guilo
72	20	31.2	14 2 Q863S0_MARPE	Q863S0 martes penn
73	20	31.2	14 2 Q863S1_MARPE	Q863S1 martes amer
74	20	31.2	14 2 Q863S2_MUSYT	Q863S2 musstela vis
75	20	31.2	14 2 Q863S3_MUSYT	Q863S3 musstela fire
76	20	31.2	14 2 Q863S4_MUSER	Q863S4 musstela erm
77	20	31.2	14 2 Q863S5_PTEBR	Q863S5 pteronura b
78	20	31.2	14 2 Q863S6_LUTMA	Q863S6 lutra macul
79	20	31.2	14 2 Q863S7_LUTMA	Q863S7 lutra lutra
80	20	31.2	14 2 Q863S8_LONLC	Q863S8 lontra long
81	20	31.2	14 2 Q863S9_LONFE	Q863S9 lontra feli
82	20	31.2	14 2 Q863T0_LONCN	Q863T0 lontra cana
83	20	31.2	14 2 Q863T1_ENHJU	Q863T1 enhya dra lut
84	20	31.2	14 2 Q863T2_AMBCT	Q863T2 amblyonyx ci
85	20	31.2	14 2 Q863T3_AONCA	Q863T3 aonyx capen
86	20	31.2	14 2 Q9R2Z4_CAMBE	Q9R2Z4 campylobact
87	20	31.2	14 2 Q9R2Z5_CAMBE	Q9R2Z5 campylobact
88	20	31.2	14 2 Q9W7Y9_CAMCO	Q9W7Y9 campylobact
89	20	31.2	14 2 Q9X715_CAMBE	Q9X715 campylobact
90	20	31.2	16 2 Q9LAP2_ENTFC	Q9LAP2 enterococcu
91	20	31.2	17 1 FIBA_PIG	FIBA sus scrofa
92	20	31.2	17 2 Q9HB76_HUMAN	Q9HB76 homo sapien
93	20	31.2	17 2 Q7RBC2_PLAYO	Q7RBC2 plasmodium
94	20	31.2	17 2 Q4XR88_PLACH	Q4XR88 plasmodium
95	20	31.2	17 2 Q7W2N4_BOVIN	Q7W2N4 bos taurus
96	20	31.2	17 2 Q8KHG3_STRGY	Q8KHG3 streptococc
97	20	31.2	17 2 Q8KRA3_9STRE	Q8KRA3 streptococc
98	20	31.2	17 2 Q9WW20_ENTFC	Q9WW20 enterococcu
99	20	31.2	17 2 Q9WW21_ENTFA	Q9WW21 enterococcu
100	20	31.2	17 2 Q9X515_ENTGA	Q9X515 enterococcu

ALIGNMENTS

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RESULT 1
Q9R5T5_PROM1 PRELIMINARY; PRT; 20 AA.
ID Q9R5T5;
AC Q9R5T5;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 21, Last annotation update)
DE Flagellin (Fragment).
OS Proteus mirabilis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Proteus.
OX NCBI_TaxID=584;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=91372967; PubMed=1680106;
RA Bahraoui F.K., Johnson D.E., Robbins D., Mobley H.L.;
RT "Proteus mirabilis flagellin and MR/P fimbriae: isolation,
RT purification, N-terminal analysis, and serum antibody response
RT following experimental urinary tract infection.";
RL Infect Immun. 59:3574-3580(1991).
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 20 AA; 2234 MW; 667024216115E099 CRC64;

Query Match 42.2%; Score 27; DB 2; Length 20;
Best Local Similarity 62.5%; Pred. No. 1.3e+03;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 NYLALVRE 11
DB 7 NYLSLVTO 14

RESULT 2
Q9R595_9SYNE PRELIMINARY; PRT; 20 AA.
ID Q9R595;
AC Q9R595;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Photosystem I subunit XII (Fragment).
OS Synecchococcus.
OC Bacteria; Cyanobacteria; Chroococcales.
OX NCBI_TaxID=1129;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=93252282; PubMed=8486290; DOI=10.1016/0378-1119(93)90618-D;
RA Muehlenhoff U., Haehnel W., Wilt H.T., Hermann R.G.;
RT "Genes encoding eleven subunits of photosystem I from the thermophilic
RT cyanobacterium Synecchococcus sp.";
RL Gene 127:71-78(1993).
DR GO; GO:0009522; C:photosystem I; IEA.
DR GO; GO:0015979; P:photosynthesis; IEA.
DR InterPro; IPR010010; Pfam.
DR Pfam; PF07465; Pfam; 1.
SQ SEQUENCE 20 AA; 2102 MW; DF585D9ED9D7C512 CRC64;

Query Match 42.2%; Score 27; DB 2; Length 20;
Best Local Similarity 66.7%; Pred. No. 1.3e+03;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DKONYALV 9
DB 5 DTQVVALV 13

RESULT 3
Q4KN88_MUSSP PRELIMINARY; PRT; 16 AA.
ID Q4KN88;
AC Q4KN88;
DT 13-SEP-2005 (TREMBLrel. 31, Created)
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)

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DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
DE MHC class I antigen (Fragment).
GN Name-H2-Tw5.
OS Mus spretus (Western wild mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Charchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10096;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SEB;
RA Guidry P.A., Stroyanowski I.;
RT "The Murine Family of Gut-Restricted Class Ib MHC includes
RT Alternatively Spliced Isoforms of the Proposed HLA-G Homolog,
RT Blastocyst MHC.";
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY989870; AY485357.1; -; Genomic_DNA.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 16 AA; 1839 MW; 236C9069F3EC01E CRC64;

Query Match 40.6%; Score 26; DB 2; Length 16;
Best Local Similarity 50.0%; Pred. No. 1.6e+03;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 NYLALVRELK 13
DB 1 DYIYNMEDLK 10

RESULT 4
ACCEA_ACICA STANDARD; PRT; 15 AA.
ID ACCEA_ACICA;
AC P28467;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Isocitrate lyase (EC 4.1.3.1) (Isocitrate) (ICL)
DE (Fragment).
GN Name=aceA.
OS Acinetobacter calcoaceticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OX NCBI_TaxID=471;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=92041568; PubMed=1938889;
RA Hoyt J.C., Johnson K.E., Reeves H.C.;
RT "Purification and characterization of Acinetobacter calcoaceticus
RT isocitrate lyase.";
RL J. Bacteriol. 173:6844-6848(1991).
CC -1- CATALYTIC ACTIVITY: Isocitrate = succinate + glyoxylate.
CC -1- PATHWAY: Glyoxylate bypass; first step.
CC -1- SUBUNIT: Homotetramer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to the isocitrate lyase family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR; A41338; A41338.
DR InterPro; IPR000918; Isocit_lyase_ph.
DR PROSITE; PS00161; ISOCITRATE_LYASE; PARTIAL.
KW Direct protein sequencing; Glyoxylate bypass; Lyase;
KW Tricarboxylic acid cycle.
FT NON_TER 15
FT NON_TER 15
SQ SEQUENCE 15 AA; 1710 MW; 83AE726B1F2F9CE3 CRC64;

Query Match 39.1%; Score 25; DB 1; Length 15;
Best Local Similarity 54.5%; Pred. No. 2.3e+03;

```


Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 ONYALVRELK 13
DB 4 Q7AIDAVRELK 14

RESULT 5

Q7M305 EUDVA PRELIMINARY; PRT; 20 AA.

AC Q7M305;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Globin (Fragment).
OS Eudictyia vancouveri.
OC Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Canalipalpata;
OC Sabellidae; Sabellidae; Eudictyia.
OX NCBI_Taxid=6364;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=9210633; PubMed=1762147;
RA Gabar A.N., Stern M.S., Walz D.A., Chiu J.T., Timkovich R., Wall J.S.,
Kapp O.H., Vinogradov S.N.;
RT "Hierarchy of globin complexes. The quaternary structure of the
RT extracellular chlorocruorin of Eudictyia vancouveri.";
RL J. Mol. Biol. 222:1109-1129 (1991).
DR FJR; S19615; S19615.
FT NON_TER 1 20
FT SEQUENCE 20 AA; 2286 MW; 42834109F06698CB CRC64;

Query Match 39.1%; Score 25; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 3.1e+03;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 DKONYLAL 8
DB 12 DRONLISM 19

RESULT 6

Q76UT2_9CAUD PRELIMINARY; PRT; 15 AA.

AC Q76UT2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Integrase (Fragment).
OS Nameint;
OC Lactococcus phage BK5-T.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
OX NCBI_Taxid=31754;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96064424; PubMed=8526525;
RA Boyce J.D., Davidson B.E., Hillier A.J.;
RT "Spontaneous deletion mutants of the Lactococcus lactis temperate
bacteriophage BK5-T and localization of the BK5-T attP site.";
RL Appl. Environ. Microbiol. 61:4105-4109 (1995).
DR EMBL; S80308; AAB35788.2; -; Genomic_DNA.
FT NON_TER 1 15
FT SEQUENCE 15 AA; 1831 MW; 12D81A642BD0B341 CRC64;

Query Match 37.5%; Score 24; DB 2; Length 15;
Best Local Similarity 41.7%; Pred. No. 3.6e+03;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 DKONYLALVREL 12
DB 4 DKOKITELMEL 15

RESULT 7

LXS_ESTAC

STANDARD; PRT; 18 AA.

AC P82175;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Lysozyme (EC 3.2.1.17) (1,4-beta-N-acetylglucosaminidase) (Fragment).
OS Bactigene acraea (Salt marsh moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
OC Acrididae; Bactigene.
OX NCBI_Taxid=56594;
RN [1]
RP PROTEIN SEQUENCE, AND ENZYME REGULATION.
RX TISSUE=Hemocyte;
RX MEDLINE=97448947; PubMed=9303271; DOI=10.1016/S0145-305X(97)00012-8;
RA Wiltner D., Weise C., Goetz P., Wiesner A.;
RT "LPS (lipopolysaccharide)-activated immune response in a hemocyte
cell line from Bactigene acraea (Lepidoptera).";
RL Dev. Comp. Immunol. 21:323-336 (1997).
CC -1- FUNCTION: Lysozymes have primarily a bacteriolytic function; those
CC in tissues and body fluids are associated with the monocyte-
CC macrophage system and enhance the activity of immunogens (By
CC similarity).
CC -1- CATALYTIC ACTIVITY: Hydrolysis of 1,4-beta-linkages between N-
CC acetylglucosaminic acid and N-acetyl-D-glucosamine residues in a
CC peptidoglycan and between N-acetyl-D-glucosamine residues in
CC chitodextrins.
CC -1- ENZYME REGULATION: By lipopolysaccharide (LPS).
CC -1- SIMILARITY: Belongs to the glycosyl hydrolase 22 family.

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CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC removed.

CC -----
CC DR InterPro: IPR001916; Glyco_hydro_22.
CC PROSITE: PS00128; LACTALBUMIN LYSOZYME, PARTIAL.
CC Antimicrobial; Bacteriolytic enzyme; Direct protein sequencing;
KM Glycosidase; Hydrolase.
FT NON_TER 18 18
FT SEQUENCE 18 AA; 2214 MW; B229D8F5ECD7F57 CRC64;

Query Match 37.5%; Score 24; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 4.3e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 LVRELK 13
DB 9 LVRELK 14

RESULT 8

Q9DS99_ADE04 PRELIMINARY; PRT; 18 AA.

AC Q9DS99;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE P23 protease (Fragment).
OS Human adenovirus 4 (HAdV-4).
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_Taxid=28280;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=2-G T95-873;
RX MEDLINE=99175282; PubMed=10074533;
RA Crawford-Miksza L.K., Nang R.N., Schnurr D.P.;
RT "Strain variation in adenovirus serotypes 4 and 7a causing acute
RT respiratory disease.";

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RL J. Clin. Microbiol. 37:1107-1112(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Z-G 795-873;
RA Crawford-Mikaza L.K.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF065064; AAD03661.3; -; Genomic_DNA.
DR HSSP; P03252; INLN.
DR GO; GO:0008233; F:peptidase activity; IEA.
KM Protease.
FT NON_TER
SQ SEQUENCE 18 AA; 1917 MW; 12FCE2715E7FB445 CRC64;

Query Match 37.5%; Score 24; DB 2; Length 18;
Best Local Similarity 45.5%; Pred. No. 4.3e+03;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 KONYALVREL 12
Db :|:|:|
4 EQELKAIVRDL 14

RESULT 9
RL10_CITFR STANDARD; PRT; 19 AA.
ID RL10_CITFR
AC P43448;
DC 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE 50S ribosomal protein L10 (Fragment).
GN Name=rplJ;
OS Citrobacter freundii.
CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
CC Enterobacteriaceae; Citrobacter.
OX NCBI_TaxID=546;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=771;
RA Zhyvoloup A.N.;
RL Submitted (AUG-1993) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the ribosomal protein L10P family.
-----
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CC removed.
-----
DR EMBL; X74448; CAAS2459.1; -; Genomic_DNA.
DR PIR; S35970; S35970.
DR HAMAP; MF_00362; -; 1.
DR InterPro; IPR002363; Ribosomal_L10eub.
DR PROSITE; PS01109; RIBOSOMAL_L10; PARTIAL.
KM Ribonucleoprotein; Ribosomal protein.
FT INIT_MET 0
FT NON_TER 0
SQ SEQUENCE 19 AA; 2026 MW; E20A02CD7851DB16 CRC64;

Query Match 37.5%; Score 24; DB 1; Length 19;
Best Local Similarity 50.0%; Pred. No. 4.6e+03;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DKONYALVREL 12
Db :|:|:|
6 DKQALVAEVS 17

RESULT 10
Q4XBH7_PLACH PRELIMINARY; PRT; 19 AA.
AC Q4XBH7;
DT 13-SEP-2005 (TREMBLrel. 31, Created)
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)

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DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=PC403822.00.0;
OS Plasmodium chabaudi.
CC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5825;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kool J.T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Duggett J., Trueman H.B., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carnucci D.J., Yates J.R., Kafatos F.C.,
RA Jansz C.D., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAJ01007928; CAH85746.1; -; Genomic_DNA.
KM Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 19 AA; 2373 MW; 3A760616CBF95A84 CRC64;

Query Match 37.5%; Score 24; DB 2; Length 19;
Best Local Similarity 50.0%; Pred. No. 4.6e+03;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKONYL 6
Db :|:|:|
14 ERQNYM 19

RESULT 11
RL10_PROVU STANDARD; PRT; 20 AA.
ID RL10_PROVU
AC P51411;
DC 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE 50S ribosomal protein L10 (Fragment).
GN Name=rplJ;
OS Proteus vulgaris.
CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
CC Enterobacteriaceae; Proteus.
OX NCBI_TaxID=585;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RA Zhyvoloup A.N.;
RL Submitted (AUG-1993) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the ribosomal protein L10P family.
-----
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CC use as long as its content is in no way modified and this statement is not
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-----
DR EMBL; X74446; CAAS2457.1; -; Genomic_DNA.
DR PIR; S35978; S35978.
DR HAMAP; MF_00362; -; 1.
DR InterPro; IPR002363; Ribosomal_L10eub.
DR PROSITE; PS01109; RIBOSOMAL_L10; PARTIAL.
KM Ribonucleoprotein; Ribosomal protein.
FT INIT_MET 0
FT NON_TER 0
SQ SEQUENCE 20 AA; 76520A02CD7851DB CRC64;

Query Match 37.5%; Score 24; DB 1; Length 20;
Best Local Similarity 50.0%; Pred. No. 4.8e+03;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

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QY 1 DKONYALVEL 12
 DB 6 DKQAIIVAEVSEV 17

RESULT 12
 Q4YD10_PLABE PRELIMINARY; PRT; 20 AA.

ID Q4YD10_PLABE PRELIMINARY; PRT; 20 AA.
 AC Q4YD10;
 DT 13-SEP-2005 (TREMBLrel. 31, Created)
 DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
 DE Hypothetical protein (Fragment).
 GN ORFNames=PB406092.00.0;
 OS Plasmodium berghei.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
 NC NCBI_TaxID=5621;
 RN [1]

RA NUCLEOTIDE SEQUENCE.
 RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
 RA Berrian M., Florens L., Janssen C.S., Pain A., Christopoulos G.K.,
 RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
 RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
 RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
 RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.,
 RT "A comprehensive survey of the Plasmodium life cycle by genomic,
 RL transcriptomic, and proteomic analyses."
 SC Science 307:82-86(2005).
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC EMBL; CAI01006376; CAI04109.1; -; Genomic_DNA.

KM Hypothetical protein. 1
 FT NON TER
 SQ SEQUENCE 20 AA; 2501 MW; 75F9BFEC2628711 CRC64;

Query Match 37.5%; Score 24; DB 2; Length 20;
 Best Local Similarity 83.3%; Pred. No. 4.8e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 LVRELK 13
 DB 5 LVRELK 10

RESULT 13
 Q9L4S9_SALTY PRELIMINARY; PRT; 21 AA.

ID Q9L4S9_SALTY PRELIMINARY; PRT; 21 AA.
 AC Q9L4S9;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Putative glycoprotein (Fragment).
 OS Salmonella typhimurium.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Salmonella.
 NC NCBI_TaxID=602;
 RN [1]

RA NUCLEOTIDE SEQUENCE.
 RA MEDLINE=22306558; PubMed=12420160; DOI=10.1007/s00203-002-0458-7;
 RA Rychlik I., Martin G., Methner U., Lovell M., Cardova L., Sebkova A.,
 RA Sevcik M., Damborsky J., Barrow P.A.,
 RT "Identification of Salmonella enterica serovar Typhimurium genes
 RT associated with growth suppression in stationary-phase nutrient broth
 RT cultures and in the chicken intestine."
 RL Arch. Microbiol. 178:411-420(2002).

DR EMBL; AF68390; AAF73476.1; -; Genomic_DNA.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0019867; C:outer membrane; IEA.
 DR GO; GO:0015288; F:porin activity; IEA.
 KW Porin.
 FT NON TER
 SQ SEQUENCE 21 AA; 2340 MW; FF537CDB3287E9E2 CRC64;

Query Match 37.5%; Score 24; DB 2; Length 21;
 Best Local Similarity 62.5%; Pred. No. 5.1e+03;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 KONYALV 9
 DB 2 KAKYLALM 9

RESULT 14
 Q5D4Q6_BACST PRELIMINARY; PRT; 9 AA.

ID Q5D4Q6_BACST PRELIMINARY; PRT; 9 AA.
 AC Q5D4Q6;
 DT 10-MAY-2005 (TREMBLrel. 30, Created)
 DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)
 DE tRNA-encoded proteolysis-inducing peptide tag (Fragment).
 GN Name=ssra;
 OS Bacillus stearothermophilus.
 OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Geobacillus.
 NC NCBI_TaxID=1422;
 RN [1]

RA NUCLEOTIDE SEQUENCE.
 RA STRAIN=LLC;
 RC Williams K.P.;
 RT "Phylogenetic analysis of tRNA."
 RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY011529; AAX12900.1; -; Genomic_DNA.
 FT NON TER
 SQ SEQUENCE 9 AA; 935 MW; 4D46D72DCB545603 CRC64;

Query Match 35.9%; Score 23; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KONY 5
 DB 2 KONY 5

RESULT 15
 Q9UC18_HUMAN PRELIMINARY; PRT; 16 AA.

ID Q9UC18_HUMAN PRELIMINARY; PRT; 16 AA.
 AC Q9UC18;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE Endozepine (Fragment).
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 NC NCBI_TaxID=9606;
 RN [1]

RA PROTEIN SEQUENCE.
 RA MEDLINE=93184488; PubMed=1292782;
 RA Apfel R., Lottspeich F., Hoppe J., Behl C., Durr G., Bogdahn U.,
 RT "Purification and analysis of growth regulating proteins secreted by a
 RT human melanoma cell line."
 RL Melanoma Res. 2:327-336(1992).
 DR HSSP; P07107; 1HB6.

SQ SEQUENCE 16 AA; 1924 MW; 9E1BDA89F501A76 CRC64;

Query Match 35.9%; Score 23; DB 2; Length 16;
 Best Local Similarity 55.6%; Pred. No. 5.8e+03;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 YIALVELK 13
 DB 3 YINKVELK 11

RT reepiratory disease.";
 RL J. Clin. Microbiol. 37:1107-1112(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=RI-67;
 RA Crawford-Mikhaez L.K.;
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF065062; AAD03655.2; -; Genomic DNA.
 DR GO: GO:0004197; F:cysteine-type endopeptidase activity; IEA.
 DR GO: GO:0008223; F:peptidase activity; IEA.
 DR GO: GO:0006508; F:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR000855; Peptidase_C5.
 DR ProDom; PD003705; Peptidase_C5; 1.
 KM Process.
 FT NON_TER
 SQ SEQUENCE 18 AA; 1929 MW; BB3CPD4C5E7FB446 CRC64;
 Query Match 35.9%; Score 23; DB 2; Length 18;
 Best Local Similarity 36.4%; Pred. No. 6.6e+03;
 Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 KNYLALVREL 12
 :|::|:
 Db 4 EQELRAIRDL 14

RESULT 20
 Q6LBF5_HUMAN
 ID Q6LBF5_HUMAN PRELIMINARY; PRT; 19 AA.
 AC Q6LBF5;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE TRA protein (Fragment).
 GN Name=CFA;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo
 NCBI_TaxID=9606;
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Liver;
 RA Sarafanov A.G.; Timofeeva M.Y., Bannikov V.M., Zakhariev V.M.,
 RT "Sequencing and primary structure analysis of a genomic sequence
 flanking the 3' terminus of human tissue plasminogen activator gene.";
 RL Mol. Biol. (Mosk.) 29:161-165(1995).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Liver;
 RA Sarafanov A.G.;
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; X77531; CAA54669.1; -; Genomic DNA.
 DR GO: GO:0030195; P:negative regulation of blood coagulation; IEA.
 FT NON_TER
 SQ SEQUENCE 19 AA; 2342 MW; SABN0749ACP2D6A4 CRC64;
 Query Match 35.9%; Score 23; DB 2; Length 19;
 Best Local Similarity 50.0%; Pred. No. 7e+03;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 NYLALVRE 11
 :|::|:
 Db 8 NYLDWIRD 15

RESULT 21
 Q967U6_LITFO
 ID Q967U6_LITFO PRELIMINARY; PRT; 19 AA.
 AC Q967U6;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)

DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Engailed (Fragment).
 OS Lithobius forficatus.
 OC Eukaryota; Metazoa; Arthropoda; Myriapoda; Chilopoda;
 OC Pleurostigmophora; Lithobiomorpha; Lithobiidae; Lithobius.
 NCBI_TaxID=7552;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=21272202; PubMed=11378385; DOI=10.1016/S0960-9822(01)00222-6;
 RA Cook C.E., Smith M.L., Telford M.J., Bastianello A., Akam M.;
 RT "Hox genes and the phylogeny of the arthropode.";
 RL Curr. Biol. 11:759-763(2001).
 DR EMBL; AF362097; AAK51952.1; -; Genomic DNA.
 FT NON_TER
 SQ SEQUENCE 19 AA; 2339 MW; 4C6F5E9A1FE03C57 CRC64;
 Query Match 35.9%; Score 23; DB 2; Length 19;
 Best Local Similarity 83.3%; Pred. No. 7e+03;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 LYRELK 13
 :|::|:
 Db 6 LARELK 11

RESULT 22
 Q9GPK3_9MYRI
 ID Q9GPK3_9MYRI PRELIMINARY; PRT; 19 AA.
 AC Q9GPK3;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Engailed protein (Fragment).
 OS Scutigereila immaculata (garden symphylan).
 OC Eukaryota; Metazoa; Arthropoda; Myriapoda; Scutigereillidae;
 OC Scutigereilla.
 NCBI_TaxID=146864;
 OX NCBI_TaxID=146864;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=21272202; PubMed=11378385; DOI=10.1016/S0960-9822(01)00222-6;
 RA Cook C.E., Smith M.L., Telford M.J., Bastianello A., Akam M.;
 RT "Hox genes and the phylogeny of the arthropode.";
 RL Curr. Biol. 11:759-763(2001).
 DR EMBL; AF318499; AAG45179.1; -; Genomic DNA.
 FT NON_TER
 SQ SEQUENCE 19 AA; 2339 MW; 4C6F5E9A1FE03C57 CRC64;
 Query Match 35.9%; Score 23; DB 2; Length 19;
 Best Local Similarity 83.3%; Pred. No. 7e+03;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 LYRELK 13
 :|::|:
 Db 6 LARELK 11

RESULT 23
 Q4X1Z2_PLACH
 ID Q4X1Z2_PLACH PRELIMINARY; PRT; 19 AA.
 AC Q4X1Z2;
 DT 13-SEP-2005 (TREMBlrel. 31, Created)
 DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
 DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
 DE Hypochemical protein (Fragment).
 GN ORFNames=PC400809.00.0;
 OS Plasmodium chabaudi.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 NCBI_TaxID=5825;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Hall N., Karris M., Raine J.D., Carlton J.M., Kooij T.W.A.,

RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
 RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
 RA Quail M.A., Ormond D., Doggett J., Trueman H.B., Mendoza J.,
 RA Bidwell S.L., Rajandream M.A., Carnucci D.J., Yates J.R., Kafatos F.C.,
 RA Janssen C.J., Barrett B., Turner C.M.R., Waters A.P., Sinden R.S.,
 RT "A comprehensive survey of the Plasmodium life cycle by genomic,
 RT transcriptomic, and proteomic analyses."; Science 307:82-86(2005).
 RL Science 307:82-86(2005).
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; CAJ01005631; CAH83122.1; -; Genomic_DNA.
 KW Hypothetical protein.
 FT NON TER 1
 SQ SEQUENCE 19 AA; 2315 MW; E6BF80132E33FD91 CRC64;
 Query Match 35.9%; Score 23; DB 2; Length 19;
 Best Local Similarity 42.9%; Pred. No. 7e+03;
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 2 KNYIAL 8
 DB 2 KKNYICI 8
 RESULT 24
 ID Q4XT43_PLACH PRELIMINARY; PRT; 19 AA.
 AC Q4XT43;
 DT 13-SEP-2005 (TREMBLrel. 31, Created)
 DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
 DE Hypothetical protein (Fragment).
 GN ORFNames=PC10647.00.0;
 OS Plasmodium chabaudi.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5825;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
 RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
 RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
 RA Quail M.A., Ormond D., Doggett J., Trueman H.B., Mendoza J.,
 RA Bidwell S.L., Rajandream M.A., Carnucci D.J., Yates J.R., Kafatos F.C.,
 RA Janssen C.J., Barrett B., Turner C.M.R., Waters A.P., Sinden R.S.,
 RT "A comprehensive survey of the Plasmodium life cycle by genomic,
 RT transcriptomic, and proteomic analyses."; Science 307:82-86(2005).
 RL Science 307:82-86(2005).
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; CAJ01003378; CAH79919.1; -; Genomic_DNA.
 KW Hypothetical protein.
 FT NON TER 1
 SQ SEQUENCE 19 AA; 2251 MW; FADCD87AB64CE02 CRC64;
 Query Match 35.9%; Score 23; DB 2; Length 19;
 Best Local Similarity 36.4%; Pred. No. 7e+03;
 Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 QY 3 ONYLALVRELK 13
 DB 1 QELIVVIOELQ 11
 RESULT 25
 ID OBWGCS_9EUCA PRELIMINARY; PRT; 20 AA.
 AC OBWGCS;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE NADH dehydrogenase subunit 1 (Fragment).

OS Blepharipoda occidentalis.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Anomura; Hippoidea;
 OC Albinidea; Blepharipoda.
 OX NCBI_TaxID=177216;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=21884466; PubMed=11886621; DOI=10.1098/rspb.2001.1886;
 RA Morrison C.L., Harvey A.W., Lavery S., Tieu K., Huang Y.,
 RA Cunningham C.W.;
 RT "Mitochondrial gene rearrangements confirm the parallel evolution of
 RT the crab-like form."
 RL Proc. R. Soc. Lond. B. Biol. Sci. 269:345-350(2002).
 DR EMBL; AF436053; AAL31625.1; -; Genomic_DNA.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON TER 20
 SQ SEQUENCE 20 AA; 2238 MW; 2DAF5888EF21F513 CRC64;
 Query Match 35.9%; Score 23; DB 2; Length 20;
 Best Local Similarity 66.7%; Pred. No. 7.4e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 4 NYLALV 9
 DB 5 NYLILI 10

Search completed: January 26, 2006, 08:03:51
 Job time : 41.6638 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 26, 2006, 07:47:09 ; Search time 81.5172 Seconds
(without alignments)
129.360 Million cell updates/sec

Title: US-09-662-293-8
Perfect score: 124
Sequence: 1 DMAQNYKXKROQFIQSULNNGATRQ 24

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378761 residues

Total number of hits satisfying chosen parameters: 897420

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

A_Geneseq 21: *
1: geneeqp19908s: *
2: geneeqp19908s: *
3: geneeqp2000s: *
4: geneeqp2001s: *
5: geneeqp2002s: *
6: geneeqp2003as: *
7: geneeqp2003bs: *
8: geneeqp2004s: *
9: geneeqp2005s: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	37	29.8	15	6	ABR30497 Human can
2	37	29.8	15	6	ABR31387 Human can
3	34	27.4	13	7	ADW34497 HLA bindi
4	34	27.4	13	7	ADW35730 HLA bindi
5	33.5	27.0	19	1	AAPE8118 hsc-relat
6	32	25.8	15	6	ABR30464 Human can
7	32	25.8	15	6	ABR31017 Human can
8	32	25.8	15	6	ABR30929 Human can
9	32	25.8	15	7	ADW37611 HLA bindi
10	31	25.0	9	5	ABJ01432 158P1D7 r
11	31	25.0	10	5	ABJ01921 158P1D7 r
12	31	25.0	10	5	ABJ01457 158P1D7 r
13	31	25.0	12	2	AAAI19443 Anti-Fung
14	31	25.0	12	2	AAAI19480 Anti-Fung
15	31	25.0	12	3	AAAI19930 Histactin-
16	31	25.0	12	3	AAAI19988 Histactin-
17	31	25.0	14	3	ABBS6747 Human SNP
18	31	25.0	15	6	ABG72213 Human CAR
19	31	25.0	15	2	ADM65333 Human NGF
20	31	25.0	16	2	AAW73692 M. tuberc
21	31	25.0	16	2	AAW73802 M. tuberc
22	31	25.0	16	4	AAU08157 Mycobacte
23	31	25.0	16	5	ABG78004 M. tuberc
24	31	25.0	17	4	AAH85946 Caenor de

25	31	25.0	17	7	ADM37099 Wild-type
26	31	25.0	17	7	ADM53387 Beta-cate
27	31	25.0	17	7	ADM95021 Wild-type
28	31	25.0	17	8	ADJ78231 Peptide S
29	31	25.0	17	8	ADJ31521 Beta-cate
30	31	25.0	17	9	AEAO1731 Human bet
31	31	25.0	19	5	ABG96178 Cyateline-
32	31	25.0	19	5	ADM11055 Clostridi-
33	31	25.0	20	8	ADH15134 Gliadin r
34	31	25.0	20	8	ADH15661 Gliadin r
35	30	24.2	9	8	ABY01496 SARS coro
36	30	24.2	10	9	ADZ86149 SARS coro
37	30	24.2	12	2	AAV24768 Lactoferr
38	30	24.2	12	9	ADZ69939 Curvulari
39	30	24.2	13	7	ADM75353 Potential
40	30	24.2	14	9	ADY49681 Severe ac
41	30	24.2	15	6	ABR30599 Human can
42	30	24.2	15	6	ABR30928 Human can
43	30	24.2	15	6	ABR31140 Human can
44	30	24.2	15	6	ABR31256 Human can
45	30	24.2	15	6	ABR31386 Human can
46	30	24.2	15	7	ADM75913 Human MHC
47	30	24.2	15	7	ADM75938 Human MHC
48	30	24.2	15	7	ADM75962 Human MHC
49	30	24.2	15	7	ADM75981 Human Fac
50	30	24.2	15	7	ADG06417 Human B-d
51	30	24.2	15	9	ADV51686 SARS-Cov
52	30	24.2	15	9	ADV51687 SARS-Cov
53	30	24.2	15	9	ADV51690 SARS-Cov
54	30	24.2	15	9	ADV51695 SARS-Cov
55	30	24.2	15	9	ADV51692 SARS-Cov
56	30	24.2	15	9	ADV51694 SARS-Cov
57	30	24.2	15	9	ADV51688 SARS-Cov
58	30	24.2	15	9	ADV51689 SARS-Cov
59	30	24.2	15	9	ADV51691 SARS-Cov
60	30	24.2	15	9	ADV51693 SARS-Cov
61	30	24.2	15	9	ADV51696 SARS-Cov
62	30	24.2	16	7	ADD23798 Breast ca
63	30	24.2	18	2	AAR43009 Peptide s
64	30	24.2	18	4	ABJ91858 Antimicro
65	30	24.2	18	8	ADN03310 Exemplary
66	30	24.2	18	8	ADR42145 CD6pepti
67	30	24.2	19	6	ABP70504 Peptide c
68	30	24.2	19	6	AEA33305 SARS prot
69	30	24.2	20	8	ADH15133 Gliadin r
70	30	24.2	20	8	ADH15660 Gliadin r
71	30	24.2	20	9	ADY77534 Peptide a
72	30	24.2	21	4	AAV31984 Ubiquitin
73	29.5	23.8	14	4	AAH98489 Human pep
74	29.5	23.8	19	7	ADF14605 Rheumatoid
75	29	23.4	9	6	ABJ43855 151P3D4 c
76	29	23.4	9	6	ABJ47304 151P3D4 c
77	29	23.4	9	6	ABJ39816 151P3D4 c
78	29	23.4	9	6	ABJ44507 151P3D4 c
79	29	23.4	9	6	ABJ45095 151P3D4 c
80	29	23.4	9	6	ABJ44772 151P3D4 c
81	29	23.4	9	6	ABJ42937 151P3D4 c
82	29	23.4	9	6	ABJ42407 151P3D4 c
83	29	23.4	9	6	ABJ45886 151P3D4 c
84	29	23.4	9	6	ABJ46596 151P3D4 c
85	29	23.4	9	6	ABJ46646 151P3D4 c
86	29	23.4	9	6	ABJ49376 151P3D4 c
87	29	23.4	9	6	ADZ57400 Cytotoxic
88	29	23.4	10	4	AAH88237 Saccharom
89	29	23.4	10	6	ABJ51147 151P3D4 c
90	29	23.4	10	6	ABJ51458 151P3D4 c
91	29	23.4	10	6	ABJ51265 151P3D4 c
92	29	23.4	10	6	ABJ51288 151P3D4 c
93	29	23.4	10	6	ABJ41268 151P3D4 c
94	29	23.4	10	6	ABJ50106 151P3D4 c
95	29	23.4	10	6	ABJ53103 151P3D4 c
96	29	23.4	10	6	ABJ50479 151P3D4 c
97	29	23.4	10	6	ABJ52255 151P3D4 c

98	29	23.4	10	6	ABJ50615	151P3D4 C
99	29	23.4	10	6	ABJ53745	151P3D4 C
100	29	23.4	10	6	ABJ53805	151P3D4 C

ALIGNMENTS

RESULT 1

ABR30497 standard; peptide; 15 AA.

ABR30497;

19-MAY-2003 (first entry)

Human cancer-related protein 83P4B8 HLA peptide #1559.

Human; cytostatic; vaccine; cancer; immune response; HLA;

human leukocyte antigen.

Homo sapiens.

MO200283921-A2.

24-OCT-2002.

10-APR-2002; 2002MO-US011654.

10-APR-2001; 2001US-0282739P.

10-APR-2001; 2001US-0283112P.

25-APR-2001; 2001US-0286630P.

(AGEN-) AGENSYS INC.

Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;

Morrison K, Morrison RK, Raitano AB;

WPI; 2003-075555/07.

New composition comprising a substance that modulates the structure of

proteins and polynucleotides, useful for therapeutic, prognostic and

diagnostic reagents for eliciting cellular or humoral immune response in

cancer patients.

Claim 13; Page 476; 1021pp; English.

The present invention relates to novel human cancer-related genes and

proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and

proteins are useful for eliciting a humoral or cellular immune response.

The genes are useful as probes and primers for the amplification and/or

detection of genes, mRNAs or their fragments, as reagents for the

diagnosis and/or prognosis of cancer, as coding sequences capable of

directing the expression of the protein, as tools for modulating or

inhibiting the expression of genes and/or translation of transcripts, and

as therapeutic agents. The proteins and peptides are useful as

therapeutic, prognostic and diagnostic reagents for cancer. The present

sequence is a human leukocyte antigen (HLA) peptide, used in an example

from the invention

SQ Sequence 15 AA;

Query Match 29.8%; Score 37; DB 6; Length 15;

Best Local Similarity 46.7%; Pred. No. 75;

Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

9 RQOFIQSVLNNGATR 23

1 RQETLEQVLNRYVTR 15

RESULT 2

ABR31387

ID ABR31387 standard; peptide; 15 AA.

ABR31387;

19-MAY-2003 (first entry)

Human cancer-related protein 83P4B8 HLA peptide #2449.

Human; cytostatic; vaccine; cancer; immune response; HLA;

human leukocyte antigen.

Homo sapiens.

MO200283921-A2.

24-OCT-2002.

10-APR-2002; 2002MO-US011654.

10-APR-2001; 2001US-0282739P.

10-APR-2001; 2001US-0283112P.

25-APR-2001; 2001US-0286630P.

(AGEN-) AGENSYS INC.

Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;

Morrison K, Morrison RK, Raitano AB;

WPI; 2003-075555/07.

New composition comprising a substance that modulates the structure of

proteins and polynucleotides, useful for therapeutic, prognostic and

diagnostic reagents for eliciting cellular or humoral immune response in

cancer patients.

Claim 13; Page 491; 1021pp; English.

The present invention relates to novel human cancer-related genes and

proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and

proteins are useful for eliciting a humoral or cellular immune response.

The genes are useful as probes and primers for the amplification and/or

detection of genes, mRNAs or their fragments, as reagents for the

diagnosis and/or prognosis of cancer, as coding sequences capable of

directing the expression of the protein, as tools for modulating or

inhibiting the expression of genes and/or translation of transcripts, and

as therapeutic agents. The proteins and peptides are useful as

therapeutic, prognostic and diagnostic reagents for cancer. The present

sequence is a human leukocyte antigen (HLA) peptide, used in an example

from the invention

SQ Sequence 15 AA;

Query Match 29.8%; Score 37; DB 6; Length 15;

Best Local Similarity 46.7%; Pred. No. 75;

Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

9 RQOFIQSVLNNGATR 23

1 RQETLEQVLNRYVTR 15

RESULT 3

ADM34497 standard; peptide; 13 AA.

ADM34497;

10-MAR-2005 (first entry)

HLA binding epitope #5247.

Virucide; cytostatic; gene therapy; vaccine; epitope; cytotoxic T cell;

MHC class I; CTL; HTL; A2-restricted cytotoxic lymphocyte; HLA;

KM viral disease; cancer.
 XX
 OS Unidentified.
 XX
 PN WO2003040165-A2.
 XX
 PD 15-MAY-2003.
 XX
 PF 18-OCT-2001; 2001WO-US051650.
 XX
 PR 19-OCT-2000; 2000US-0242350P.
 PR 20-APR-2001; 2001US-0285624P.
 XX
 PA (EPIM-) EPIMMUNE INC.
 XX
 PI Sette A, Sidney J, Southwood S;
 XX
 DR WPI; 2003-441519/41.
 XX
 PT New composition comprising at least one peptide having allele-specific
 PT binding motifs for HLA, useful for preventing, treating or diagnosing
 PT viral diseases and cancer.
 XX
 PS Claim 1; Page 52-379; 382pp; English.
 XX
 CC The invention relates to a composition comprising at least one peptide
 CC having an isolated, prepared epitope selected from any of the sequences
 CC from 30 lists given in the specification. Also disclosed is a method for
 CC inducing a cytotoxic T cell response against a pre-selected antigen in a
 CC patient expressing a specific MHC class I allele by contacting cytotoxic
 CC T cells from the patient with the composition cited above. The
 CC composition comprises an epitope that is joined by an amino acid linker.
 CC The epitope is admixed or joined to a CTL or HTL epitope. The epitope is
 CC bound to an HLA molecule on the antigen-presenting cell, where when an A2
 CC -restricted cytotoxic lymphocyte (CTL) is present, a receptor of the CTL
 CC binds to a complex of the HLA molecule and the epitope. Specifically
 CC claimed are peptides having allele-specific binding motifs for HLA. The
 CC compositions and methods are useful for preventing, treating or
 CC diagnosing viral diseases and cancer. The peptide epitopes are useful as
 CC diagnostic agents for evaluating immune responses, for making antibodies
 CC and for evaluating efficacy of a vaccine. Sequences given in ADW29251-
 CC ADW37745 represent epitopes of the invention as given in Tables 2-31.
 CC
 XX
 SQ Sequence 13 AA;
 Query Match 27.4%; Score 34; DB 7; Length 13;
 Best Local Similarity 56.2%; Pred. No. 2e+02;
 Matches 9; Conservative 1; Mismatches 2; Indels 4; Gaps 1;
 QY 7 KYRQPFQSVLNGAT 22
 DB 2 KYRKQFIL---KGAT 13
 ID ADM35730 standard; peptide; 13 AA.
 XX
 AC ADM35730;
 XX
 DT 10-MAR-2005 (first entry)
 XX
 DE HLA binding epitope #6480.
 XX
 KM Viruslike; cytosolic; gene therapy; vaccine; epitope; cytotoxic T cell;
 KM MHC class I; CTL; HTL; A2-restricted cytotoxic lymphocyte; HLA;
 KM viral disease; cancer.
 XX
 OS Unidentified.
 XX
 PN WO2003040165-A2.
 XX
 PD 15-MAY-2003.

XX
 PF 18-OCT-2001; 2001WO-US051650.
 XX
 PR 19-OCT-2000; 2000US-0242350P.
 PR 20-APR-2001; 2001US-0285624P.
 XX
 PA (EPIM-) EPIMMUNE INC.
 XX
 PI Sette A, Sidney J, Southwood S;
 XX
 DR WPI; 2003-441519/41.
 XX
 PT New composition comprising at least one peptide having allele-specific
 PT binding motifs for HLA, useful for preventing, treating or diagnosing
 PT viral diseases and cancer.
 XX
 PS Claim 1; Page 52-379; 382pp; English.
 XX
 CC The invention relates to a composition comprising at least one peptide
 CC having an isolated, prepared epitope selected from any of the sequences
 CC from 30 lists given in the specification. Also disclosed is a method for
 CC inducing a cytotoxic T cell response against a pre-selected antigen in a
 CC patient expressing a specific MHC class I allele by contacting cytotoxic
 CC T cells from the patient with the composition cited above. The
 CC composition comprises an epitope that is joined by an amino acid linker.
 CC The epitope is admixed or joined to a CTL or HTL epitope. The epitope is
 CC bound to an HLA molecule on the antigen-presenting cell, where when an A2
 CC -restricted cytotoxic lymphocyte (CTL) is present, a receptor of the CTL
 CC binds to a complex of the HLA molecule and the epitope. Specifically
 CC claimed are peptides having allele-specific binding motifs for HLA. The
 CC compositions and methods are useful for preventing, treating or
 CC diagnosing viral diseases and cancer. The peptide epitopes are useful as
 CC diagnostic agents for evaluating immune responses, for making antibodies
 CC and for evaluating efficacy of a vaccine. Sequences given in ADW29251-
 CC ADW37745 represent epitopes of the invention as given in Tables 2-31.
 CC
 XX
 SQ Sequence 13 AA;
 Query Match 27.4%; Score 34; DB 7; Length 13;
 Best Local Similarity 56.2%; Pred. No. 2e+02;
 Matches 9; Conservative 1; Mismatches 2; Indels 4; Gaps 1;
 QY 7 KYRQPFQSVLNGAT 22
 DB 2 KYRKQFIL---KGAT 13
 ID AAP81118 standard; protein; 19 AA.
 XX
 AC AAP81118;
 XX
 DT 25-MAR-2003 (revised)
 DT 01-JUL-2002 (revised)
 DT 08-OCT-1990 (first entry)
 XX
 DE hsc-related peptide hsc (169-187).
 XX
 KM oncogene related peptide; hsc-related.
 XX
 OS Synthetic.
 XX
 PN EP253325-A.
 XX
 PD 20-JAN-1988.
 XX
 PF 10-JUL-1987; 87EP-00109985.
 XX
 PR 11-JUL-1986; 86JP-00164331.
 PR 10-JUL-1987; 87JP-00173671.
 XX
 PA (YANA/) YANAIHARA N.

```

XX Abe K, Yanaihara N;
XX WPI; 1988-015700/03.
XX New oncogene related peptide(s) - useful in prepn. of antigen and then
XX antibodies having specific reactivity with cancer proteins.
XX Claim 6; Page 33; 53pp; English.
XX Prepared by solid phase or soln. methods. One of 2 het-related peptides
XX among 23 claimed oncogene-related peptides. See also AAP114-7 and
XX AAP119-P81134. (Updated on 01-JUL-2002 to add missing PI field.)
XX (Updated on 25-MAR-2003 to correct PR field.)
XX Sequence 19 AA;
SQ
Query Match      27.0%; Score 33.5; DB 1; Length 19;
Best Local Similarity 42.1%; Pred. No. 3.7e+02;
Matches 8; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

OY      4 QNYKROQFIQSVLNNGAT 22
       ::|||::|||::|||
Db      2 ESYKYPGMFI-ALSKNGKT 19

RESULT 6
ABR30464
ID ABR30464 standard; peptide; 15 AA.
XX ABR30464;
XX
XX 19-MAY-2003 (first entry)
XX
XX Human cancer-related protein 83P4B8 HLA peptide #1526.
XX
XX Human; cytostatic; vaccine; cancer; immune response; HLA;
XX human leukocyte antigen.
XX
XX Homo sapiens.
XX
XX WO200283921-A2.
XX
XX 24-OCT-2002.
XX
XX 10-APR-2002; 2002WO-US011654.
XX
XX 10-APR-2001; 2001US-0282739P.
XX 10-APR-2001; 2001US-0283112P.
XX 25-APR-2001; 2001US-0286630P.
XX
XX (AGEN-) AGENSYS INC.
XX
XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
XX Morrison K, Morrison RK, Raitano AB;
XX
XX WPI; 2003-075555/07.
XX
XX New composition comprising a substance that modulates the structure of
XX proteins and polynucleotides, useful for therapeutic, prognostic and
XX diagnostic reagents for eliciting cellular or humoral immune response in
XX cancer patients.
XX
XX Claim 13; Page 475; 1021pp; English.
XX
XX The present invention relates to novel human cancer-related genes and
XX proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
XX proteins are useful for eliciting a humoral or cellular immune response.
XX The genes are useful as probes and primers for the amplification and/or
XX detection of genes, mRNAs or their fragments, as reagents for the
XX diagnosis and/or prognosis of cancer, as coding sequences capable of
XX directing the expression of the protein, as tools for modulating or
XX inhibiting the expression of genes and/or translation of transcripts, and

```

```

CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention
XX
XX Sequence 15 AA;
SQ
Query Match      25.8%; Score 32; DB 6; Length 15;
Best Local Similarity 42.9%; Pred. No. 4.9e+02;
Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY      10 QQFIQSVLNNGATR 23
       ::|||::|||::|||
Db      1 QEILIEQVLNRYVTR 14

RESULT 7
ABR31017
ID ABR31017 standard; peptide; 15 AA.
XX ABR31017;
XX
XX 19-MAY-2003 (first entry)
XX
XX Human cancer-related protein 83P4B8 HLA peptide #2079.
XX
XX Human; cytostatic; vaccine; cancer; immune response; HLA;
XX human leukocyte antigen.
XX
XX Homo sapiens.
XX
XX WO200283921-A2.
XX
XX 24-OCT-2002.
XX
XX 10-APR-2002; 2002WO-US011654.
XX
XX 10-APR-2001; 2001US-0282739P.
XX 10-APR-2001; 2001US-0283112P.
XX 25-APR-2001; 2001US-0286630P.
XX
XX (AGEN-) AGENSYS INC.
XX
XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
XX Morrison K, Morrison RK, Raitano AB;
XX
XX WPI; 2003-075555/07.
XX
XX New composition comprising a substance that modulates the structure of
XX proteins and polynucleotides, useful for therapeutic, prognostic and
XX diagnostic reagents for eliciting cellular or humoral immune response in
XX cancer patients.
XX
XX Claim 13; Page 485; 1021pp; English.
XX
XX The present invention relates to novel human cancer-related genes and
XX proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
XX proteins are useful for eliciting a humoral or cellular immune response.
XX The genes are useful as probes and primers for the amplification and/or
XX detection of genes, mRNAs or their fragments, as reagents for the
XX diagnosis and/or prognosis of cancer, as coding sequences capable of
XX directing the expression of the protein, as tools for modulating or
XX inhibiting the expression of genes and/or translation of transcripts, and
XX as therapeutic agents. The proteins and peptides are useful as
XX therapeutic, prognostic and diagnostic reagents for cancer. The present
XX sequence is a human leukocyte antigen (HLA) peptide, used in an example
XX from the invention
XX
XX Sequence 15 AA;
SQ
Query Match      25.8%; Score 32; DB 6; Length 15;
Best Local Similarity 42.9%; Pred. No. 4.9e+02;
Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

```

OY 10 QOFIQSVLNGATR 23
 ID 1 QEILEQVLRVVR 14

RESULT 8
 ABR30929
 ID ABR30929 standard; peptide; 15 AA.

AC ABR30929;

DT 19-MAY-2003 (first entry)

XX Human cancer-related protein 83P4B8 HLA peptide #191.

XX Human, cytostatic; vaccine; cancer; immune response; HLA;
 KM human leukocyte antigen.

OS Homo sapiens.

XX WO200283921-A2.

XX 24-OCT-2002.

XX 10-APR-2002; 2002WO-US011654.

XX 10-APR-2001; 2001US-0282739P.

XX 10-APR-2001; 2001US-0283112P.

XX 25-APR-2001; 2001US-0286630P.

XX (AGEN-) AGENSYS INC.

XX Jakobovits A, Chailite-Bid PM, Farris M, Ge W, Hubert RS;
 PI Morrison K, Morrison RK, Raitano AB;

XX WPI; 2003-075555/07.

XX New composition comprising a substance that modulates the structure of
 PT proteins and polynucleotides, useful for therapeutic, prognostic and
 PT diagnostic reagents for eliciting cellular or humoral immune response in
 PT cancer patients.

XX Claim 13; Page 483; 1021pp; English.

XX The present invention relates to novel human cancer-related genes and
 CC proteins (AB278120-AB278168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention

XX Sequence 15 AA;

Query Match 25.8%; Score 32; DB 6; Length 15;
 Best Local Similarity 42.9%; Pred. No. 4.9e+02;

Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 10 QOFIQSVLNGATR 23
 ID 1 QEILEQVLRVVR 14

RESULT 9
 ADW37611
 ID ADW37611 standard; peptide; 15 AA.

AC ADW37611;

XX 10-MAR-2005 (first entry)

XX HLA binding epitope #8361.

XX Virucide; cytostatic; gene therapy; vaccine; epitope; cytotoxic T cell;

XX MHC class I; CTL; HTL; A2-restricted cytotoxic lymphocyte; HLA;

XX viral disease; cancer.

XX Unidentified.

XX WO2003040165-A2.

XX 15-MAY-2003.

XX 18-OCT-2001; 2001WO-US051650.

XX 19-OCT-2000; 2000US-0242350P.

XX 20-APR-2001; 2001US-0285624P.

XX (EPIM-) EPIMMUNE INC.

XX Sette A, Sidney J, Southwood S;

XX WPI; 2003-441519/41.

XX Claim 1; Page 52-379; 382pp; English.

XX The invention relates to a composition comprising at least one peptide
 CC having an isolated, prepared epitope selected from any of the sequences
 CC from 30 lists given in the specification. Also disclosed is a method for
 CC inducing a cytotoxic T cell response against a pre-selected antigen in a
 CC patient expressing a specific MHC class I allele by contacting cytotoxic
 CC T cells from the patient with the composition cited above. The
 CC composition comprises an epitope that is joined by an amino acid linker.
 CC The epitope is admixed or joined to a CTL or HTL epitope. The epitope is
 CC bound to an HLA molecule on the antigen-presenting cell, where when an A2
 CC -restricted cytotoxic lymphocyte (CTL) is present, a receptor of the CTL
 CC binds to a complex of the HLA molecule and the epitope. Specifically
 CC claimed are peptides having allele-specific binding motifs for HLA. The
 CC compositions and methods are useful for preventing, treating or
 CC diagnosing viral diseases and cancer. The peptide epitopes are useful as
 CC diagnostic agents for evaluating immune responses, for making antibodies
 CC and for evaluating efficacy of a vaccine. Sequences given in ADW29251-
 CC ADW37745 represent epitopes of the invention as given in Tables 2-31.

XX Sequence 15 AA;

Query Match 25.8%; Score 32; DB 7; Length 15;
 Best Local Similarity 41.7%; Pred. No. 4.9e+02;

Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 4 QNYKXROQFIQS 15
 ID 2 ESYKHEQVYIRS 13

RESULT 10
 ABJ01432
 ID ABJ01432 standard; peptide; 9 AA.

XX ABJ01432;

XX 19-SEP-2002 (first entry)

XX 158PID7 related HLA peptide SEQ ID No 132.

XX Cytostatic; 158PID7; cancer; bladder cancer; mouse; rat; rabbit; dog;

KM cat; cow; horse; human; vaccine; gene therapy; human leukocyte antigen;
KW HLA.
XX
OS Homo sapiens.
XX
PN WO200216593-A2.
XX
PD 28-FEB-2002.
XX
PP 22-AUG-2001; 2001WO-US026276.
XX
XX 22-AUG-2000; 2000US-0227098P.
PR 10-APR-2001; 2001US-0282739P.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Faris M, Hubert RS, Raitano AB, Afar DEH, Levin E;
PI Chailita-Eid PM, Jakobovits A;
XX
XX WPI; 2002-425659/45.
DR
XX New compositions comprising a gene (designated 158PID7), its encoded
PT protein or their modulators, useful for treating or diagnosing cancers,
PT particularly bladder cancer, in mammals (e.g. dogs, cats, cows, horses or
PT humans).
XX
PS Disclosure; Page 130; 181pp; English.
XX
CC The invention relates to a novel nucleic acid, designated 158PID7. The
CC compositions are useful for treating or diagnosing cancers, particularly
CC bladder cancer, in mammals (e.g. mice, rats, rabbits, dogs, cats, cows,
CC horses or humans). The compositions are also useful for monitoring
CC genetic abnormalities and in preparing cancer vaccines. The nucleic acid
CC of the invention can be used in gene therapy to treat the said disorders.
CC This sequence represents a human leukocyte antigen (HLA) peptide relating
CC to the 158PID7 protein of the invention
CC
XX
SQ Sequence 9 AA;
XX
Query Match 25.0%; Score 31; DB 5; Length 9;
Best Local Similarity 75.0%; Pred. No. 2e+06; 1; Indels 0; Gaps 0;
Matches 6; Conservative 1; Mismatches 1;
XX
QY 15 SLVNGAT 22
Db |:|||||
1 SLNNGLT 8
XX
RESULT 11
ABJ01921
ID ABJ01921 standard; peptide; 10 AA.
XX
AC ABJ01921;
XX
DT 19-SEP-2002 (first entry)
XX
DE 158PID7 related HLA peptide SEQ ID No 621.
XX
KW Cytostatic; 158PID7; cancer; bladder cancer; mouse; rat; rabbit; dog;
KW cat; cow; horse; human; vaccine; gene therapy; human leukocyte antigen;
KW HLA.
XX
OS Homo sapiens.
XX
PN WO200216593-A2.
XX
PD 28-FEB-2002.
XX
PP 22-AUG-2001; 2001WO-US026276.
XX
XX 22-AUG-2000; 2000US-0227098P.
PR 10-APR-2001; 2001US-0282739P.
XX

PA (AGEN-) AGENSYS INC.
XX
PI Faris M, Hubert RS, Raitano AB, Afar DEH, Levin E;
PI Chailita-Eid PM, Jakobovits A;
XX
XX WPI; 2002-425659/45.
DR
XX New compositions comprising a gene (designated 158PID7), its encoded
PT protein or their modulators, useful for treating or diagnosing cancers,
PT particularly bladder cancer, in mammals (e.g. dogs, cats, cows, horses or
PT humans).
XX
PS Disclosure; Page 148; 181pp; English.
XX
CC The invention relates to a novel nucleic acid, designated 158PID7. The
CC compositions are useful for treating or diagnosing cancers, particularly
CC bladder cancer, in mammals (e.g. mice, rats, rabbits, dogs, cats, cows,
CC horses or humans). The compositions are also useful for monitoring
CC genetic abnormalities and in preparing cancer vaccines. The nucleic acid
CC of the invention can be used in gene therapy to treat the said disorders.
CC This sequence represents a human leukocyte antigen (HLA) peptide relating
CC to the 158PID7 protein of the invention
CC
XX
SQ Sequence 10 AA;
XX
Query Match 25.0%; Score 31; DB 5; Length 10;
Best Local Similarity 75.0%; Pred. No. 4.4e+02; 1; Indels 0; Gaps 0;
Matches 6; Conservative 1; Mismatches 1;
XX
QY 15 SLVNGAT 22
Db |:|||||
2 SLNNGLT 9
XX
RESULT 12
ABJ01457
ID ABJ01457 standard; peptide; 10 AA.
XX
AC ABJ01457;
XX
DT 19-SEP-2002 (first entry)
XX
DE 158PID7 related HLA peptide SEQ ID No 157.
XX
KW Cytostatic; 158PID7; cancer; bladder cancer; mouse; rat; rabbit; dog;
KW cat; cow; horse; human; vaccine; gene therapy; human leukocyte antigen;
KW HLA.
XX
OS Homo sapiens.
XX
PN WO200216593-A2.
XX
PD 28-FEB-2002.
XX
PP 22-AUG-2001; 2001WO-US026276.
XX
XX 22-AUG-2000; 2000US-0227098P.
PR 10-APR-2001; 2001US-0282739P.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Faris M, Hubert RS, Raitano AB, Afar DEH, Levin E;
PI Chailita-Eid PM, Jakobovits A;
XX
XX WPI; 2002-425659/45.
DR
XX New compositions comprising a gene (designated 158PID7), its encoded
PT protein or their modulators, useful for treating or diagnosing cancers,
PT particularly bladder cancer, in mammals (e.g. dogs, cats, cows, horses or
PT humans).
XX
PS Disclosure; Page 131; 181pp; English.
XX

CC The invention relates to a novel nucleic acid, designated 158PID7. The
 CC compositions are useful for treating or diagnosing cancers, particularly
 CC bladder cancer, in mammals (e.g. mice, rats, rabbits, dogs, cats, cows,
 CC horses or humans). The compositions are also useful for monitoring
 CC genetic abnormalities and in preparing cancer vaccines. The nucleic acid
 CC of the invention can be used in gene therapy to treat the said disorders.
 CC This sequence represents a human leukocyte antigen (HLA) peptide relating
 CC to the 158PID7 protein of the invention

XX
 SQ Sequence 10 AA;

Query Match 25.0%; Score 31; DB 5; Length 10;
 Best Local Similarity 75.0%; Pred. No. 4.4e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 15 SVLNGAT 22
 | : | | | | |
 Db 1 SLNNGLT 8

RESULT 13

AAW19443
 ID AAW19443 standard; peptide; 12 AA.

XX
 AC AAW19443;

XX
 DT 05-SEP-1997 (first entry)

DE Anti-fungal and anti-bacterial histatin-based peptide 13-Q2.3.9.10.

XX Candida albicans; periodontitis; caries; tooth decay; oral infection;
 KM vaginal infection; urethral infection; mucosal infection; ear infection;
 KM respiratory infection; skin infection; ophthalmic infection;
 KM bacterial disease; Streptococcus mutans; Porphyromonas gingivalis;
 KM Clostridium histolyticum.

XX
 OS Synthetic.

XX
 FH Key Location/Qualifiers
 FT Region 1..12
 FT /note= "At least one amino acid must have a D-
 configuration"

XX
 PN W09640768-A2.

XX
 PD 19-DEC-1996.

XX
 PF 07-JUN-1996; 96WO-US009374.

XX
 PR 07-JUN-1995; 95US-00481888.

XX
 PA (PERI-) PERIODONTIX INC.

XX
 PA (UYBO-) UNIV BOSTON.

XX
 PI Oppenheim FG, Xu T, Roberts FD, Spacciapoli P, Friden PM;

XX
 DR WPI; 1997-052232/05.

XX
 PT Anti-fungal and anti-bacterial histatin-based peptide(s) - useful esp for
 PT treating Candidal infections, periodontitis and caries.

XX
 PS Disclosure; Fig 1; 72pp; English.

XX
 CC The present sequence represents peptide Q2.3.9.10, where at least one
 CC amino acid is in the D-configuration. The peptide preferably is modified
 CC by an acetyl or carbamyl addition at the N-terminus and/or amidation at
 CC the C-terminus. The peptide, based on the naturally occurring histidine-
 CC rich human histatins, have anti-fungal and anti-bacterial activity and
 CC are useful in compositions for the treatment of oral, vaginal, urethral,
 CC mucosal, respiratory, skin, ear and ophthalmic fungal or bacterial
 CC infections. It is particularly effective against local and systemic
 CC Candida albicans infection, against oral bacterial diseases such as
 CC caries and periodontitis (by inhibiting e.g. Streptococcus mutans and

CC Porphyromonas gingivalis) and against Clostridium histolyticum. The
 CC peptide has superior anti-fungal (especially anti-Candidal) and anti-
 CC bacterial activity, particularly on a weight basis, compared to the
 CC longer, naturally occurring histatins. Peptides containing D-residues are
 CC also more resistant to degradation than L-amino acid versions

XX
 SQ Sequence 12 AA;

Query Match 25.0%; Score 31; DB 2; Length 12;
 Best Local Similarity 55.6%; Pred. No. 5.5e+02;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 4 ONYKYROOF 12
 | : | : | | |
 Db 3 QHNGYKQOF 11

RESULT 14

AAW19480
 ID AAW19480 standard; peptide; 12 AA.

XX
 AC AAW19480;

XX
 DT 05-SEP-1997 (first entry)

DE Anti-fungal and anti-bacterial D-amino acid peptide 113-Q2.3.9.10.

XX Candida albicans; periodontitis; caries; tooth decay; oral infection;
 KM vaginal infection; urethral infection; mucosal infection; ear infection;
 KM respiratory infection; skin infection; ophthalmic infection;
 KM bacterial disease; Streptococcus mutans; Porphyromonas gingivalis;
 KM Clostridium histolyticum.

XX
 OS Synthetic.

XX
 FH Key Location/Qualifiers
 FT Region 1..12
 FT /note= "At least one amino acid must have D-
 configuration"

XX
 PN W09640770-A2.

XX
 PD 19-DEC-1996.

XX
 PF 07-JUN-1996; 96WO-US009962.

XX
 PR 07-JUN-1995; 95US-00485273.

XX
 PA (PERI-) PERIODONTIX INC.

XX
 PA (UYBO-) UNIV BOSTON.

XX
 PI Oppenheim FG, Xu T, Spacciapoli P, Roberts FD, Friden PM;

XX
 DR WPI; 1997-052234/05.

XX
 PT Anti-fungal and anti-bacterial D-amino acid histatins and histatin-based
 PT peptide(s) - useful esp for treating Candidal infections, periodontitis
 PT and caries.

XX
 PS Disclosure; Fig 1; 63pp; English.

XX
 CC The present sequence represents an anti-fungal and anti-bacterial D-amino
 CC acid histatin-based peptide 113-Q2.3.9.10, found in human paratoid
 CC secretion, where at least one amino acid in the peptide is in the D-
 CC configuration. The peptide is preferably modified by an acetyl or
 CC carbamyl addition at the N-terminus and/or amidation at the C-terminus.
 CC The novel D-amino acid-containing peptide, based on the naturally
 CC occurring histidine-rich human histatins, have anti-fungal and anti-
 CC bacterial activity and are useful in compositions for the treatment of
 CC oral, vaginal, urethral, mucosal, respiratory, skin, ear and ophthalmic
 CC fungal or bacterial infections. It is particularly effective against
 CC local and systemic Candida albicans infection, against oral bacterial
 CC diseases such as caries and periodontitis (by inhibiting e.g.

CC Streptococcus mutans and Porphyromonas gingivalis) and against
 CC Clostridium histolyticum. The D-amino acid-containing peptide has
 CC superior anti-fungal (especially anti-candidal) and anti-bacterial
 CC activity, particularly on a weight basis, compared to the natural L-
 CC amino acid forms of histatins and histatin-based peptides. The presence
 CC of D-residues also makes the peptides more resistant to degradation than
 CC corresponding L-amino acid versions
 XX
 SQ Sequence 12 AA;
 Query Match 25.0%; Score 31; DB 2; Length 12;
 Best Local Similarity 55.6%; Pred. No. 5.5e+02;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 4 QNYKYRROOF 12
 DB 3 QHHGYKQOF 11
 RESULT 15
 AAB11993 standard; peptide: 12 AA.
 XX AAB11993;
 AC
 XX 24-NOV-2000 (first entry)
 DT
 XX Histatin-related peptide, P-113-KR2.3.9.10Q.
 DE
 XX Histatin-related peptide; cystic fibrosis; Pseudomonas aeruginosa;
 KW antibiotic resistance; pulmonary infection; antibacterial; antibiotic.
 KM
 XX Homo sapiens.
 OS Synthetic.
 OS
 XX Key Location/Qualifiers
 FH Modified-site 12
 FT /note= "C-terminal amide"
 FT
 XX WO200040204-A2.
 PN
 XX 13-JUL-2000.
 PD
 XX 07-JAN-2000; 2000WO-US000480.
 PF
 XX 08-JAN-1999; 99US-00226666.
 PR
 XX (PERI-) PERIODONTIX INC.
 PA
 XX Spacciapoli P, Rothstein DM, Friden PM;
 PI
 XX WPI: 2000-465852/40.
 DR
 XX Treating cystic fibrosis and combating Pseudomonas and other pulmonary
 XX infections in a mammal comprises administering histatin or a fragment of
 PT it.
 PT
 XX Example 6; Page 13; 27pp; English.
 PS
 XX The invention relates to treating cystic fibrosis via the administration
 CC of a histatin, a fragment of histatin, or a histatin-related peptide. The
 CC peptide that is administered contains between 8 and 20 amino acids and
 CC has the sequence: X1-X2-X3-X4-X5-X6-X7-X8-X9-X10-X11-X12-X13-X14-X15-X16-
 CC X17-X18-X19-X20- X21-X22-X23 where X1 is Asp or absent; X2 is Ser or
 CC absent; X3 is His or absent; X4 is Ala, His, Leu or absent; X5 is Lys,
 CC Gln, Arg, Orn, or another basic amino acid; X6 is Arg, Gln, Lys, or
 CC another basic amino acid; X7 is His, Phe, Tyr Leu, or another hydrophobic
 CC amino acid; X8 is His, Phe, Tyr Leu, or another hydrophobic amino acid;
 CC X9 is Gly, Lys, Arg, Ser, or a basic amino acid; X10 is Tyr; X11 is Lys,
 CC His, Phe, Leu, or another hydrophobic amino acid; X12 is Lys, Gln, Arg,
 CC Orn, or another basic amino acid; X13 is Lys, Gln, Arg, Orn, another
 CC basic amino acid, or absent; X14 is Phe or absent X15 is His, Phe, Tyr,
 CC Leu, another hydrophobic amino acid, or absent; X16 is Gln or absent; X17

CC is Lys or absent; X18 is His or absent; X19 is His or absent; X20 is Ser
 CC or absent; X21 is His or absent; X22 is Arg or absent; and X23 is Gly or
 CC absent. Optionally, the peptide may contain at least one modification
 CC selected from an N-terminal acyl addition, an N-terminal carbamyl
 CC addition and a C-terminal amide addition. Histatin, histatin fragments
 CC and histatin-related peptides have activity against Pseudomonas
 CC aeruginosa. They may therefore be used to combat Pseudomonas infections
 CC and other pulmonary infections in cystic fibrosis patients. Such
 CC infections are often resistant to the antibiotics normally used to treat
 CC pulmonary infections. Sequences AAB11985-B11993 represent histatin-
 CC related peptides used in the exemplifications of the invention. With the
 CC exception of P-113-Q2.3.9.10 (AAB11988), all these peptides showed
 CC activity against Pseudomonas aeruginosa
 XX
 SQ Sequence 12 AA;
 Query Match 25.0%; Score 31; DB 3; Length 12;
 Best Local Similarity 55.6%; Pred. No. 5.5e+02;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 4 QNYKYRROOF 12
 DB 3 QHHGYKQOF 11
 RESULT 16
 AAB11988 standard; peptide: 12 AA.
 XX AAB11988;
 AC
 XX 24-NOV-2000 (first entry)
 DT
 XX Histatin-related peptide, P-113-Q2.3.9.10.
 DE
 XX Histatin-related peptide; cystic fibrosis; Pseudomonas aeruginosa;
 KW antibiotic resistance; pulmonary infection; antibacterial; antibiotic.
 KM
 XX Homo sapiens.
 OS Synthetic.
 OS
 XX Key Location/Qualifiers
 FH Modified-site 12
 FT /note= "C-terminal amide"
 FT
 XX WO200040204-A2.
 PN
 XX 13-JUL-2000.
 PD
 XX 07-JAN-2000; 2000WO-US000480.
 PF
 XX 08-JAN-1999; 99US-00226666.
 PR
 XX (PERI-) PERIODONTIX INC.
 PA
 XX Spacciapoli P, Rothstein DM, Friden PM;
 PI
 XX WPI: 2000-465852/40.
 DR
 XX Treating cystic fibrosis and combating Pseudomonas and other pulmonary
 XX infections in a mammal comprises administering histatin or a fragment of
 PT it.
 PT
 XX Example 5; Page 12; 27pp; English.
 PS
 XX The invention relates to treating cystic fibrosis via the administration
 CC of a histatin, a fragment of histatin, or a histatin-related peptide. The
 CC peptide that is administered contains between 8 and 20 amino acids and
 CC has the sequence: X1-X2-X3-X4-X5-X6-X7-X8-X9-X10-X11-X12-X13-X14-X15-X16-
 CC X17-X18-X19-X20- X21-X22-X23 where X1 is Asp or absent; X2 is Ser or
 CC absent; X3 is His or absent; X4 is Ala, His, Leu or absent; X5 is Lys,
 CC Gln, Arg, Orn, or another basic amino acid; X6 is Arg, Gln, Lys, or
 CC another basic amino acid; X7 is His, Phe, Tyr Leu, or another hydrophobic

CC amino acid; X8 is His, Phe, Tyr Leu, or another hydrophobic amino acid;
 CC X9 is Gly, Lys, Arg, Ser, or a basic amino acid; X10 is Tyr; X11 is Lys,
 CC His, Phe, Leu, or another hydrophobic amino acid; X12 is Lys, Gln, Arg,
 CC Orn, or another basic amino acid; X13 is Lys, Gln, Arg, Orn, another
 CC basic amino acid, or absent; X14 is Phe or absent; X15 is His, Phe, Tyr,
 CC Leu, another hydrophobic amino acid, or absent; X16 is Glu or absent; X17
 CC is Lys or absent; X18 is His or absent; X19 is His or absent; X20 is Ser
 CC or absent; X21 is His or absent; X22 is Arg or absent; and X23 is Gly or
 CC absent. Optionally, the peptide may contain at least one modification
 CC selected from an N-terminal acyl addition, an N-terminal carbamyl
 CC addition and a C-terminal amide addition. Histatin, histatin fragments
 CC and histatin-related peptides have activity against *Pseudomonas*
 CC aeruginosa. They may therefore be used to combat *Pseudomonas* infections
 CC and other pulmonary infections in cystic fibrosis patients. Such
 CC infections are often resistant to the antibiotics normally used to treat
 CC pulmonary infections. Sequences ABB11985-B11993 represent histatin-
 CC related peptides used in the exemplifications of the invention. With the
 CC exception of the present sequence, all these peptides showed activity
 CC against *Pseudomonas aeruginosa*
 XX

SO Sequence 12 AA;
 Query Match 25.0%; Score 31; DB 3; Length 12;
 Best Local Similarity 55.6%; Pred. No. 5.5e+02;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 QNTKYRQOF 12
 DB 3 QNHGYKQOF 11

RESULT 17
 ABB56747
 ID ABB56747 standard; peptide; 14 AA.
 AC ABB56747;
 XX
 DT 05-MAR-2002 (first entry)
 DE Human SNP related amino acid sequence SEQ ID NO:1112.
 XX
 KW Human; single nucleotide polymorphism; SNP; polymorphism; cytostatic;
 KW immunosuppressive; antiinflammatory; neuroprotective; antimicrobial;
 KW autoimmune disease; inflammation; cancer; nervous system disease;
 KW infection; polymorphic protein.
 XX
 OS Homo sapiens.
 XX
 PN WO200138586-A2.
 XX
 PD 31-MAY-2001.
 XX
 PF 22-NOV-2000; 2000WO-US032311.
 XX
 PR 24-NOV-1999; 99US-0167383P.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Shinketsu RA, Leach M;
 XX
 DR WPI; 2001-355949/37.
 XX
 PT Isolated human nucleic acids comprising one or more single nucleotide
 PT polymorphisms, useful for treating a subject suffering from a pathology,
 PT e.g. autoimmune diseases, ascribed to the presence of a sequence
 PT polymorphism.
 XX
 PS Claim 1; Page 636; 674pp; English.
 XX
 CC ABL00010 to ABL01104 represent human nucleic acid oligonucleotides
 CC comprising one or more single nucleotide polymorphisms (SNPs). ABB56531
 CC to ABB56903 represent human peptides encoded by some of the SNP
 CC oligonucleotides. The sequences from the present invention can have

CC immunosuppressive, cytostatic, antiinflammatory, neuroprotective and
 CC antimicrobial activities. Nucleic acids, polypeptides, oligonucleotides
 CC and antibodies from the present invention can be used for treating a
 CC subject suffering from, at risk for, or suspected of, suffering from a
 CC pathology ascribed to the presence of a sequence polymorphism. The
 CC pathology may be autoimmune diseases, inflammation, cancer, diseases of
 CC the nervous system, and infection by pathogenic microorganisms. The SNPs
 CC are also useful for determining which forms of a characterized
 CC polymorphism are present in individuals. The antibodies may be used in
 CC the detection, quantitation and/or cellular or tissue localisation of a
 CC polymorphic protein (e.g., for use in measuring levels of the polymorphic
 CC protein within appropriate physiological samples)
 XX

SO Sequence 14 AA;
 Query Match 25.0%; Score 31; DB 4; Length 14;
 Best Local Similarity 60.0%; Pred. No. 6.5e+02;
 Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 DMAQNTKYRQ 10
 DB 4 DRTANVYRQ 13

RESULT 18
 ABG72213
 ID ABG72213 standard; peptide; 15 AA.
 AC ABG72213;
 XX
 DT 14-FEB-2003 (first entry)
 DE Human CARD-12 peptide used to raise CARD-12 antibodies.
 XX
 DE Human CARD-12 peptide used to raise CARD-12 antibodies.
 XX
 KW Human; caspase recruitment domain-12; CARD-12; apoptosis; transgenic;
 KW inflammatory disorder; immune disorder; Crohn's disease;
 KW reactive arthritis; insulin-dependent diabetes; multiple sclerosis;
 KW contact dermatitis; psoriasis; graft versus host disease; sarcoidosis;
 KW graft rejection; atopic condition; asthma; allergic rhinitis;
 KW gastrointestinal allergy; food allergy; eosinophilia; conjunctivitis;
 KW glomerular nephritis; viral infection; bacterial infection;
 KW Alzheimer's disease; Parkinson's disease; retinitis pigmentosa;
 KW Huntington's disease; anaemia; myocardial infarction; stroke; cancer;
 KW cytostatic; antiinflammatory; immunosuppressive; neuroprotective;
 KW dermatological; nephrotropic; ophthalmological; cardiac;
 KW cerebroprotective; immunogen.
 XX
 OS Homo sapiens.
 XX
 PN WO200285939-A1.
 XX
 PD 31-OCT-2002.
 XX
 PF 24-APR-2002; 2002WO-US013009.
 XX
 PR 24-APR-2001; 2001US-00841739.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Bertin J;
 XX
 DR WPI; 2003-093098/08.
 XX
 PT Novel caspase recruitment domain-12, CARD-12, polypeptide useful for
 PT treating inflammatory disorders and immune disorders e.g., Crohn's
 PT disease, diabetes, multiple sclerosis, Hashimoto's thyroiditis and
 PT Grave's disease.
 XX
 PS Example 3; Page 18; 112pp; English.
 XX
 CC The present invention relates to the isolation of human caspase
 CC recruitment domain-12 (CARD-12), and the polynucleotide sequence encoding
 CC it. The CARD family of proteins are involved in apoptosis. The invention

Query Match	25.0%	Score 31;	DB 2;	Length 16;
Best Local Similarity	33.3%	Pred. No. 7.6e+02;		
Matches	5;	Conservative	6;	Mismatches 4;
				Indels 0;
				Gaps 0;

```
QY      5 NYKYRQQFIQSVLNN 19
      ||::|||::|:
Db      2 NYEQQEQASQQLSS 16
```

RESULT	22
AAU08157	
ID	AAU08157 standard; peptide; 16 AA

DE Mycobacterium tuberculosis overlapping peptide ORF-1-16

Tuberculosis; Mycobacterium infection; gene therapy; anti bacterial;

05 Mycobacterium tuberculosis

PN WO200162893-A2

PF 26-FEB-2001; 2001WO-US005992.

PR 08-AUG-2000; 2000US-0223828P.

PA (CORI-) CORIXA CORP.

PI Campos-Neto A, Skeiky Y, Owendale P, Jen S, Lodes M,

DR WPI; 2001-536638/59

PT An isolated polypeptide comprising a Mycobacterium antigen, e.g., from

PT response to and inhibiting development of a *Mycobacterium tuberculosis* infection.

CC The present invention relates to the

The present invention relates to the isolation of Mycobacterium tuberculosis antigen polypeptides (e.g. Tb224) and the nucleic acids encoding them. The invention describes compounds and methods for the diagnosis of tuberculosis or for inducing protective immunity against tuberculosis. The compounds comprise at least one immunogenic portion of one or more Mycobacterium proteins and nucleic acid molecules encoding such polypeptides. The Mycobacterium proteins and nucleic acid molecules encoding them can be used in diagnostic kits for the detection of Mycobacterium infection in patients and biological samples. The compounds of the invention and antibodies directed against the Mycobacterium proteins may be used in vaccines for immunisation against Mycobacterium infections. The nucleic acids encoding the Mycobacterium proteins may be used in gene therapy. AAU08142-AAU08158 represent peptides (ORF-1-1 to ORF-1-17) which overlap to the open reading frame ORF-1

```
RESULT 23
ABG78004
ID ABG78004 standard; peptide; 16 AA.
XX
AC ABG78004;
XX
DT 15-NOV-2002 (first entry)
XX
DE M. tuberculosis CD4+ antigen ORF-1.1-1-17 peptide #16.
XX
KM Antigen; CD4+; infectious disease; tumour; tuberculosis;
XX autoimmune disease; Leishmaniasis; dendritic cell; T cell.
XX
OS Mycobacterium tuberculosis.
XX
PN US2002081579-A1.
XX
PD 27-JUN-2002.
XX
PF 13-FEB-1998; 98US-00023588.
XX
PR 13-FEB-1998; 98US-00023588.
XX
PA (POT)/ POTTER J E R.
XX
PI Skeiky YAW, Dillon DC, Alderson MR;
XX
DR WPI; 2002-617730/66.
XX
PT Identifying DNAs encoding CD4+ T cell stimulating antigens, for isolating
PT new CD4+ T cell-stimulating antigens associated with e.g. infections,
PT comprises measuring the levels of interferon-gamma production or cell
PT proliferation.
XX
PS Example 2; Page 33; 46pp; English.
XX
CC The invention relates to identifying DNA sequences that encode CD4+ T
CC cell stimulating antigens or antigens containing antibody epitopes
CC comprising determining the level of CD4+ T cell stimulation when incubated
CC with dendritic cells that have been exposed with a host cell transformed
CC with a plasmid suspected of containing a DNA sequence that encodes a CD4+
CC T cell stimulating antigen. Also included are (1) an isolated DNA
CC sequence consisting of DNA sequences isolated using the new method, their
CC complement or DNA sequences that hybridise to them; (2) an expression
CC vector comprising (1); (3) a host cell transformed with the expression
CC vector of (2); and (4) a polypeptide comprising an immunogenic portion of
CC antigen, or a variant of the antigen that differs only in conservative
CC substitutions and/or modifications, where the antigen comprises an amino
CC acid sequence encoded by (1). The method is useful for identifying and
CC isolating new antigens that stimulate CD4+ T cells. In particular, the
CC method is useful for isolating antigens associated with any disorder in
CC which the stimulation of CD4+ T cells is believed to play a role in the
CC body's immune response, e.g. CD4+ T cell-stimulating antigens associated
CC with infectious disease agents such as Mycobacterium tuberculosis or
CC Leishmaniasis, tumour tissue, or autoimmune disorders. The present method
CC is less technically difficult and less time-consuming than prior methods.
CC The present method is also more suitable for high-throughput use. The
CC present sequence represents an overlapping peptide derived from a CD4+ T
CC cell-stimulating antigen from M. tuberculosis
XX
SQ Sequence 16 AA;
XX
Query Match 25.0%; Score 31; DB 5; Length 16;
Best Local Similarity 33.3%; Pred. No. 7.6e+02;
Matches 5; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 5 NYKXROQFIQSVLN 19
||:|:|:|:|:|:|
Db 2 NYEOQEQASQOILSS 16
```

```
RESULT 24
AAB85946
```

```
ID AAB85946 standard; peptide; 17 AA.
XX
AC AAB85946;
XX
DT 30-NOV-2001 (first entry)
XX
DE Castor bean 2S small subunit protein fragment.
XX
KM Nadin gene; promoter; Brassica; phenotype; transcription; EA9; 3H11;
XX 2A11; alpha-amylase.
XX
OS Ricinus communis.
XX
PN US6281410-B1.
XX
PD 28-AUG-2001.
XX
PF 15-JAN-1999; 99US-00232861.
XX
PR 31-JUL-1986; 86US-00891529.
PR 26-MAY-1987; 87US-00054369.
PR 28-JUL-1987; 87US-00078538.
PR 25-JAN-1988; 88US-00147781.
PR 15-MAR-1988; 88US-00168190.
PR 29-APR-1988; 88US-00188361.
PR 02-NOV-1988; 88US-00267685.
PR 21-MAY-1990; 90US-00526123.
PR 09-JUL-1990; 90US-00550804.
PR 10-AUG-1993; 93US-00105852.
PR 07-JUN-1995; 95US-00484941.
PR 07-MAR-1997; 97US-00812665.
XX
PA (CALJ ) CALGENE LLC.
XX
PI Knauf VC, Kridl JC;
XX
DR WPI; 2001-564354/63.
XX
PT Obtaining a plant that produces a seed with a modified phenotype or
PT altering a seed phenotype, comprises transforming a plant cell with a DNA
PT construct consisting of operably linked components in the direction of
PT transcription.
XX
PS Example 9; Fig 6; 68pp; English.
XX
CC The invention provides a method for obtaining a plant which produces at
CC least one seed having a modified phenotype. The method involves
CC transforming a host plant cell with a DNA construct which consists of
CC operably linked components in the direction of transcription, a promoter
CC region from a Brassica plant gene, a DNA sequence of interest other than
CC the native coding sequence, and a transcription termination region. The
CC method is useful for obtaining plants having modified phenotype or for
CC altering the phenotype of a plant seed or tissue. The DNA constructs are
CC used in manipulating plant cells to provide for regulated transcription,
CC such as light inducible transcription, in a plant tissue or plant part of
CC interest at particular stages of plant growth or in response to external
CC control. These constructs are also used for modulation of expression of
CC endogenous products as well as production of exogenous products in the
CC seed. Sequences AAB85941-47 represent fragments of storage proteins used
CC in comparison studies with the storage protein 2A11
XX
SQ Sequence 17 AA;
XX
Query Match 25.0%; Score 31; DB 4; Length 17;
Best Local Similarity 46.2%; Pred. No. 8.2e+02;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 4 QNYKYROQFIQSV 16
||:|:|:|:|:|:|
Db 2 QNLRQCEYIQOV 14
```

```
RESULT 25
```

Search completed: January 26, 2006, 07:57:58
Job time : 84.5172 secs

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ADM37099
ID ADM37099 standard; peptide; 17 AA.
XX
AC ADM37099;
XX
DT 03-JUN-2004 (first entry)
XX
DE Wild-type Betacatenin 34-50.
XX
KM Beta-catenin; AKT kinase; kinase; phosphorylation substrate;
XX kinase recognition domain; E3 binding region.
XX
OS Unidentified.
XX
PN US2003170611-A1.
XX
PD 11-SEP-2003.
XX
PF 09-MAR-2002; 2002US-00093840.
XX
PR 09-MAR-2002; 2002US-00093840.
XX
PA (CARD/) CARDONE M H.
XX (YAFF/) YAFFE M.
XX
PI Cardone MH, Yaffe M;
XX
DR WPI; 2003-863752/80.
XX
PT Identifying a molecule capable of modulating a kinase activity in situ
XX using a substrate with an altered kinase recognition domain and an
XX associated label is useful in drug discovery.
XX
PS Disclosure; Fig 3b; 25pp; English.
XX
CC The invention relates to identifying a molecule capable of modulating a
XX kinase activity in situ, comprising exposing a candidate molecule to a
XX cell comprising a phosphorylation substrate associated with a detectable
XX label and having a kinase recognition domain altered to be recognised by
XX a kinase that does not recognise the substrate in its unaltered state,
XX and determining whether the candidate molecule causes a change in an
XX expression of the label. Also included are a molecule capable of
XX modulating activity of at least one kinase in situ identified by the
XX claimed method, a fusion protein (comprising an E3 binding region, a
XX kinase recognition domain and a green fluorescent protein, where the
XX kinase recognition domain is the domain of beta-catenin, HIV protein VPU,
XX p27, Bcl-2 or c-Jun), a fusion protein (comprising an E3 binding region,
XX a kinase recognition domain and an enzyme capable of producing a
XX detectable enzymatic product, where the kinase recognition domain is the
XX domain of beta-catenin, HIV protein VPU, p27, Bcl-2 or c-Jun), an
XX isolated genetic molecule encoding one of the above fusion proteins, a
XX vector capable of expressing the above genetic molecule and a cell
XX transfected with the above vector. Expression of the label requires
XX phosphorylation of the phosphorylation substrate by the kinase. The
XX kinase recognition domain is altered to include a consensus recognition
XX motif for the kinase (e.g. AKT kinase). The invention is useful to study
XX kinase activity in situ and to screen for molecules that modulate kinase
XX activities in situ, for example in drug discovery. The invention allows
XX for information on multiple kinases to be provided simultaneously, which
XX prior art does not provide. The present sequence is the wild-type region
XX of Beta-catenin, which may be mutated to an AKT (not defined)
XX phosphorylation site.
XX
SQ Sequence 17 AA;
XX
Query Match 25.0%; Score 31; DB 7; Length 17;
Best Local Similarity 35.7%; Pred. No. 8.2e+02;
Matches 5; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
QY 9 RQOFIQSVLNNGAT 22
Db 4 QQSYLDGSHSGAT 17

```

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OM protein - protein search, using sw model

Run on: January 26, 2006, 07:50:06 ; Search time 22.5517 Seconds
(without alignments)
87.985 Million cell updates/sec

Title: US-09-662-293-8

Perfect score: 124
Sequence: 1 DMAQNYKRRQFIQSVMNGATRG 24

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 229350

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Issued Patents AA: *
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2: /cgn2_6/ptodata/1/1aa/6_COMB.pep: *
3: /cgn2_6/ptodata/1/1aa/H_COMB.pep: *
4: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep: *
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6: /cgn2_6/ptodata/1/1aa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	25.0	9	2	US-09-935-430-132
2	31	25.0	10	2	US-09-935-430-157
3	31	25.0	10	2	US-09-935-430-621
4	31	25.0	12	1	US-08-973-563A-37
5	31	25.0	12	1	US-08-973-559-37
6	31	25.0	12	1	US-08-926-666-14
7	31	25.0	14	2	US-08-505-250-14
8	31	25.0	14	2	US-08-505-250-14
9	31	25.0	16	2	US-09-073-009-49
10	31	25.0	16	2	US-09-073-010-49
11	30	24.2	12	2	US-09-462-118-30
12	30	24.2	18	2	US-09-623-548A-1034
13	30	24.2	18	2	US-09-657-276-1034
14	30	24.2	18	1	PCT-US93-03748-1
15	28.5	23.0	18	1	US-08-816-105A-14
16	28	22.6	10	2	US-09-935-430-180
17	28	22.6	10	2	US-09-935-430-125
18	28	22.6	12	2	US-09-411-706-6
19	28	22.6	13	2	US-09-935-032-6
20	28	22.6	13	2	US-09-543-940-9
21	28	22.6	15	1	US-07-918-181A-20
22	28	22.6	15	1	US-08-231-575-20
23	28	22.6	15	4	PCT-US93-06928-20
24	28	22.6	16	1	US-08-346-849-58
25	28	22.6	16	1	US-08-346-849-59
26	28	22.6	16	1	US-08-934-222-60
27	28	22.6	16	1	US-08-933-402-60
28	28	22.6	16	1	US-09-207-621-60
29	28	22.6	16	1	US-08-293-284A-58
30	28	22.6	16	1	US-08-293-284A-59
31	28	22.6	16	1	US-08-532-818-60
32	28	22.6	16	2	US-09-231-797-60
33	28	22.6	16	2	US-08-934-224-60
34	28	22.6	16	2	US-08-933-443-60
35	28	22.6	16	2	US-08-934-223-60
36	28	22.6	16	2	US-09-413-992-60
37	28	22.6	16	2	US-08-898-300-58
38	28	22.6	16	2	US-08-898-300-59
39	28	22.6	16	2	US-08-824-513-58
40	28	22.6	16	2	US-08-824-513-59
41	28	22.6	21	1	US-08-280-373B-5
42	27	21.8	9	2	US-09-935-430-114
43	27	21.8	9	2	US-09-935-430-130
44	27	21.8	9	2	US-09-935-430-492
45	27	21.8	10	2	US-08-159-339A-932
46	27	21.8	10	2	US-08-159-339A-992
47	27	21.8	12	1	US-07-598-416-1
48	27	21.8	12	1	US-08-441-818-1
49	27	21.8	12	1	US-08-973-563A-36
50	27	21.8	12	1	US-08-973-559-36
51	27	21.8	12	1	US-08-628-183-1
52	27	21.8	12	2	US-09-226-666-13
53	27	21.8	14	1	US-08-082-849B-19
54	27	21.8	14	4	PCT-US94-01624-19
55	27	21.8	15	2	US-09-009-953-129
56	27	21.8	16	1	US-08-480-190-58
57	27	21.8	16	1	US-08-488-379-58
58	27	21.8	16	2	US-09-171-705-16
59	27	21.8	16	2	US-09-009-953-187
60	27	21.8	16	2	US-08-475-399A-58
61	27	21.8	16	2	US-09-311-784A-315
62	27	21.8	16	2	US-08-077-255A-58
63	27	21.8	16	2	US-09-657-757-16
64	27	21.8	16	4	PCT-US93-07545-58
65	27	21.8	17	1	US-08-467-420A-10
66	27	21.8	17	1	US-08-470-110A-10
67	27	21.8	17	1	US-08-667-769A-10
68	27	21.8	17	1	US-08-940-371-10
69	27	21.8	17	2	US-08-637-647-10
70	27	21.8	17	2	US-09-563-222C-26
71	27	21.8	17	2	US-09-830-748B-11
72	27	21.8	17	2	US-10-700-740-10
73	27	21.8	17	4	PCT-US95-17082A-10
74	27	21.8	21	2	US-09-674-674D-45
75	26.5	21.4	20	1	US-08-107-676-22
76	26.5	21.4	20	2	US-09-295-820-22
77	26.5	21.4	20	2	US-08-406-597-1
78	26	21.0	10	1	US-08-556-530-1
79	26	21.0	10	1	US-08-556-530-1
80	26	21.0	10	2	US-09-270-542-30
81	26	21.0	11	1	US-08-471-044-16
82	26	21.0	11	1	US-08-471-044-16
83	26	21.0	11	1	US-08-463-483A-16
84	26	21.0	11	1	US-08-471-046A-16
85	26	21.0	11	1	US-08-470-566B-16
86	26	21.0	11	1	US-08-838-119B-16
87	26	21.0	11	1	US-08-766-858A-44
88	26	21.0	11	1	US-08-469-834-16
89	26	21.0	11	2	US-09-300-529-16
90	26	21.0	11	2	US-09-333-336A-16
91	26	21.0	11	2	US-09-233-352A-16
92	26	21.0	11	2	US-09-402-036-16
93	26	21.0	11	2	US-09-904-226-16
94	26	21.0	12	1	US-08-392-973A-2
95	26	21.0	12	1	US-08-973-563A-29
96	26	21.0	12	1	US-08-973-559-29
97	26	21.0	12	2	US-08-933-235-9
98	26	21.0	12	2	US-09-147-208-20
99	26	21.0	12	2	US-08-469-260A-480
100	26	21.0	12	2	US-09-434-476A-19

ALIGNMENTS

```
RESULT 1
US-09-935-430-132
; Sequence 132, Application US/09935430
; Patent No. 6863892
; GENERAL INFORMATION:
; APPLICANT: PARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-ELD, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/09/935,430
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 132
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-935-430-132

Query Match          25.0%; Score 31; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy          15 SVLNNGAT 22
|:|||||
Db          1 SLNNGLT 8

RESULT 2
US-09-935-430-157
; Sequence 157, Application US/09935430
; Patent No. 6863892
; GENERAL INFORMATION:
; APPLICANT: PARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-ELD, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/09/935,430
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 157
; LENGTH: 10
; TYPE: PRT
```

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-935-430-157

Query Match          25.0%; Score 31; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 79;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy          15 SVLNNGAT 22
|:|||||
Db          1 SLNNGLT 8

RESULT 3
US-09-935-430-621
; Sequence 621, Application US/09935430
; Patent No. 6863892
; GENERAL INFORMATION:
; APPLICANT: PARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-ELD, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/09/935,430
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 621
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-935-430-621

Query Match          25.0%; Score 31; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 79;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy          15 SVLNNGAT 22
|:|||||
Db          2 SLNNGLT 9

RESULT 4
US-08-973-563A-37
; Sequence 37, Application US/08973563A
; Patent No. 5885965
; GENERAL INFORMATION:
; APPLICANT: Oppenheim, Frank G.
; APPLICANT: Xu, Tao
; APPLICANT: Spacciopoli, Peter
; APPLICANT: Roberts, F. D.
; APPLICANT: Friden, Philip M.
; TITLE OF INVENTION: Anti-Fungal D-Amino Acid Histatin-Based
; TITLE OF INVENTION: Peptides
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Millicia Drive
; CITY: Lexington
; STATE: MA
```

```

; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/973,563A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,273
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: PER95-02A2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 781-861-6240
; TELEFAX: 781-861-9540
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..12
; OTHER INFORMATION: /note="At least one amino acid
; OTHER INFORMATION: must have a D configuration."
; US-08-973-563A-37

Query Match 25.0%; Score 31; DB 1; Length 12;
Best Local Similarity 55.6%; Pred. No. 98;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 QNYKYRQOF 12
DB 3 QHHGYKQOF 11

RESULT 5
US-08-973-559-37
; Sequence 37, Application US/08973559
; Patent No. 5912230
; GENERAL INFORMATION:
; APPLICANT: OPENHEIM, FRANK G.
; APPLICANT: XU, TAO
; APPLICANT: ROBERTS, F. D.
; APPLICANT: SPACCIAPOLI, PETER
; APPLICANT: FRIDEN, PHILIP M.
; TITLE OF INVENTION: Anti-Fungal and Anti-Bacterial
; TITLE OF INVENTION: Histatin-Based Peptides
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Miltia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/973,559
; FILING DATE: 07-JUN-1996
; CLASSIFICATION: 514

```

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/481,888
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: PER95-01A2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 781-861-6240
; TELEFAX: 781-861-9540
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-973-559-37

Query Match 25.0%; Score 31; DB 1; Length 12;
Best Local Similarity 55.6%; Pred. No. 98;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 QNYKYRQOF 12
DB 3 QHHGYKQOF 11

RESULT 6
US-09-226-666-14
; Sequence 14, Application US/09226666A
; Patent No. 6528488
; GENERAL INFORMATION:
; APPLICANT: Spacciapoli, Peter
; APPLICANT: Rotheisen, David M.
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: METHOD FOR TREATING CYSTIC FIBROSIS
; FILE REFERENCE: 50032/007001
; CURRENT APPLICATION NUMBER: US/09/226,666A
; CURRENT FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Derived from Homo sapiens
; US-09-226-666-14

Query Match 25.0%; Score 31; DB 2; Length 12;
Best Local Similarity 55.6%; Pred. No. 98;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 QNYKYRQOF 12
DB 3 QHHGYKQOF 11

RESULT 7
US-08-505-250-14
; Sequence 14, Application US/08505250
; Patent No. 6183983
; GENERAL INFORMATION:
; APPLICANT: Sato, Haruya
; APPLICANT: Yamamoto, Keiji
; APPLICANT: Suzuki, Kokichi
; APPLICANT: Ikeda, Masahiro
; APPLICANT: Sakagami, Masahiro
; APPLICANT: Taniguchi, Makoto
; TITLE OF INVENTION: PROTEIN MODIFICATION METHOD
; FILE REFERENCE: 110-511
; CURRENT APPLICATION NUMBER: US/08/505,250

```

CURRENT FILING DATE: 1995-11-29
; EARLIER APPLICATION NUMBER: PCT/JP95/00298
; EARLIER FILING DATE: 1995-02-27
; EARLIER APPLICATION NUMBER: JP 198187/94
; EARLIER FILING DATE: 1994-08-23
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-08-505-250-14

Query Match 25.0%; Score 31; DB 2; Length 14;
Best Local Similarity 58.3%; Pred. No. 1.2e+02;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 7 KYROQFIQSVLN 18
| | | | |
Db 3 KKRSHFDQDVLN 14

RESULT 8
; US-08-505-250-14
; Sequence 14, Application US/08505250
; Patent No. 6322996
; GENERAL INFORMATION:
; APPLICANT: Sato, Haruya
; APPLICANT: Yamamoto, Keiji
; APPLICANT: Suzuki, Kokichi
; APPLICANT: Ikeda, Masahiro
; APPLICANT: Sakagami, Masahiro
; APPLICANT: Taniguchi, Makoto
; TITLE OF INVENTION: PROTEIN MODIFICATION METHOD
; FILE REFERENCE: 110-511
; CURRENT APPLICATION NUMBER: US/08/505,250
; CURRENT FILING DATE: 1995-11-29
; PRIOR APPLICATION NUMBER: PCT/JP95/00298
; PRIOR FILING DATE: 1995-02-27
; PRIOR APPLICATION NUMBER: JP 198187/94
; PRIOR FILING DATE: 1994-08-23
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-08-505-250-14

Query Match 25.0%; Score 31; DB 2; Length 14;
Best Local Similarity 58.3%; Pred. No. 1.2e+02;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 7 KYROQFIQSVLN 18
| | | | |
Db 3 KKRSHFDQDVLN 14

RESULT 9
; US-09-073-009-49
; Sequence 49, Application US/09073009
; Patent No. 6555653
; GENERAL INFORMATION:
; APPLICANT: Alderson, Mark
; APPLICANT: Dillon, Davin C.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Campos-Neto, Antonio

TUBERCULOSIS AND ME
; TITLE OF INVENTION: COMPOUNDS AND DIAGNOSIS OF
; NUMBER OF SEQUENCES: 144
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY
; STREET: 6300 Columbia Center, 701 Fifth Ave.
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/073,009
; FILING DATE: 05-MAY-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.441C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-8900
; TELEFAX: 206-682-6031
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium tuberculosis
US-09-073-009-49

Query Match 25.0%; Score 31; DB 2; Length 16;
Best Local Similarity 33.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

OY 5 NYKROQFIQSVLNN 19
| | | | |
Db 2 NYEQEQASQQLLS 16

RESULT 10
; US-09-073-010-49
; Sequence 49, Application US/09073010
; Patent No. 6613881
; GENERAL INFORMATION:
; APPLICANT: Alderson, Mark
; APPLICANT: Dillon, Davin C.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Campos-Neto, Antonio
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS OF TUBERCULOSIS AND
; NUMBER OF SEQUENCES: 144
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY
; STREET: 6300 Columbia Center, 701 Fifth Ave.
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/073,010
; FILING DATE: 05-MAY-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:


```

PRT-09-657-276-1034
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: 60/159,783
PRIOR FILING DATE: 1999-10-18
NUMBER OF SEQ ID NOS: 1617
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1034
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-623-548A-1034

Query Match      24.2%   Score 30; DB 2; Length 18;
Best Local Similarity 41.7%; Pred. No. 2.3e+02;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0

QY      3 AONKYRQOFIQ 14
       |::|::|::|
Db      7 AASHIYQNQFVQ 18

RESULT 13
US-09-657-276-1034
Sequence 1034, Application US/09657276
Patent No. 6887470
GENERAL INFORMATION:
APPLICANT: ConjuChem, Inc.
APPLICANT: Bridon, Dominique
APPLICANT: Ezrin, Alan
APPLICANT: Milner, Peter
APPLICANT: Holmes, Darren
APPLICANT: Thibaudeau, Karen
TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
TITLE OF INVENTION: COMPONENTS
FILE REFERENCE: 2110
CURRENT APPLICATION NUMBER: US/09/657,276
CURRENT FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: 60/134,406
PRIOR FILING DATE: 1999-05-17
PRIOR APPLICATION NUMBER: 60/153,406
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: 60/159,783
PRIOR FILING DATE: 1999-10-18
NUMBER OF SEQ ID NOS: 1617
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1034
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-657-276-1034

Query Match      24.2%   Score 30; DB 2; Length 18;
Best Local Similarity 41.7%; Pred. No. 2.3e+02;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0

QY      3 AONKYRQOFIQ 14
       |::|::|::|
Db      7 AASHIYQNQFVQ 18

RESULT 14
PCT-US93-03748-1
Sequence 1, Application PC/TUS9303748
GENERAL INFORMATION:
APPLICANT: Howard, Russell J.
APPLICANT: Leung, Lawrence L.K.
TITLE OF INVENTION: Modulation of Thrombospondin-CD36 Interactions

```


RESULT 17
US-09-935-430-425
; Sequence 425, Application US/09935430
; Patent No. 6663892
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: APAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLOVITZ, PIA
; APPLICANT: JAKOBOWITZ, AVA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/09/935.430
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 425
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-935-430-425

Query Match 22.6%; Score 28; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 12 FIOSLNNG 20
| : |||
Db 1 FIOSLNNG 9

RESULT 18
US-09-411-706-6
; Sequence 6, Application US/09411706
; Patent No. 6312956
; GENERAL INFORMATION:
; APPLICANT: Lane, Kirk B.
; TITLE OF INVENTION: NUCLEAR TARGETED PEPTIDE NUCLEIC ACID OLIGOMER
; FILE REFERENCE: 3765
; CURRENT APPLICATION NUMBER: US/09/411.706
; CURRENT FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 6
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: consensus NLS
; OTHER INFORMATION: peptide
US-09-411-706-6

Query Match 22.6%; Score 28; DB 2; Length 12;
Best Local Similarity 57.1%; Pred. No. 3.1e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 6 YKYRQGF 12
| : |||
Db 5 YKYRPEY 11

RESULT 19

US-09-935-032-6
; Sequence 6, Application US/09935032
; Patent No. 6623966
; GENERAL INFORMATION:
; APPLICANT: Lane, Kirk B.
; TITLE OF INVENTION: NUCLEAR TARGETED PEPTIDE NUCLEIC ACID OLIGOMER
; FILE REFERENCE: 3765
; CURRENT APPLICATION NUMBER: US/09/935.032
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: US/09/411.706
; PRIOR FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 6
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: consensus NLS
US-09-935-032-6

Query Match 22.6%; Score 28; DB 2; Length 12;
Best Local Similarity 57.1%; Pred. No. 3.1e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 6 YKYRQGF 12
| : |||
Db 5 YKYRPEY 11

RESULT 20
US-09-543-940-9
; Sequence 9, Application US/09543940
; Patent No. 6613742
; GENERAL INFORMATION:
; APPLICANT: Huang, Ziwei
; APPLICANT: Zhou, Zhaowen
; APPLICANT: Luo, Jiansong
; APPLICANT: Luo, Jiansong
; TITLE OF INVENTION: Chemokine-Derived Synthetic Peptides
; FILE REFERENCE: 8321-40
; CURRENT APPLICATION NUMBER: US/09/543.940
; CURRENT FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/128,106
; PRIOR FILING DATE: 1999-04-07
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 9
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide containing segment from C-terminal region
; OTHER INFORMATION: of human SDF-1 protein
US-09-543-940-9

Query Match 22.6%; Score 28; DB 2; Length 13;
Best Local Similarity 33.3%; Pred. No. 3.4e+02;
Matches 4; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 7 KYRQFIQSVLN 18
| : |||
Db 2 KWIQVEYLEKALN 13

RESULT 21
US-07-918-181A-20
; Sequence 20, Application US/07918181A
; Patent No. 5338833
; GENERAL INFORMATION:
; APPLICANT: Fowlkes, Dana M.

TITLE OF INVENTION: C-Terminal IL-6 Muteins
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Imclone Systems Incorporated
STREET: 180 Varick Street
CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10014
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/918,181A
FILING DATE: 23-JUL-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sheets, Eric J.
REGISTRATION NUMBER: 30,326
REFERENCE/DOCKET NUMBER: FOM-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLECULE TYPE: linear
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: C-terminal
US-07-918-181A-20
Query Match 22.6%; Score 28; DB 1; Length 15;
Best Local Similarity 53.3%; Pred. No. 4e+02;
Matches 8; Conservative 2; Mismatches 3; Indels 2; Gaps 1;
QY 10 QQFIQSVLNGATRO 24
Db 2 QEFQSSLR--ALRQ 14
RESULT 22
US-08-231-575-20
Sequence 20, Application US/08231575
Patent No. 5565336
GENERAL INFORMATION:
APPLICANT: Fowikes, Dana M.
TITLE OF INVENTION: C-Terminal IL-6 Muteins
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Imclone Systems Incorporated
STREET: 180 Varick Street
CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10014
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/231,575
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/918,181
FILING DATE: 23-JUL-1992

ATTORNEY/AGENT INFORMATION:
NAME: Sheets, Eric J.
REGISTRATION NUMBER: 30,326
REFERENCE/DOCKET NUMBER: FOM-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLECULE TYPE: linear
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: C-terminal
US-08-231-575-20
Query Match 22.6%; Score 28; DB 1; Length 15;
Best Local Similarity 53.3%; Pred. No. 4e+02;
Matches 8; Conservative 2; Mismatches 3; Indels 2; Gaps 1;
QY 10 QQFIQSVLNGATRO 24
Db 2 QEFQSSLR--ALRQ 14
RESULT 23
PCT-US93-06928-20
Sequence 20, Application PC/TUS9306928
GENERAL INFORMATION:
APPLICANT: Fowikes, Dana M.
TITLE OF INVENTION: Carboxy Terminal IL-6 Muteins
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Imclone Systems Incorporated
STREET: 180 Varick Street
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 11014
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06928
FILING DATE: 19930723
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/918,181
FILING DATE: 23-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Felt, Irving N.
REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: FOM-2-T
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLECULE TYPE: linear
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: C-terminal
PCT-US93-06928-20

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OM protein - protein search, using sw model

Run on: January 26, 2006, 08:04:12 : Search time 78 seconds
(without alignments)
128.563 Million cell updates/sec

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Perfect score: 124
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Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqe, 417829326 residues

Total number of hits satisfying chosen parameters: 369445

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

Published Applications AA Main:*

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- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	26.6	17	4	US-10-057-789-250 Sequence 250, App
2	33	26.6	17	4	US-10-212-628-250 Sequence 250, App
3	31	25.0	9	3	US-09-935-430-132 Sequence 132, App
4	31	25.0	9	4	US-10-277-292-132 Sequence 132, App
5	31	25.0	9	4	US-10-280-340-132 Sequence 132, App
6	31	25.0	9	5	US-10-990-137-132 Sequence 132, App
7	31	25.0	10	3	US-09-935-430-157 Sequence 157, App
8	31	25.0	10	3	US-09-935-430-621 Sequence 621, App
9	31	25.0	10	4	US-10-277-292-157 Sequence 157, App
10	31	25.0	10	4	US-10-277-292-621 Sequence 621, App
11	31	25.0	10	4	US-10-280-340-157 Sequence 157, App
12	31	25.0	10	4	US-10-280-340-621 Sequence 621, App
13	31	25.0	10	5	US-10-990-137-157 Sequence 157, App
14	31	25.0	10	5	US-10-990-137-621 Sequence 621, App
15	31	25.0	12	3	US-09-226-666-14 Sequence 14, App
16	31	25.0	14	5	US-10-813-638-1312 Sequence 1312, App
17	31	25.0	16	3	US-09-073-009-49 Sequence 49, App
18	31	25.0	16	3	US-09-023-588-49 Sequence 49, App
19	31	25.0	16	3	US-09-793-306-49 Sequence 49, App
20	30	24.2	10	5	US-10-936-237-11 Sequence 11, App
21	30	24.2	12	4	US-10-247-946-30 Sequence 30, App
22	30	24.2	12	4	US-10-251-526-30 Sequence 30, App
23	30	24.2	15	6	US-11-009-460-104 Sequence 104, App
24	30	24.2	18	4	US-10-197-954-35 Sequence 35, App
25	30	24.2	18	5	US-10-760-085-35 Sequence 35, App
26	30	24.2	18	6	US-11-066-697-1034 Sequence 1034, App
27	30	24.2	19	5	US-10-479-166-17 Sequence 17, App

28	29	23.4	16	5	US-10-656-721-13 Sequence 13, App
29	29	23.4	17	5	US-10-837-269-156 Sequence 156, App
30	29	23.4	17	5	US-10-837-269-157 Sequence 157, App
31	29	23.4	19	5	US-10-837-269-157 Sequence 157, App
32	29	23.4	19	5	US-10-837-269-160 Sequence 160, App
33	29	23.4	21	3	US-09-853-830-45 Sequence 45, App
34	29	23.4	21	4	US-10-139-146-3 Sequence 3, App
35	29	23.4	21	4	US-10-133-973-14 Sequence 14, App
36	29	23.4	21	4	US-10-438-729-45 Sequence 45, App
37	28.5	23.0	17	4	US-10-471-220-47 Sequence 47, App
38	28.5	23.0	21	4	US-10-745-069-37 Sequence 37, App
39	28.5	23.0	21	4	US-10-768-288A-37 Sequence 37, App
40	28.5	23.0	21	4	US-10-780-325A-37 Sequence 37, App
41	28.5	23.0	21	5	US-10-869-649-37 Sequence 37, App
42	28	22.6	10	3	US-09-935-430-180 Sequence 180, App
43	28	22.6	10	3	US-09-935-430-425 Sequence 425, App
44	28	22.6	10	4	US-10-277-292-180 Sequence 180, App
45	28	22.6	10	4	US-10-277-292-425 Sequence 425, App
46	28	22.6	10	4	US-10-280-340-180 Sequence 180, App
47	28	22.6	10	4	US-10-280-340-425 Sequence 425, App
48	28	22.6	10	5	US-10-990-137-180 Sequence 180, App
49	28	22.6	13	5	US-10-990-137-425 Sequence 425, App
50	28	22.6	13	5	US-10-222-703A-867 Sequence 867, App
51	28	22.6	15	4	US-10-203-915A-248 Sequence 248, App
52	28	22.6	15	4	US-10-203-915A-249 Sequence 249, App
53	28	22.6	15	5	US-10-886-773-130 Sequence 130, App
54	28	22.6	15	5	US-10-886-773-131 Sequence 131, App
55	28	22.6	15	5	US-10-505-929-525 Sequence 525, App
56	28	22.6	15	5	US-10-505-929-526 Sequence 526, App
57	28	22.6	15	5	US-10-505-929-527 Sequence 527, App
58	28	22.6	15	5	US-10-505-929-528 Sequence 528, App
59	28	22.6	15	5	US-10-505-929-529 Sequence 529, App
60	28	22.6	15	5	US-10-505-929-530 Sequence 530, App
61	28	22.6	15	5	US-10-505-929-531 Sequence 531, App
62	28	22.6	16	4	US-10-390-472-58 Sequence 58, App
63	28	22.6	16	4	US-10-390-472-59 Sequence 59, App
64	28	22.6	16	6	US-11-065-970-19 Sequence 19, App
65	28	22.6	17	5	US-10-996-316-170 Sequence 170, App
66	28	22.6	17	6	US-11-036-098-10 Sequence 10, App
67	28	22.6	20	5	US-10-482-284A-68 Sequence 68, App
68	28	22.6	20	5	US-10-690-276-311 Sequence 311, App
69	28	22.6	21	5	US-10-505-929-584 Sequence 584, App
70	27.5	22.2	18	4	US-10-685-998-99 Sequence 99, App
71	27.5	22.2	20	6	US-11-107-086-35 Sequence 35, App
72	27	21.8	9	3	US-09-935-430-114 Sequence 114, App
73	27	21.8	9	3	US-09-935-430-130 Sequence 130, App
74	27	21.8	9	3	US-09-935-430-192 Sequence 192, App
75	27	21.8	9	4	US-10-062-257-9 Sequence 9, App
76	27	21.8	9	4	US-10-277-292-114 Sequence 114, App
77	27	21.8	9	4	US-10-277-292-130 Sequence 130, App
78	27	21.8	9	4	US-10-277-292-492 Sequence 492, App
79	27	21.8	9	4	US-10-280-340-114 Sequence 114, App
80	27	21.8	9	4	US-10-280-340-132 Sequence 132, App
81	27	21.8	9	4	US-10-280-340-492 Sequence 492, App
82	27	21.8	9	5	US-10-865-478-133 Sequence 133, App
83	27	21.8	9	5	US-10-990-137-114 Sequence 114, App
84	27	21.8	9	5	US-10-990-137-130 Sequence 130, App
85	27	21.8	9	5	US-10-990-137-492 Sequence 492, App
86	27	21.8	12	3	US-09-226-666-13 Sequence 13, App
87	27	21.8	14	4	US-10-953-901-594 Sequence 594, App
88	27	21.8	15	4	US-10-103-395-129 Sequence 129, App
89	27	21.8	16	3	US-09-775-805-8 Sequence 8, App
90	27	21.8	16	4	US-10-103-395-187 Sequence 187, App
91	27	21.8	16	4	US-10-371-525-315 Sequence 315, App
92	27	21.8	16	4	US-10-371-525-315 Sequence 315, App
93	27	21.8	16	4	US-10-371-525-315 Sequence 315, App
94	27	21.8	16	4	US-10-371-525-315 Sequence 315, App
95	27	21.8	16	4	US-10-371-525-315 Sequence 315, App
96	27	21.8	17	3	US-09-563-222-26 Sequence 26, App
97	27	21.8	17	3	US-09-995-529-70 Sequence 70, App
98	27	21.8	17	3	US-09-995-529-70 Sequence 70, App
99	27	21.8	17	3	US-09-995-529-76 Sequence 76, App
100	27	21.8	17	3	US-09-995-529-76 Sequence 76, App

ALIGNMENTS

RESULT 1

US-10-057-789-250
; Sequence 250, Application US/10057789
; Publication No. US20030082522a1
; GENERAL INFORMATION:
; APPLICANT: Paul Haynes
; APPLICANT: Jing Wei
; APPLICANT: John Yates
; APPLICANT: Nancy Andon
; TITLE OF INVENTION: DIFFERENTIAL LABELING FOR QUANTITATIVE
; TITLE OF INVENTION: ANALYSIS OF COMPLEX PROTEIN MIXTURES
; FILE REFERENCE: NADII.022A
; CURRENT APPLICATION NUMBER: US/10/057,789
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 60/264,576
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 60/305,232
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 311
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 250
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 4
; OTHER INFORMATION: Xaa = Modified Cysteine
US-10-057-789-250

Query Match 26.6%; Score 33; DB 4; Length 17;
Best Local Similarity 43.8%; Pred. No. 3.6e+02;
Matches 7; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Oy 8 YRQFIQSVLNGATR 23

Db 2 YTXQFVDMVLPNTALK 17

RESULT 2
US-10-212-628-250
; Sequence 250, Application US/10212628
; Publication No. US20030087329a1
; GENERAL INFORMATION:
; APPLICANT: Paul Haynes
; APPLICANT: Jing Wei
; APPLICANT: John Yates
; APPLICANT: Nancy Andon
; TITLE OF INVENTION: DIFFERENTIAL LABELING FOR QUANTITATIVE
; TITLE OF INVENTION: ANALYSIS OF COMPLEX PROTEIN MIXTURES
; FILE REFERENCE: NADII.022CPI
; CURRENT APPLICATION NUMBER: US/10/212,628
; CURRENT FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 60/264,576
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 60/305,232
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 10/057,789
; PRIOR FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 311
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 250
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 4
; OTHER INFORMATION: Xaa = Modified Cysteine
US-10-057-789-250

Query Match 26.6%; Score 33; DB 4; Length 17;
Best Local Similarity 43.8%; Pred. No. 3.6e+02;
Matches 7; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Oy 8 YRQFIQSVLNGATR 23

Db 2 YTXQFVDMVLPNTALK 17

RESULT 3
US-09-935-430-132
; Sequence 132, Application US/09935430
; Publication No. US20030017466a1
; GENERAL INFORMATION:
; APPLICANT: HUBERT, RENE
; APPLICANT: RAYTANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALILITA-EID, PIA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/277,292
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22

Query Match 25.0%; Score 31; DB 3; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 15 SVLNGAT 22

Db 1 SLVNGAT 8

RESULT 4
US-10-277-292-132
; Sequence 132, Application US/10277292
; Publication No. US20030199470A1
; GENERAL INFORMATION:
; APPLICANT: FARI, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAYTANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALILITA-EID, PIA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/277,292
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22

OTHER INFORMATION: Xaa = Modified Cysteine
US-10-212-628-250

Query Match 26.6%; Score 33; DB 4; Length 17;
Best Local Similarity 43.8%; Pred. No. 3.6e+02;
Matches 7; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Oy 8 YRQFIQSVLNGATR 23

Db 2 YTXQFVDMVLPNTALK 17

RESULT 3

US-09-935-430-132
; Sequence 132, Application US/09935430
; Publication No. US20030017466a1
; GENERAL INFORMATION:
; APPLICANT: FARI, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAYTANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALILITA-EID, PIA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/09/935,430
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 132
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-935-430-132

Query Match 25.0%; Score 31; DB 3; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 15 SVLNGAT 22

Db 1 SLVNGAT 8

RESULT 4
US-10-277-292-132
; Sequence 132, Application US/10277292
; Publication No. US20030199470A1
; GENERAL INFORMATION:
; APPLICANT: FARI, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAYTANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALILITA-EID, PIA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/277,292
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22

Query Match 25.0%; Score 31; DB 3; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 15 SVLNGAT 22

Db 1 SLVNGAT 8

RESULT 4
US-10-277-292-132
; Sequence 132, Application US/10277292
; Publication No. US20030199470A1
; GENERAL INFORMATION:
; APPLICANT: FARI, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAYTANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALILITA-EID, PIA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/277,292
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22

Query Match 25.0%; Score 31; DB 3; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 15 SVLNGAT 22

Db 1 SLVNGAT 8


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; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 132
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-277-292-132
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Query Match      25.0%; Score 31; DB 4; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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QY      15 SVLNNGAT 22
      |||||
Db      1 SLNNGLT 8
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RESULT 5
; Sequence 132, Application US/10280340
; Publication No. US20030207835A1
; GENERAL INFORMATION:
; APPLICANT: FARRIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RATTANO, ARTHUR
; APPLICANT: APEAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/280,340
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 132
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-280-340-132
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Query Match      25.0%; Score 31; DB 4; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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QY      15 SVLNNGAT 22
      |||||
Db      1 SLNNGLT 8
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RESULT 6
; Sequence 132, Application US/10990137
; Publication No. US20050227253A1
; GENERAL INFORMATION:
; APPLICANT: FARRIS, MARY
; APPLICANT: HUBERT, RENE
```

```

; APPLICANT: RATTANO, ARTHUR
; APPLICANT: APEAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 511582005003
; CURRENT APPLICATION NUMBER: US/10/990,137
; PRIOR FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: 09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 132
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-990-137-132
```

```

Query Match      25.0%; Score 31; DB 5; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      15 SVLNNGAT 22
      |||||
Db      1 SLNNGLT 8
```

```

RESULT 7
; Sequence 157, Application US/09935430
; Publication No. US20030017466A1
; GENERAL INFORMATION:
; APPLICANT: FARRIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RATTANO, ARTHUR
; APPLICANT: APEAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 157
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-935-430-157
```

```

Query Match      25.0%; Score 31; DB 3; Length 10;
Best Local Similarity 75.0%; Pred. No. 4.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      15 SVLNNGAT 22
```

Db 1 SLINNGLT 8

RESULT 8

US-09-935-430-621
; Sequence 621, Application US/09935430
; Publication No. US20030017466A1
; GENERAL INFORMATION:
; APPLICANT: PARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 621
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-935-430-621

Query Match 25.0%; Score 31; DB 3; Length 10;
Best Local Similarity 75.0%; Pred. No. 4.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 15 SVLNNGAT 22
|:|||||
Db 2 SLINNGLT 9

RESULT 9

US-10-277-292-157
; Sequence 157, Application US/10277292
; Publication No. US20030199470A1
; GENERAL INFORMATION:
; APPLICANT: PARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/277,292
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 157
; LENGTH: 10

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-277-292-157

Query Match 25.0%; Score 31; DB 4; Length 10;
Best Local Similarity 75.0%; Pred. No. 4.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 15 SVLNNGAT 22
|:|||||
Db 1 SLINNGLT 8

RESULT 10

US-10-277-292-621
; Sequence 621, Application US/10277292
; Publication No. US20030199470A1
; GENERAL INFORMATION:
; APPLICANT: PARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/277,292
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 621
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-277-292-621

Query Match 25.0%; Score 31; DB 4; Length 10;
Best Local Similarity 75.0%; Pred. No. 4.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 15 SVLNNGAT 22
|:|||||
Db 2 SLINNGLT 9

RESULT 11

US-10-280-340-157
; Sequence 157, Application US/10280340
; Publication No. US20030207835A1
; GENERAL INFORMATION:
; APPLICANT: PARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/280,340
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 157
; LENGTH: 10

```

FILE REFERENCE: 51158-20050.00
CURRENT APPLICATION NUMBER: US/10/280.340
CURRENT FILING DATE: 2002-10-25
PRIORITY APPLICATION NUMBER: US/09/935.430
PRIORITY FILING DATE: 2001-08-22
PRIORITY APPLICATION NUMBER: 60/227,098
PRIORITY FILING DATE: 2000-08-22
PRIORITY APPLICATION NUMBER: 60/282,739
PRIORITY FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 700
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 157
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-280-340-157

```

```

Query Match      25.0%; Score 31; DB 4; Length 10;
Best Local Similarity 75.0%; Pred. No. 4.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      15 SVLNNGAT 22
      |||||
Db      1 SLNNGLT 8

```

```

RESULT 12
US-10-280-340-621
Sequence 621, Application US/10280340
Publication No. US20030207835A1
GENERAL INFORMATION:
APPLICANT: PARIS, MARY
APPLICANT: HUBERT, RENE
APPLICANT: RAITANO, ARTHUR
APPLICANT: AFAR, DANIEL
APPLICANT: LEVIN, ELANA
APPLICANT: CHALLITA-EID, PIA
APPLICANT: JAKOBOWITZ, AVA
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7
TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
TITLE OF INVENTION: OTHER CANCERS
FILE REFERENCE: 51158-20050.00
CURRENT APPLICATION NUMBER: US/10/280.340
CURRENT FILING DATE: 2002-10-25
PRIORITY APPLICATION NUMBER: US/09/935.430
PRIORITY FILING DATE: 2001-08-22
PRIORITY APPLICATION NUMBER: 60/227,098
PRIORITY FILING DATE: 2000-08-22
PRIORITY APPLICATION NUMBER: 60/282,739
PRIORITY FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 700
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 621
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-280-340-621

```

```

Query Match      25.0%; Score 31; DB 4; Length 10;
Best Local Similarity 75.0%; Pred. No. 4.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      15 SVLNNGAT 22
      |||||
Db      2 SLNNGLT 9

```

```

RESULT 13
US-10-990-137-157

```

```

Sequence 157, Application US/10990137
Publication No. US20050227253A1
GENERAL INFORMATION:
APPLICANT: PARIS, MARY
APPLICANT: HUBERT, RENE
APPLICANT: RAITANO, ARTHUR
APPLICANT: AFAR, DANIEL
APPLICANT: LEVIN, ELANA
APPLICANT: CHALLITA-EID, PIA
APPLICANT: JAKOBOWITZ, AVA
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7
TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
TITLE OF INVENTION: OTHER CANCERS
FILE REFERENCE: 511582005003
CURRENT APPLICATION NUMBER: US/10/990.137
CURRENT FILING DATE: 2004-11-15
PRIORITY APPLICATION NUMBER: 09/935,430
PRIORITY FILING DATE: 2001-08-22
PRIORITY APPLICATION NUMBER: 60/282,739
PRIORITY FILING DATE: 2001-04-10
PRIORITY APPLICATION NUMBER: 60/227,098
PRIORITY FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 700
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 157
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-990-137-157

```

```

Query Match      25.0%; Score 31; DB 5; Length 10;
Best Local Similarity 75.0%; Pred. No. 4.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      15 SVLNNGAT 22
      |||||
Db      1 SLNNGLT 8

```

```

RESULT 14
US-10-990-137-621
Sequence 621, Application US/10990137
Publication No. US20050227253A1
GENERAL INFORMATION:
APPLICANT: PARIS, MARY
APPLICANT: HUBERT, RENE
APPLICANT: RAITANO, ARTHUR
APPLICANT: AFAR, DANIEL
APPLICANT: LEVIN, ELANA
APPLICANT: CHALLITA-EID, PIA
APPLICANT: JAKOBOWITZ, AVA
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7
TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
TITLE OF INVENTION: OTHER CANCERS
FILE REFERENCE: 511582005003
CURRENT APPLICATION NUMBER: US/10/990.137
CURRENT FILING DATE: 2004-11-15
PRIORITY APPLICATION NUMBER: 09/935,430
PRIORITY FILING DATE: 2001-08-22
PRIORITY APPLICATION NUMBER: 60/282,739
PRIORITY FILING DATE: 2001-04-10
PRIORITY APPLICATION NUMBER: 60/227,098
PRIORITY FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 700
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 621
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Peptide motif

```

US-10-990-137-621

Query Match 25.0%; Score 31; DB 5; Length 10;
Best Local Similarity 75.0%; Pred. No. 4.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 15 SVLNNGAT 22
Db 2 SLNNGLT 9

RESULT 15
US-09-226-666-14
Sequence 14, Application US/09226666A
Patent No. US20020077282A1

GENERAL INFORMATION:
APPLICANT: Spacciapoli, Peter
APPLICANT: Rothstein, David M.
APPLICANT: Friden, Phillip M.
TITLE OF INVENTION: METHOD FOR TREATING CYSTIC FIBROSIS
FILE REFERENCE: 50032/007001
CURRENT APPLICATION NUMBER: US/09/226.666A
CURRENT FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Derived from Homo sapiens
US-09-226-666-14

Query Match 25.0%; Score 31; DB 3; Length 12;
Best Local Similarity 55.6%; Pred. No. 5.1e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 4 QNYKYROOF 12
Db 3 QHGYKQOF 11

RESULT 16
US-10-813-638-1312

Sequence 1312, Application US/10813638
Publication No. US20040235026A1
GENERAL INFORMATION:
APPLICANT: Shinkets, Richard A.
APPLICANT: Leach, Martin D.
TITLE OF INVENTION: NUCLEIC ACIDS CONTAINING SINGLE NUCLEIC ACID POLYMORPHISMS AND ME
FILE REFERENCE: 15966-599
CURRENT APPLICATION NUMBER: US/10/813.638
CURRENT FILING DATE: 2004-03-29
PRIOR APPLICATION NUMBER: 60/163,783
PRIOR FILING DATE: 1999-11-24
NUMBER OF SEQ ID NOS: 1468
SOFTWARE: Curagen Patent Formatter Version 0.9
SEQ ID NO 1312
LENGTH: 14
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: VARIANT
LOCATION: (7)...(0)
OTHER INFORMATION: cSNP translation
US-10-813-638-1312

Query Match 25.0%; Score 31; DB 5; Length 14;
Best Local Similarity 60.0%; Pred. No. 6.1e+02;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DMAQNYKYRQ 10

Db 4 DRTANVXYRQ 13

RESULT 17
US-09-073-009-49
Sequence 49, Application US/09073009
Patent No. US20010012888A1

GENERAL INFORMATION:
APPLICANT: Alderson, Mark
APPLICANT: Dillon, Davin C.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Campos-Neco, Antonio
TITLE OF INVENTION: COMPOUNDS AND DIAGNOSIS OF
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY
STREET: 6300 Columbia Center, 701 Fifth Ave.
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104

TUBERCULOSIS AND ME

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073.009
FILING DATE: 05-MAY-1998

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Makl, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.441C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
TELEFAX: 206-682-6031

INFORMATION FOR SEQ ID NO: 49:

SEQUENCE CHARACTERISTICS:

LENGTH: 16 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

ORIGINAL SOURCE:

ORGANISM: Mycobacterium tuberculosis

US-09-073-009-49

Query Match 25.0%; Score 31; DB 3; Length 16;
Best Local Similarity 33.3%; Pred. No. 7e+02;
Matches 5; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy 5 NYKYRQFIQSVLNN 19
Db 2 NYEQEQASQOILIS 16

RESULT 18
US-09-023-588-49

Sequence 49, Application US/09023588
Patent No. US20020081579A1

GENERAL INFORMATION:

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Dillon, Davin C.

APPLICANT: Alderson, Mark R.

TITLE OF INVENTION: METHOD FOR THE ISOLATION OF NOVEL ANTIGENS

NUMBER OF SEQUENCES: 69

CORRESPONDENCE ADDRESS:

ADDRESSEE: SEED and BERRY LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: Washington

Query Match	25.0%	Score 31	DB 3	Length 16
Best Local Similarity	33.3%	Pred. NO.	7e+02	
Matches	5	Conservative	6	Mismatches 4
				Indels 0
				Gaps 0

; PRIOR FILING DATE: 1999-12-18
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Human
US-10-251-526-30

Query March 24.2%; Score 30; DB 4; Length 12;
Best Local Similarity 55.6%; Pred. No. 7.4e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 2 AONYKXRYQ 10
|::|::|::|
Db 1 LAENYKSOQ 9

RESULT 23
US-11-009-460-104
; Sequence 104, Application US//11009460
; Publication No. US20050181459A1
; GENERAL INFORMATION:
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis J.
; APPLICANT: CARTER, Graham
; TITLE OF INVENTION: METHOD FOR MAPPING AND ELIMINATING
; TITLE OF INVENTION: T-CELL EPITOPES
; FILE REFERENCE: MER-135
; CURRENT APPLICATION NUMBER: US/11/009,460
; CURRENT FILING DATE: 2004-12-10
; PRIOR APPLICATION NUMBER: PCT/EP03/06110
; PRIOR FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: EP02012919.3
; PRIOR FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 104
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Potential T-cell Epitopes
US-11-009-460-104

Query March 24.2%; Score 30; DB 6; Length 15;
Best Local Similarity 43.8%; Pred. No. 9.5e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 4; Gaps 1;

OY 8 YROQFIOSVLNNGATR 23
|::|::|::|::|
Db 2 YKSGY----LNNGPQR 13

RESULT 24
US-10-197-954-35
; Sequence 35, Application US//10197954
; Publication No. US20030119021A1
; GENERAL INFORMATION:
; APPLICANT: K"ster, Hubert
; APPLICANT: Siddiqi, Suhail
; APPLICANT: Little, Daniel
; TITLE OF INVENTION: Capture Compounds, Collections Thereof
; TITLE OF INVENTION: And Methods For Analyzing The Proteome And Complex
; TITLE OF INVENTION: Compositions
; FILE REFERENCE: 24743-2305
; CURRENT APPLICATION NUMBER: US//10/197,954
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 60/306,019
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/314,123
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 60/363,433

; PRIOR FILING DATE: 2002-03-11
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-197-954-35

Query March 24.2%; Score 30; DB 4; Length 18;
Best Local Similarity 41.7%; Pred. No. 1.2e+03;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 3 AONYKXRYQFIQ 14
|::|::|::|::|
Db 7 AASHIYONQFVQ 18

RESULT 25
US-10-760-085-35
; Sequence 35, Application US//10760085
; Publication No. US20050042771A1
; GENERAL INFORMATION:
; APPLICANT: Hubert, K"ster
; APPLICANT: Daniel Paul Little
; APPLICANT: Suhail Mahmood Siddiqi
; APPLICANT: Matthew Peter Grealish
; APPLICANT: Subramaniam Marappan
; APPLICANT: Chester Frederick Haseman III
; APPLICANT: Ping Yip
; TITLE OF INVENTION: Capture Compounds, Collections Thereof
; TITLE OF INVENTION: And Methods For Analyzing The Proteome And Complex
; TITLE OF INVENTION: Compositions
; FILE REFERENCE: 24743-2309
; CURRENT APPLICATION NUMBER: US/10/760,085
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: 60/441,398
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-760-085-35

Query March 24.2%; Score 30; DB 5; Length 18;
Best Local Similarity 41.7%; Pred. No. 1.2e+03;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 3 AONYKXRYQFIQ 14
|::|::|::|::|
Db 7 AASHIYONQFVQ 18

Search completed: January 26, 2006, 08:38:35
Job time : 79 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 26, 2006, 08:05:12 : Search time 4.55172 Seconds
(without alignments)
57.099 Million cell updates/sec

Title: US-09-662-293-8
Perfect score: 124
Sequence: 1 DMAQNYKXROQFIQSVLNGATRQ 24

Scoring table: BIOSUM62
Gapop 10.0, Gapext 0.5

Searched: 75621 seqs, 10829074 residues

Total number of hits satisfying chosen parameters: 37628

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

Published Applications AA New:*
1: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	26.6	19	7	US-11-033-039-1123 Sequence 1123, App
2	30	24.2	15	6	US-10-511-559-255 Sequence 255, App
3	30	24.2	15	6	US-10-511-559-255 Sequence 75, App
4	29.5	23.8	19	6	US-10-503-575-110 Sequence 110, App
5	28	22.6	11	7	US-11-045-024-2254 Sequence 2254, App
6	28	22.6	11	7	US-11-045-024-2254 Sequence 9528, App
7	28	22.6	13	6	US-10-945-6744-77 Sequence 77, App
8	28	22.6	15	7	US-11-045-024-13293 Sequence 13293, App
9	27	21.8	9	7	US-11-111-463-12 Sequence 12, App
10	27	21.8	13	6	US-10-511-559-254 Sequence 254, App
11	27	21.8	15	7	US-11-022-562-43 Sequence 43, App
12	27	21.8	15	7	US-11-022-562-44 Sequence 44, App
13	27	21.8	15	7	US-11-106-932-114 Sequence 114, App
14	27	21.8	15	7	US-11-045-024-13006 Sequence 13006, App
15	27	21.8	15	7	US-11-045-024-13016 Sequence 13016, App
16	27	21.8	16	6	US-10-973-977-8 Sequence 8, App
17	27	21.8	17	7	US-11-145-861-215 Sequence 215, App
18	27	21.8	19	7	US-11-033-039-1125 Sequence 1125, App
19	27	21.8	20	7	US-11-022-562-249 Sequence 249, App
20	27	21.8	20	7	US-11-022-562-250 Sequence 250, App
21	26	21.0	19	6	US-10-503-575-329 Sequence 329, App
22	26	21.0	20	7	US-11-196-400-16 Sequence 16, App
23	26	20.2	9	7	US-11-041-893-54 Sequence 54, App
24	25	20.2	12	7	US-11-054-515-2823 Sequence 2823, App
25	25	20.2	13	6	US-10-511-559-256 Sequence 256, App

26	25	20.2	13	6	US-10-511-559-257 Sequence 257, App
27	25	20.2	19	6	US-10-503-575-203 Sequence 203, App
28	25	20.2	19	6	US-10-880-238-115 Sequence 115, App
29	25	20.2	20	6	US-10-485-788A-600 Sequence 600, App
30	24	19.4	8	7	US-11-045-024-1054 Sequence 1054, App
31	24	19.4	9	7	US-11-111-463-13 Sequence 13, App
32	24	19.4	9	7	US-11-033-039-615 Sequence 615, App
33	24	19.4	10	6	US-10-501-411A-321 Sequence 321, App
34	24	19.4	11	7	US-11-045-024-1387 Sequence 1387, App
35	24	19.4	12	7	US-11-069-834-16 Sequence 16, App
36	24	19.4	13	7	US-11-145-861-197 Sequence 197, App
37	24	19.4	14	7	US-11-033-039-121 Sequence 121, App
38	24	19.4	14	7	US-11-152-697-41 Sequence 41, App
39	24	19.4	15	7	US-11-045-024-13015 Sequence 13015, App
40	24	19.4	15	7	US-11-045-024-13059 Sequence 13059, App
41	24	19.4	16	7	US-11-033-039-123 Sequence 123, App
42	24	19.4	17	6	US-10-665-658-44 Sequence 44, App
43	24	19.4	17	6	US-10-834-397-196 Sequence 196, App
44	24	19.4	17	7	US-11-007-428-4 Sequence 4, App
45	24	19.4	18	6	US-10-509-787A-92 Sequence 92, App
46	24	19.4	18	7	US-11-054-515-2795 Sequence 2795, App
47	24	19.4	19	6	US-10-503-575-282 Sequence 282, App
48	24	19.4	19	6	US-10-503-575-283 Sequence 283, App
49	24	19.4	19	6	US-10-503-575-284 Sequence 284, App
50	24	19.4	19	7	US-11-212-443-153 Sequence 153, App
51	24	19.4	20	7	US-11-022-562-292 Sequence 292, App
52	24	19.4	20	7	US-11-022-562-293 Sequence 293, App
53	24	19.4	20	7	US-11-026-403-74 Sequence 74, App
54	24	19.0	20	7	US-11-125-837-13 Sequence 13, App
55	23.5	19.0	20	6	US-10-518-599-21 Sequence 21, App
56	23	18.5	9	7	US-11-045-024-13662 Sequence 13662, App
57	23	18.5	9	7	US-11-136-079-652 Sequence 652, App
58	23	18.5	10	7	US-11-045-024-2026 Sequence 2026, App
59	23	18.5	10	7	US-11-045-024-6448 Sequence 6448, App
60	23	18.5	10	7	US-11-045-024-9521 Sequence 9521, App
61	23	18.5	11	7	US-11-045-024-1389 Sequence 1389, App
62	23	18.5	11	7	US-11-045-024-1190 Sequence 1190, App
63	23	18.5	16	6	US-10-929-888-445 Sequence 445, App
64	23	18.5	17	6	US-10-507-662-4 Sequence 4, App
65	23	18.5	17	6	US-10-665-658-41 Sequence 41, App
66	23	18.5	17	7	US-11-102-743-9 Sequence 9, App
67	23	18.5	19	6	US-10-503-575-140 Sequence 140, App
68	23	18.5	19	6	US-10-503-575-215 Sequence 215, App
69	23	18.5	19	6	US-10-503-575-313 Sequence 313, App
70	23	18.5	19	7	US-11-212-443-155 Sequence 155, App
71	23	18.5	20	6	US-10-939-890-148 Sequence 148, App
72	23	18.5	20	6	US-10-467-657-8826 Sequence 8826, App
73	22.5	18.1	15	7	US-11-045-024-13464 Sequence 13464, App
74	22.5	18.1	19	6	US-10-503-575-237 Sequence 237, App
75	22.5	18.1	20	6	US-10-623-155-413 Sequence 413, App
76	22.5	18.1	20	6	US-10-623-155-524 Sequence 524, App
77	22.5	18.1	20	6	US-10-501-411A-218 Sequence 218, App
78	22.5	18.1	20	6	US-10-501-411A-252 Sequence 252, App
79	22	17.7	7	7	US-11-097-749-11 Sequence 11, App
80	22	17.7	8	7	US-11-045-024-3567 Sequence 3574, App
81	22	17.7	8	7	US-11-045-024-10576 Sequence 10566, App
82	22	17.7	8	7	US-11-045-024-12478 Sequence 12478, App
83	22	17.7	9	7	US-11-026-403-26 Sequence 26, App
84	22	17.7	9	7	US-11-136-079-648 Sequence 648, App
85	22	17.7	10	6	US-10-467-657-8944 Sequence 8944, App
86	22	17.7	10	6	US-10-491-096-19 Sequence 19, App
87	22	17.7	11	7	US-11-035-846-18 Sequence 18, App
88	22	17.7	12	7	US-11-021-441-100 Sequence 100, App
89	22	17.7	12	7	US-11-152-666-264 Sequence 264, App
90	22	17.7	13	6	US-10-511-559-504 Sequence 504, App
91	22	17.7	14	6	US-10-503-575-79 Sequence 79, App
92	22	17.7	16	7	US-11-226-325-9 Sequence 9, App
93	22	17.7	17	6	US-10-834-397-203 Sequence 203, App
94	22	17.7	18	6	US-10-503-575-77 Sequence 77, App
95	22	17.7	19	6	US-10-503-575-177 Sequence 177, App
96	22	17.7	20	6	US-10-939-890-147 Sequence 147, App
97	22	17.7	20	6	US-10-485-788A-585 Sequence 585, App
98	22	17.7	20	7	US-11-022-562-191 Sequence 191, App

99 22 17.7 20 7 US-11-094-142-34
100 22 17.7 20 7 US-11-166-412-154

ALIGNMENTS

RESULT 1
US-11-033-039-1123

/ Sequence 1123, Application US/11033039
/ Publication No. US20060002947A1
/ GENERAL INFORMATION:
/ APPLICANT: HUMPHREYS, ROBERT
/ TITLE OF INVENTION: LI-KEY/ANTIGENIC EPIOTOPE HYBRID PEPTIDE VACCINES
/ FILE REFERENCE: REF-2017US01
/ CURRENT APPLICATION NUMBER: US/11/033.039
/ CURRENT FILING DATE: 2005-01-11
/ PRIOR APPLICATION NUMBER: 10/245,871
/ PRIOR FILING DATE: 2002-09-17
/ PRIOR APPLICATION NUMBER: 10/197,000
/ PRIOR FILING DATE: 2002-07-17
/ PRIOR APPLICATION NUMBER: 09/396,813
/ PRIOR FILING DATE: 1999-09-14
/ NUMBER OF SEQ ID NOS: 1452
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 1123
/ LENGTH: 19
/ TYPE: PRT
/ ORGANISM: Artificial Sequence

/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
/ OTHER INFORMATION: hybrid peptide

/ NAME/KEY: MOD_RES
/ LOCATION: (5)..(5)
/ OTHER INFORMATION: Ava
US-11-033-039-1123

Query Match 26.6%; Score 33; DB 7; Length 19;
Best Local Similarity 75.0%; Pred. No. 17;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 MAONKYR 9
Db 3 MKXNYKR 10

RESULT 2
US-10-511-559-255

/ Sequence 255, Application US/10511559
/ Publication No. US20050256304A1
/ GENERAL INFORMATION:

/ APPLICANT: JONES, Tim
/ APPLICANT: BAKER, Matthew
/ TITLE OF INVENTION: MODIFIED FACTOR VIII
/ FILE REFERENCE: MER-133
/ CURRENT APPLICATION NUMBER: US/10/511.559
/ CURRENT FILING DATE: 2004-10-15
/ PRIOR APPLICATION NUMBER: PCT/EP03/04063
/ PRIOR FILING DATE: 2003-04-17
/ PRIOR APPLICATION NUMBER: EP 02008712.8
/ PRIOR FILING DATE: 2002-04-18
/ PRIOR APPLICATION NUMBER: EP 03006554.4
/ PRIOR FILING DATE: 2003-03-24
/ NUMBER OF SEQ ID NOS: 1147
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 255
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Artificial Sequence

Sequence 34, Appl
Sequence 154, App

/ OTHER INFORMATION: Potential Epitope of human Factor VIII
US-10-511-559-255

Query Match 24.2%; Score 30; DB 6; Length 13;
Best Local Similarity 43.8%; Pred. No. 34;
Matches 7; Conservative 2; Mismatches 3; Indels 4; Gaps 1;

Oy 8 YROOFIOSVNLNGATR 23
Db 1 YKSQY---LNGEPQR 12

RESULT 3
US-10-511-559-75

/ Sequence 75, Application US/10511559
/ Publication No. US20050256304A1
/ GENERAL INFORMATION:
/ APPLICANT: JONES, Tim
/ APPLICANT: BAKER, Matthew
/ TITLE OF INVENTION: MODIFIED FACTOR VIII
/ FILE REFERENCE: MER-133
/ CURRENT APPLICATION NUMBER: US/10/511.559
/ CURRENT FILING DATE: 2004-10-15
/ PRIOR APPLICATION NUMBER: PCT/EP03/04063
/ PRIOR FILING DATE: 2003-04-17
/ PRIOR APPLICATION NUMBER: EP 02008712.8
/ PRIOR FILING DATE: 2002-04-18
/ PRIOR APPLICATION NUMBER: EP 03006554.4
/ PRIOR FILING DATE: 2003-03-24
/ NUMBER OF SEQ ID NOS: 1147
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 75
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Epitope of human Factor VIII
US-10-511-559-75

Query Match 24.2%; Score 30; DB 6; Length 15;
Best Local Similarity 43.8%; Pred. No. 40;
Matches 7; Conservative 2; Mismatches 3; Indels 4; Gaps 1;

Oy 8 YROOFIOSVNLNGATR 23
Db 2 YKSQY---LNGEPQR 13

RESULT 4
US-10-503-575-110

/ Sequence 110, Application US/10503575
/ Publication No. US20050244823A1
/ GENERAL INFORMATION:
/ APPLICANT: Drijfhout, Jan Wouter
/ APPLICANT: van Veelen, Petrus Antonius
/ TITLE OF INVENTION: NOVEL EPIOTOPES FOR CELLAC DISEASE AND AUTOIMMUNE DISEASES, METHOD
/ FILE REFERENCE: 2799/72843-PCT-US
/ CURRENT APPLICATION NUMBER: US/10/503.575
/ CURRENT FILING DATE: 2004-08-04
/ PRIOR APPLICATION NUMBER: PCT/NL03/00077
/ PRIOR FILING DATE: 2003-02-04
/ PRIOR APPLICATION NUMBER: EP 02075456.0
/ PRIOR FILING DATE: 2002-02-04
/ NUMBER OF SEQ ID NOS: 340
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 110
/ LENGTH: 19
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-503-575-110

10

```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: SDF-1 CXCR4 receptor antagonist analogue
; OTHER INFORMATION: C-terminal residues 55-67 linked by -(CH-2)-n-
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Xaa = Leu linked via -(CH-2)-n-, where n = 1 to 20.
; OTHER INFORMATION: to the C-terminal amino acid of any one of SEQ ID NOS:76,
; OTHER INFORMATION: 78, 87-94, 103-110, and 117-122
US-10-945-674A-77

Query Match          22.6%; Score 28; DB 6; Length 13;
Best Local Similarity 33.3%; Pred. No. 70;
Matches 4; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY      7 KYRQQTQSIVLN 18
      |:::|
Db      2 KWIOEYLEKALN 13

RESULT 8
US-11-045-024-13293
; Sequence 13293, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Cheenut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esreban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: EpiImmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13293
; LENGTH: 15
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-13293

Query Match          22.6%; Score 28; DB 7; Length 15;
Best Local Similarity 45.5%; Pred. No. 82;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      11 QFIQSIVLNNGA 21
      |:::|
Db      3 QLIBALLDTGA 13
```

```

RESULT 9
US-11-111-463-12
; Sequence 12, Application US/11111463
; Publication No. US20050261196A1
; GENERAL INFORMATION:
; APPLICANT: Turner, Jerrold R.
; APPLICANT: Mccay, Derek
; APPLICANT: Mccay, Derek
; TITLE OF INVENTION: MYOSIN LIGHT CHAIN KINASE INHIBITORS AND METHODS OF USE
; FILE REFERENCE: 092234-9030-US01
; CURRENT APPLICATION NUMBER: US/11/111,463
; CURRENT FILING DATE: 2005-04-21
; PRIOR APPLICATION NUMBER: 60/564,313
; PRIOR FILING DATE: 2004-04-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-11-111-463-12

Query Match          21.8%; Score 27; DB 7; Length 9;
Best Local Similarity 50.0%; Pred. No. 5,8e+04;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      4 QNKYKRRQ 11
      |:::|
Db      2 KKKYKRRK 9

RESULT 10
US-10-511-559-254
; Sequence 254, Application US/10511559
; Publication No. US20050256304A1
; GENERAL INFORMATION:
; APPLICANT: JONES, Tim
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis, J.
; TITLE OF INVENTION: MODIFIED FACTOR VIII
; FILE REFERENCE: MER-133
; CURRENT APPLICATION NUMBER: US/10/511,559
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: PCT/EP03/04063
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: EP 02008712.8
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: EP 03006554.4
; PRIOR FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 1147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 254
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Potential Epitope of human Factor VIII
US-10-511-559-254

Query Match          21.8%; Score 27; DB 6; Length 13;
Best Local Similarity 46.2%; Pred. No. 1e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 4; Gaps 1;

QY      8 YRQFIQSIVLNNG 20
      |:::|
Db      3 YKSGY-----LNNG 11

RESULT 11
```

```
US-11-022-562-43
; Sequence 43, Application US/11022562
; Publication No. US20050249742A1
; GENERAL INFORMATION:
; APPLICANT: Ruprecht, Ruth M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
; TITLE OF INVENTION: A CYTOTOXIC T LYMPHOCYTE IMMUNE RESPONSE
; FILE REFERENCE: DEN-043CN
; CURRENT APPLICATION NUMBER: US/11/022,562
; PRIOR FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: PCT/US03/20322
; PRIOR FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 60/392718
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus
US-11-022-562-43

Query Match      21.8%; Score 27; DB 7; Length 15;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY      15 SVLNCGATRQ 24
DB      5 SALSEGATPQ 14

RESULT 12
US-11-022-562-44
; Sequence 44, Application US/11022562
; Publication No. US20050249742A1
; GENERAL INFORMATION:
; APPLICANT: Ruprecht, Ruth M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
; TITLE OF INVENTION: A CYTOTOXIC T LYMPHOCYTE IMMUNE RESPONSE
; FILE REFERENCE: DEN-043CN
; CURRENT APPLICATION NUMBER: US/11/022,562
; PRIOR FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: PCT/US03/20322
; PRIOR FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 60/392718
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus
US-11-022-562-44

Query Match      21.8%; Score 27; DB 7; Length 15;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY      15 SVLNCGATRQ 24
DB      1 SAUSEGATPQ 10

RESULT 13
US-11-106-932-114
; Sequence 114, Application US/11106932
; Publication No. US20050260697A1
; GENERAL INFORMATION:
; APPLICANT: WANG, KA-WANG KEVIN
; APPLICANT: HAYES, RONALD
; APPLICANT: LIU, MING CHEN
```

```
APPLICANT: OLI, MONIKA
; TITLE OF INVENTION: PROTEOLYTIC MARKERS AS DIAGNOSTIC BIOMARKERS FOR CANCER, ORGAN
; TITLE OF INVENTION: INJURY AND MUSCLE REHABILITATION/EXERCISE OVERTRAINING
; FILE REFERENCE: 5853-549-1
; CURRENT APPLICATION NUMBER: US/11/106,932
; PRIOR FILING DATE: 2005-04-15
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 114
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-106-932-114

Query Match      21.8%; Score 27; DB 7; Length 15;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY      15 SVLNCGATRQ 24
DB      2 SEMVNGATEQ 11

RESULT 14
US-11-045-024-13006
; Sequence 13006, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060, 0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; PRIOR FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13006
; LENGTH: 15
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-13006

Query Match      21.8%; Score 27; DB 7; Length 15;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY      15 SVLNCGATRQ 24
```

```
Db          2 SALSEGATPQ 11

RESULT 15
US-11-045-024-13016
; Sequence 13016, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: EpiImmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2000.0040007
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13016
; LENGTH: 15
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-13016

Query Match          21.8%; Score 27; DB 7; Length 15;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY          15 SVLNNGATRQ 24
Db          6 SALSEGATPQ 15

RESULT 16
US-10-973-977-8
; Sequence 8, Application US/10973977
; Publication No. US20060008467A1
; GENERAL INFORMATION:
; APPLICANT: HAYNES, BARTON F.
; APPLICANT: LIAO, HUA-XIN
; APPLICANT: LETVIN, NORMAN
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS VACCINE
; FILE REFERENCE: 1579-942
; CURRENT FILING DATE: 2004-10-27
; PRIOR APPLICATION NUMBER: 09/775,805
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 09/497,497
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 107

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-973-977-8

Query Match          21.8%; Score 27; DB 6; Length 16;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY          15 SVLNNGATRQ 24
Db          5 SALSEGATPQ 14

RESULT 17
US-11-145-861-215
; Sequence 215, Application US/11145861
; Publication No. US20060014138A1
; GENERAL INFORMATION:
; APPLICANT: Chinaiyan, Arul
; APPLICANT: Wang, Xiaoju
; TITLE OF INVENTION: Phage Microarray Profiling of the Humoral Response to Disease
; FILE REFERENCE: UM-09899
; CURRENT FILING DATE: 2005-06-06
; PRIOR APPLICATION NUMBER: US/11/145,861
; NUMBER OF SEQ ID NOS: 464
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 215
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-145-861-215

Query Match          21.8%; Score 27; DB 7; Length 17;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY          10 QOQFQSVLNN 19
Db          2 KQILSSVLNS 11

RESULT 18
US-11-033-039-1125
; Sequence 1125, Application US/11033039
; Publication No. US20060002947A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPIOTOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2017US01
; CURRENT FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: US/11/033,039
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 1452
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1125
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (5)..(5)
```

OTHER INFORMATION: Ava
US-11-033-039-1125

Query Match 21.8% Score 27; DB 7; Length 19;
Best Local Similarity 38.5%; Pred. No. 1.5e+02;
Matches 5; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 9 RQGFIOGVLNNGA 21
DB 2 RMXKLDVWQNA 14

RESULT 19
US-11-022-562-249
Sequence 249, Application US/11022562
Publication No. US20050249742A1
GENERAL INFORMATION:
APPLICANT: Ruprecht, Ruth M.
APPLICANT: Shisong, Jiang
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
TITLE OF INVENTION: A CYTOTOXIC T LYMPHOCYTE IMMUNE RESPONSE
FILE REFERENCE: DEN-043CN
CURRENT APPLICATION NUMBER: US/11/022,562
CURRENT FILING DATE: 2004-12-22
PRIOR APPLICATION NUMBER: PCT/US03/20322
PRIOR FILING DATE: 2003-06-27
PRIOR APPLICATION NUMBER: 60/392718
PRIOR FILING DATE: 2002-06-27
NUMBER OF SEQ ID NOS: 340
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 249
LENGTH: 20
TYPE: PRT
ORGANISM: Human Immunodeficiency Virus
US-11-022-562-249

Query Match 21.8% Score 27; DB 7; Length 20;
Best Local Similarity 60.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 15 SVLNGATQ 24
DB 3 SALSEGATPQ 12

RESULT 20
US-11-022-562-250
Sequence 250, Application US/11022562
Publication No. US20050249742A1
GENERAL INFORMATION:
APPLICANT: Ruprecht, Ruth M.
APPLICANT: Shisong, Jiang
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
TITLE OF INVENTION: A CYTOTOXIC T LYMPHOCYTE IMMUNE RESPONSE
FILE REFERENCE: DEN-043CN
CURRENT APPLICATION NUMBER: US/11/022,562
CURRENT FILING DATE: 2004-12-22
PRIOR APPLICATION NUMBER: PCT/US03/20322
PRIOR FILING DATE: 2003-06-27
PRIOR APPLICATION NUMBER: 60/392718
PRIOR FILING DATE: 2002-06-27
NUMBER OF SEQ ID NOS: 340
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 250
LENGTH: 20
TYPE: PRT
ORGANISM: Human Immunodeficiency Virus
US-11-022-562-250

Query Match 21.8% Score 27; DB 7; Length 20;
Best Local Similarity 60.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 15 SVLNGATQ 24
DB 3 SALSEGATPQ 12

RESULT 21
US-10-503-575-329
Sequence 329, Application US/10503575
Publication No. US20050244823A1
GENERAL INFORMATION:
APPLICANT: Drijfhout, Jan Mouter
APPLICANT: van Veelen, Petrus Antonius
TITLE OF INVENTION: NOVEL EPITOPES FOR CELIAC DISEASE AND AUTOIMMUNE DISEASES, METHO
TITLE OF INVENTION: DETECTING THOSE AND NOVEL NON-ANTIGENIC FOOD COMPOUNDS
FILE REFERENCE: 2799/72843-PCT-US
CURRENT APPLICATION NUMBER: US/10/503,575
CURRENT FILING DATE: 2004-08-04
PRIOR APPLICATION NUMBER: PCT/NL03/00077
PRIOR FILING DATE: 2003-02-04
PRIOR APPLICATION NUMBER: EP 02075456.0
PRIOR FILING DATE: 2002-02-04
NUMBER OF SEQ ID NOS: 340
SOFTWARE: PatentIn version 3.1
SEQ ID NO 329
LENGTH: 19
TYPE: PRT
ORGANISM: Homo sapiens
US-10-503-575-329

Query Match 21.0% Score 26; DB 6; Length 19;
Best Local Similarity 50.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 7 KYRQGFIOGVLN 18
DB 3 RMXKLDVWQNA 14

RESULT 22
US-11-196-400-16
Sequence 16, Application US/11196400
Publication No. US20050287166A1
GENERAL INFORMATION:
APPLICANT: DRUTHE, PIERRE
APPLICANT: DAUBERSIES, PIERRE
TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES
FILE REFERENCE: 200773USODIV
CURRENT APPLICATION NUMBER: US/11/196,400
CURRENT FILING DATE: 2005-08-04
PRIOR APPLICATION NUMBER: US/09/742,096
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 08/973,462
PRIOR FILING DATE: 1998-02-06
PRIOR APPLICATION NUMBER: PCT/FR96/00894
PRIOR FILING DATE: 1996-06-12
PRIOR APPLICATION NUMBER: FR 95/07007
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn version 3.3
SEQ ID NO 16
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Peptide
US-11-196-400-16

Query Match 21.0% Score 26; DB 7; Length 20;
Best Local Similarity 36.4%; Pred. No. 2.4e+02;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 9 RQGFIOGVLN 19

Db 9 KENIIDNLLNN 19

RESULT 23
US-11-041-893-54
; Sequence 54, Application US/11041893
; Publication No. US2006002941A1
; GENERAL INFORMATION:
; APPLICANT: Mahbarez, Gregory G.
; TITLE OF INVENTION: COMPOSITIONS COMPRISING IMMUNE RESPONSE
; FILE REFERENCE: 100123.401
; CURRENT APPLICATION NUMBER: US/11/041,893
; CURRENT FILING DATE: 2005-01-24
; PRIOR APPLICATION NUMBER: US 60/616,855
; PRIOR FILING DATE: 2004-10-06
; PRIOR APPLICATION NUMBER: US 60/538,713
; PRIOR FILING DATE: 2004-01-23
; NUMBER OF SEQ ID NOS: 295
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-11-041-893-54

Query Match 20.2%; Score 25; DB 7; Length 9;
Best Local Similarity 62.5%; Pred. No. 5.8e+04;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 14 QSVLNNGA 21
Db 1 QAVANGGA 8

RESULT 24
US-11-054-515-2823
; Sequence 2823, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2823
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2823

Query Match 20.2%; Score 25; DB 7; Length 12;
Best Local Similarity 62.5%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 DMAQVYKY 8
Db 1 DMKVYKY 8

RESULT 25
US-10-511-559-256
; Sequence 256, Application US/10511559
; Publication No. US20050256304A1
; GENERAL INFORMATION:
; APPLICANT: JONES, Tim
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis, J.
; TITLE OF INVENTION: MODIFIED FACTOR VIII
; FILE REFERENCE: MER-133
; CURRENT APPLICATION NUMBER: US/10/511,559
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: PCT/EP03/04063
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: EP 02008712.8
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: EP 0306554.4
; PRIOR FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 1147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 256
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Potential Epitope of human Factor VIII
US-10-511-559-256

Query Match 20.2%; Score 25; DB 6; Length 13;
Best Local Similarity 71.4%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 17 LNNGATR 23
Db 4 LNNGPOR 10

Search completed: January 26, 2006, 08:39:06
Job time : 4.55172 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 26, 2006, 07:48:50 : Search time 12 Seconds
(without alignments)
192.434 Million cell updates/sec

Title: US-09-662-293-8
Perfect score: 124
Sequence: 1 DMAQNYKRYROFQISVLNNGATRQ 24

Scoring table: BIOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 4071

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	24.2	20	2	TS0757
2	28	22.6	10	2	S4282
3	27	21.8	21	2	CS6817
4	26	21.0	12	2	PH0771
5	26	21.0	17	2	J02330
6	25	20.2	17	2	J02310
7	25	20.2	19	2	A44239
8	25	20.2	20	2	S18582
9	25	20.2	20	2	S03508
10	24	19.4	10	2	F44644
11	24	19.4	18	2	B57789
12	23	18.5	9	2	C36730
13	23	18.5	14	2	F48394
14	23	18.5	14	2	S72217
15	23	18.5	15	2	JN0730
16	23	18.5	20	2	S00494
17	23	18.5	20	2	S80028
18	22	17.7	9	2	D58503
19	22	17.7	12	2	S10624
20	22	17.7	12	2	PH0746
21	22	17.7	17	2	PS0454
22	22	17.7	18	2	PH0768
23	22	17.7	20	2	S17461
24	22	17.7	20	2	JN0142
25	22	17.7	20	2	D42842
26	22	17.7	20	2	S35970
27	22	17.7	20	2	A54519
28	22	17.7	20	2	S28779
29	22	17.7	21	2	S35978

30	22	17.7	21	2	P00257
31	22	17.7	21	2	S57568
32	22	17.7	21	2	S69350
33	21.5	17.3	19	2	B60977
34	21	16.9	7	2	A38081
35	21	16.9	9	2	PC7076
36	21	16.9	11	2	S42587
37	21	16.9	11	2	A32428
38	21	16.9	15	2	PH1329
39	21	16.9	15	2	A56049
40	21	16.9	15	2	S33781
41	21	16.9	16	2	S10807
42	21	16.9	17	2	S48655
43	21	16.9	18	2	PH1368
44	21	16.9	19	2	PH1313
45	21	16.9	21	2	S71602
46	21	16.9	21	2	T06566
47	20	16.1	10	2	S28055
48	20	16.1	10	2	F41839
49	20	16.1	10	2	S30348
50	20	16.1	10	2	JN0025
51	20	16.1	10	2	A44871
52	20	16.1	11	2	C59151
53	20	16.1	11	2	S23306
54	20	16.1	13	2	A33208
55	20	16.1	13	2	S29488
56	20	16.1	13	2	S47362
57	20	16.1	13	2	G44644
58	20	16.1	14	2	S39932
59	20	16.1	14	2	S39931
60	20	16.1	15	2	B33208
61	20	16.1	15	2	S32677
62	20	16.1	15	2	P00182
63	20	16.1	15	2	G60977
64	20	16.1	16	2	PH1588
65	20	16.1	17	2	PD0005
66	20	16.1	18	2	I73024
67	20	16.1	18	2	A38890
68	20	16.1	19	2	S00495
69	20	16.1	19	2	T50329
70	20	16.1	19	2	A33361
71	20	16.1	20	2	A53875
72	20	16.1	20	2	S46205
73	20	16.1	20	2	S46204
74	20	16.1	20	2	S00493
75	20	16.1	20	2	A48394
76	20	16.1	20	2	S17501
77	20	16.1	20	2	P00544
78	20	16.1	20	2	S33291
79	20	16.1	21	2	S78574
80	20	16.1	21	2	A60420
81	20	16.1	21	2	PC4443
82	19.5	15.7	19	2	B53145
83	19.5	15.7	21	2	E44101
84	19	15.3	11	2	S35490
85	19	15.3	12	2	I39390
86	19	15.3	13	2	PC1149
87	19	15.3	13	2	S47361
88	19	15.3	14	1	QMWAP
89	19	15.3	14	2	S39930
90	19	15.3	14	2	PT0210
91	19	15.3	14	2	EC7079
92	19	15.3	15	2	PQ0174
93	19	15.3	15	2	PQ0175
94	19	15.3	15	2	S00706
95	19	15.3	15	2	PH1314
96	19	15.3	15	2	PQ0073
97	19	15.3	15	2	PT0096
98	19	15.3	17	2	PH0769
99	19	15.3	17	2	S16144
100	19	15.3	17	2	B31435

microbial serine p
T cell receptor V-
4-hydroxybenzoate
14-3-3 protein hom
amine oxidase (cop
spectrin alpha cha
cellf protein - Esc
amine oxidase (cop
Ig heavy chain DJ
urinary tract ston
acetylcholine synth
protein kinase C i
glutathione dehydr
Ig heavy chain DJ
recombination prot
ribulose-bisphosph
cytochrome b559 co
ribosomal protein
clotting protein -
mosact - sea urchi
monodehydroascorba
protein-tyrosine k
substance P - Alia
calreticulin, hepa
GTP-binding protei
T-cell antigen rec
neurotoxin-associat
S-allele-associate
calreticulin, uret
nitrogenase cofact
scylar glycoprotei
protein 425 - Cal i
Ig H chain V-D-J r
very-high-density l
T cell receptor be
11k protein 5306 f
hemocyanin chain I
wc-repeat protein
CAMP-regulated pho
creatine kinase (E
comosarin (EC 3.4.2
ananasin (EC 3.4.22
hemocyanin chain I
major fat-globule
glutaminase - Alca
capsid protein VP5
lipopolyasaccharide
protein kinase C i
lens intrinsinc mem
cytochrome c3 - De
high conductance c
calmodulin, vasocac
type II site-speci
acetylcholine rece
equinactoxin IA - 8
T-cell antigen rec
poliactes mastopara
S-allele-associate
T-cell receptor al
unidentified 27.2K
ethylar glycoprotei
ethylar glycoprotei
actin - sea urchin
Ig heavy chain DJ
T-cell receptor be
pyruvate dehydroge
T-cell receptor be
spova protein - Ba
adherence lectin 1

ALIGNMENTS

RESULT 1

T50757

pufk protein [imported] - Rhodobacter sphaeroides

C/Species: Rhodobacter sphaeroides

C/Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004

C/Accession: T50757

R/Choudhary, M.; Kaplan, S.

Nucleic Acids Res. 28, 862-867, 2000

A/Title: DNA sequence analysis of the photosynthesis region of Rhodobacter sphaeroides 2

A/Reference number: 225222; MUID:20115911; PMID:10648776

A/Accession: T50757

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-20 <CHO>

A/Cross-references: UNIPROT:Q53121; UNIPARC:UPI00001329F3; EMBL:AF195122; PIDN:AAF24301.

A/Experimental source: strain 2.4.1

C/Genetics:

A/Gene: pufK

Query Match

Best Local Similarity 24.2%; Score 30; DB 2; Length 20;

Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 9 RQRFIQSVLNNNG 20

DB 8 RHQHVASVLRSG 19

RESULT 2

S42282

paraportal crystal protein cryIIB - Bacillus thuringiensis plasmid (fragment)

N/Alternate names: delta-endotoxin

C/Species: Bacillus thuringiensis

C/Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 24-Jul-1998

C/Accession: S42282

R/Crickmore, N.; Wheeler, V.C.; Ellar, D.J.

Mol. Gen. Genet. 242, 365-368, 1994

A/Title: Use of an operon fusion to induce expression and crystallization of a Bacillus

A/Reference number: S42282; MUID:94150472; PMID:7906381

A/Accession: S42282

A/Molecule type: protein

A/Residues: 1-10 <CR>

A/Cross-references: UNIPARC:UPI000017ACD4

A/Experimental source: subsp. galleriae 916

C/Genetics:

A/Gene: cryIIB

C/Keywords: delta-endotoxin

Query Match

Best Local Similarity 22.6%; Score 28; DB 2; Length 10;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 13 IQSVLNNNG 20

DB 1 MNTVLNNG 8

RESULT 3

C56817

photosystem I protein Psal - Synechococcus sp. (PCC 6301) (fragment)

C/Species: Synechococcus sp.

C/Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 18-Aug-1995

C/Accession: C56817

R/Li, N.; Warren, P.V.; Golbeck, J.H.; Frank, G.; Zuber, H.; Bryant, D.A.

Biochim. Biophys. Acta 1059, 215-225, 1991

A/Title: Polypeptide composition of the Photosystem I complex and the Photosystem I core

A/Reference number: A56817; MUID:91355213; PMID:1653017

A/Accession: C56817

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-21

A/Cross-references: UNIPARC:UPI0000132581

A/Note: Sequence extracted from NCBI backbone (NCBI:P:57972)

C/Genetics:

A/Gene: psal

Query Match

Best Local Similarity 21.8%; Score 27; DB 2; Length 21;

Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 14 QSVLNNNGATRO 24

DB 2 QDVIANNGTAE 12

RESULT 4

PH0771

T-cell receptor beta chain (P55.1.1) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999

C/Accession: PH0771

R/Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.

J. Exp. Med. 174, 1371-1383, 1991

A/Title: T cell receptor genes in a series of class I major histocompatibility complex-r

allelic exclusion and antigen-specific repertoire.

A/Reference number: PH0746; MUID:92078846; PMID:1836010

A/Accession: PH0771

A/Molecule type: mRNA

A/Residues: 1-12 <CAS>

A/Cross-references: UNIPARC:UPI0000115FBE; EMBL:X60865; NID:953624; PIDN:CAA43255.1; PID

A/Experimental source: T lymphocyte

C/Keywords: T-cell receptor

Query Match

Best Local Similarity 21.0%; Score 26; DB 2; Length 12;

Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 AQNVYKROQF 12

DB 2 ASRFQYQYF 11

RESULT 5

JQ2320

hypothetical 2.1k protein - potato chloroplast

C/Species: chloroplast Solanum tuberosum (potato)

C/Date: 10-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004

C/Accession: JQ2320; JQ2315

R/Kawagoe, Y.; Kikuta, Y.

Theor. Appl. Genet. 81, 13-20, 1991

A/Title: Chloroplast DNA evolution in potato (Solanum tuberosum L.).

A/Reference number: JQ2306

A/Accession: JQ2320

A/Molecule type: DNA

A/Residues: 1-17 <KWL>

A/Cross-references: UNIPARC:UPI000017B0C3

A/Experimental source: cv. W553-4

A/Accession: JQ2315

A/Molecule type: DNA

A/Residues: 1-17 <KWL>

A/Cross-references: UNIPARC:UPI000017B0C3

A/Experimental source: cv. 150

C/Genetics:

A/Genome: chloroplast

C/Keywords: chloroplast

Query Match

Best Local Similarity 21.0%; Score 26; DB 2; Length 17;

Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 MAQNYKXR 9

DB 1 MNTVLNNG 8

Db 1 MKNYSYK 8

RESULT 6

Q02310

hypothetical 2.1k protein - tomato chloroplast (strain Toko)

C:Species: chloroplast Lycopersicon esculentum (tomato)

C:Date: 10-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004

C:Accession: J02310

R:Kawagoe, Y.; Kikuta, Y.

Theor. Appl. Genet. 81, 13-20, 1991

A:Title: Chloroplast DNA evolution in potato (Solanum tuberosum L.).

A:Reference number: J02306

A:Accession: J02310

A:Molecule type: DNA

A:Residues: 1-17 <KAW>

A:Cross-references: UNIPROT:Q7M2E9, UNIPARC:UPI000017B098

A:Experimental source: strain Toko

C:Genetics:

A:Genome: chloroplast

C:Keywords: chloroplast

Query Match 20.2%; Score 25; DB 2; Length 17;

Best Local Similarity 50.0%; Pred. No. 1.7e+03;

Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 MAQNYKTR 9

Db 1 MKPNYSYK 8

RESULT 7

A44239

amine oxidase (copper-containing) (EC 1.4.3.6), kidney - pig (fragment)

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004

C:Accession: A44239

R:Jurner, S.M.; Patcic, M.M.; Scaman, C.H.; Smith, A.J.; Brown, D.E.; Dooley, D.M.; Mure,

Biochemistry 31, 12147-12154, 1992

A:Title: Identification of topaguinone and its consensus sequence in copper amine oxidase

A:Reference number: A44239; PMID:93090748; PMID:1457410

A:Accession: A44239

A:Molecule type: protein

A:Residues: 1-7, 'X', '9-19 <JAN>

A:Cross-references: UNIPROT:Q9TRK6, UNIPARC:UPI000008701B; PIDN:AAB24426.1; PID:9261360

A:Experimental source: kidney

A:Note: sequence extracted from NCBI backbone (NCBIP:119897)

A:Note: we show one of the unidentified residues as tyrosine forming the topaguinone pro

C:Superfamily: amiloride-binding protein

C:Keywords: oxidoreductase; quinoprotein; topaguinone

F/B/Modified site: topaguinone (Tyr) #status experimental

Query Match 20.2%; Score 25; DB 2; Length 19;

Best Local Similarity 55.6%; Pred. No. 1.9e+03;

Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 NYKYRQCFI 13

Db 7 NYDYIXDFI 15

RESULT 8

S18582

hypothetical protein K (puG 3' region) - Rhodobacter sphaeroides

C:Species: Rhodobacter sphaeroides

C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 03-May-1994

C:Accession: S18582; S32855

R:Hunter, C.N.; McGlynn, P.; Ashby, M.K.; Burgess, J.G.; Olsen, J.D.

Mol. Microbiol. 5, 2649-2661, 1991

A:Title: DNA sequencing and complementation/deletion analysis of the bchA-puf operon reg

A:Reference number: S18580; PMID:92140030; PMID:1779756

A:Accession: S18582

A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-20 <HUN>
A:Cross-references: UNIPARC:UPI000017AB8B; EMBL:X68795

Query Match

Best Local Similarity 20.2%; Score 25; DB 2; Length 20;

Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 9 RQFIQSVLNG 20

Db 8 RHNHVASVLRSG 19

RESULT 9

S03508

T-cell receptor alpha chain J region (19) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 05-Nov-1999

C:Accession: S03508

R:Minoto, A.; Mjolsness, S.; Hood, L.

Nature 316, 832-836, 1985

A:Title: Genomic organization of the genes encoding mouse T-cell receptor alpha-chain.

A:Reference number: S03503; PMID:85296332; PMID:2993908

A:Accession: S03508

A:Molecule type: DNA

A:Residues: 1-20 <MIN>

A:Cross-references: UNIPARC:UPI0000115262; EMBL:X03058; NID:954521; PIDN:CAA26865.1; PI

A:Note: this sequence was determined from the germline gene

C:Keywords: T-cell receptor

Query Match 20.2%; Score 25; DB 2; Length 20;

Best Local Similarity 100.0%; Pred. No. 2e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 NYKY 8

Db 5 NYKY 8

RESULT 10

F44644

neurotoxin-associated protein type B Hn+ 35k chain, band 3a - Clostridium botulinum (fr

C:Species: Clostridium botulinum

C:Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004

C:Accession: F44644

R:Somers, E.; DasGupta, B.R.

J. Protein Chem. 10, 415-425, 1991

A:Title: Clostridium botulinum types A, B, C1, and E produce proteins with or without h

A:Reference number: A44644; PMID:92143938; PMID:1781887

A:Contents: type B

A:Accession: F44644

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-10 <SOM>

A:Cross-references: UNIPROT:Q9RSN6; UNIPARC:UPI00000B2EFF

A:Note: sequence extracted from NCBI backbone (NCBIP:83787)

C:Keywords: hemagglutinin

Query Match 19.4%; Score 24; DB 2; Length 10;

Best Local Similarity 57.1%; Pred. No. 1.4e+03;

Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 13 IQSVLNN 19

Db 1 IQNVLND 7

RESULT 11

B57789

kidney stone matrix protein - human (fragment)

C:Species: Homo sapiens (hmn)

C:Date: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 23-Feb-1996

C:Accession: B57789

R:Binette, J.P.; Binette, M.B.
 submitted to the Protein Sequence Database, February 1996
 A:Description: The proteins of gallbladder stones.
 A:Reference number: A57789
 A:Accession: B57789
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-18 <BIN>
 A:Cross-references: UNIPARC:UPI000017C28A
 A:Experimental source: urate calcium oxalate kidney stone

Query Match 19.4%; Score 24; DB 2; Length 18;
 Best Local Similarity 36.4%; Pred. No. 2.5e+03;
 Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 5 NYKRYOPIQS 15
 Db 4 NYKFTGEIVQS 14

RESULT 12

C36730
 hutu protein - Klebsiella pneumoniae (fragment)
 C:Species: Klebsiella pneumoniae
 C:Date: 19-Apr-1991 #sequence_revision 19-Apr-1991 #text_change 08-Oct-1999
 C:Accession: C36730

R:Schwacha, A.; Bender, R.A.
 J. Bacteriol. 172, 5477-5481, 1990
 A:Title: Nucleotide sequence of the gene encoding the repressor for the histidine utililz
 A:Reference number: A36730; MUID:90368611; PMID:2203754
 A:Accession: C36730
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-9 <SCH>

A:Cross-references: UNIPARC:UPI000012CEC3; GB:M34604; NID:G149203; PIDN:AAA25076.1; PID:

Query Match 19.0%; Score 23.5; DB 2; Length 9;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;
 Matches 6; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

OY 2 MAQNYKXRO 10
 Db 1 MSQS-KYRQ 8

RESULT 13

F48394
 glycoprotein component 16/major fat-globule membrane protein/MFG-E8 homolog - bovine (fr
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 07-Feb-1997
 C:Accession: F48394

R:Mahter, J.H.; Banghart, L.R.; Lane, W.S.
 Biochem. Mol. Biol. Int. 29, 545-554, 1993
 A:Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig
 II-like sequences.
 A:Reference number: A48394; MUID:93250576; PMID:8485470

A:Accession: F48394
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-14 <MAT>
 A:Cross-references: UNIPARC:UPI000014C319
 A:Experimental source: milk
 A:Note: sequence extracted from NCBI backbone (NCBI:111455)
 C:Keywords: glycoprotein

Query Match 18.5%; Score 23; DB 2; Length 14;
 Best Local Similarity 36.4%; Pred. No. 2.8e+03;
 Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 13 IQSVLNNNGATR 23
 Db 4 VTXYVTOGASR 14

RESULT 14

S72217
 D-arabinose 1-dehydrogenase [NAD(P)] (EC 1.1.1.117) - yeast (Candida albicans) (fragment)

C:Species: Candida albicans
 C:Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 03-Jun-2002
 C:Accession: S72217
 R:Kim, S.T.; Huh, W.K.; Kim, J.Y.; Hwang, S.W.; Kang, S.O.
 Biochim. Biophys. Acta 1297, 1-8, 1996
 A:Title: D-arabinose dehydrogenase and biosynthesis of erythroascorbic acid in Candida al

A:Reference number: S72217; MUID:96439039; PMID:8841374
 A:Accession: S72217
 A:Molecule type: protein
 A:Residues: 1-14 <KIM>
 A:Cross-references: UNIPARC:UPI000017CDB9
 C:Keywords: oxidoreductase

Query Match 18.5%; Score 23; DB 2; Length 14;
 Best Local Similarity 62.5%; Pred. No. 2.8e+03;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 13 IQSVLNNNG 20
 Db 7 IDPXLNNG 14

RESULT 15

JN0730
 hypothetical 1.7k protein - phage SP1
 N:Alternate names: hypothetical protein 42.1
 C:Species: phage SP1
 C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 17-Mar-1999
 C:Accession: JN0730

R:Chai, S.; Stjepan, U.; Lueder, G.; Trautner, T.A.; Alonso, J.C.
 Gene 129, 41-49, 1993
 A:Title: Sequence analysis of the left end of the Bacillus subtilis bacteriophage SP1 g

A:Reference number: JN0729; MUID:93328123; PMID:8335259
 A:Accession: JN0730
 A:Molecule type: DNA
 A:Residues: 1-15 <CHA>

A:Cross-references: UNIPARC:UPI000017A84E; EMBL:X65941

Query Match 18.5%; Score 23; DB 2; Length 15;
 Best Local Similarity 80.0%; Pred. No. 3e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 16 VLNNG 20
 Db 1 MLNNG 5

RESULT 16

S00494
 hemocyanin chain II - Japanese spiny lobster (fragment)
 C:Species: Panulirus japonicus (Japanese spiny lobster)
 C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
 C:Accession: S00494

R:Makino, N.; Kimura, S.
 Eur. J. Biochem. 173, 423-430, 1988
 A:Title: Subunits of Panulirus japonicus hemocyanin. 1. Isolation and properties.
 A:Reference number: S00492; MUID:88196131; PMID:3360019
 A:Accession: S00494
 A:Molecule type: protein

A:Residues: 1-20 <MAK>
 A:Cross-references: UNIPROT:P82312; UNIPARC:UPI000012C37C
 A:Superfamily: hemocyanin
 C:Keywords: copper; hemolymph; hexamer; oxygen carrier

Query Match 18.5%; Score 23; DB 2; Length 20;
 Best Local Similarity 29.4%; Pred. No. 4e+03;
 Matches 5; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

OY 2 MAQNYKROPIQSVLN 18

Db 3 VASSTAHKQDINHLD 19

RESULT 17

PS0028
Flagellar motor switch protein flbd - Escherichia coli (fragment)
C/Species: Escherichia coli
C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 18-Jun-1993
C/Accession: PS0028
R/Malakooti, J.; Kameda, Y.; Matsumura, P.
J. Bacteriol. 171, 2728-2734, 1989
A/Title: DNA sequence analysis, gene product identification, and localization of flagellin
A/Reference number: PS0027; MUID:89213963; PMID:2651416
A/Accession: PS0028
A/Molecule type: DNA
A/Residues: 1-20 <MAL>
A/Cross-references: UNIPARC:UPI000017AA3D
C/Genetics:
A/Gene: flbd

Query Match 18.5%; Score 23; DB 2; Length 20;
Best Local Similarity 62.5%; Pred. No. 4e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 17 LNNGATRG 24
Db 1 MNHATVQ 8

RESULT 18

D58503
translation elongation factor EF-Tu - unidentified bacterium (fragment)
C/Species: unidentified bacterium
C/Date: 07-Feb-1997 #sequence_revision 07-Feb-1997 #text_change 09-Jul-2004
C/Accession: D58503
R/Binette, J.P.; Binette, M.B.
submitted to the Protein Sequence Database, October 1996
A/Description: The proteins of kidney and gallbladder stones.
A/Reference number: A58501
A/Accession: D58503
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-9 <BIN>
A/Cross-references: UNIPROT:Q7M151, UNIPARC:UPI000017827D
A/Experimental source: human bile and stones
C/Superfamily: translation elongation factor Tu; translation elongation factor Tu homolog
C/Keywords: GTP binding

Query Match 17.7%; Score 22; DB 2; Length 9;
Best Local Similarity 80.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 YRQGF 12
Db 2 YRQGF 6

RESULT 19

S10624
lipovitelin - African clawed frog
C/Species: Xenopus laevis (African clawed frog)
C/Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 10-Nov-1995
C/Accession: S10624
R/Wallace, R.A.; Hoch, K.L.; Carnevali, O.
J. Mol. Biol. 213, 407-409, 1990
A/Title: Placement of small lipovitelin subunits within the vitellogenin precursor in X
A/Reference number: S10624; MUID:90278951; PMID:2352275
A/Accession: S10624
A/Molecule type: protein
A/Residues: 1-12 <WAL>
A/Cross-references: UNIPARC:UPI000017BF94

Query Match 17.7%; Score 22; DB 2; Length 12;
Best Local Similarity 60.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 8 YRQGF 12
Db 6 YRQGF 10

RESULT 20

PH0746
T-cell receptor beta chain (B28) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
C/Accession: PH0746
R/Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A/Title: T cell receptor genes in a series of class I major histocompatibility complex-
allelic exclusion and antigen-specific repertoire.
A/Reference number: PH0746; MUID:92078846; PMID:1836010
A/Accession: PH0746
A/Molecule type: mRNA
A/Residues: 1-12 <CAS>
A/Cross-references: UNIPARC:UPI0000115FA5; EMBL:X60837; NID:950098; PIDN:CAA43230.1; PI
A/Experimental source: T lymphocyte
C/Keywords: T-cell receptor

Query Match 17.7%; Score 22; DB 2; Length 12;
Best Local Similarity 40.0%; Pred. No. 3.4e+03;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 AONKYRQGF 12
Db 2 ASSRYEQYF 11

RESULT 21

PS0454
38k protein 3129 - rice (strain Nihonbare) (fragment)
C/Species: Oryza sativa (rice)
C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Mar-1995
C/Accession: PS0454
R/Tsugita, A.
submitted to JIPID, April 1993
A/Reference number: PS0206
A/Accession: PS0454
A/Molecule type: protein
A/Residues: 1-17 <TSU>
A/Cross-references: UNIPARC:UPI000017B100
A/Experimental source: leaf, chloroplast, stem
A/Note: molecular weight 38k, pI 5.9

Query Match 17.7%; Score 22; DB 2; Length 17;
Best Local Similarity 80.0%; Pred. No. 4.9e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 19 NGATR 23
Db 11 NGXTR 15

RESULT 22

PH0768
T-cell receptor beta chain (M2) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
C/Accession: PH0768
R/Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A/Title: T cell receptor genes in a series of class I major histocompatibility complex-
allelic exclusion and antigen-specific repertoire.
A/Reference number: PH0746; MUID:92078846; PMID:1836010
A/Accession: PH0768

A:Molecule type: mRNA
 A:Residues: 1-18 <C>
 A:Cross-references: UNIPARC:UPI0000115FBB, EMBL:X60862, NID:952972, PIDN:CAA4252.1, PID
 A:Experimental source: T lymphocyte
 C:Keywords: T-cell receptor

Query Match 17.7% Score 22; DB 2; Length 18;
 Best Local Similarity 42.9%; Pred. No. 5.2e+03;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 YKXROOF 12
 : | : |
 Db 10 FNVAEQF 16

RESULT 23

S17461
 Flavodoxin B - Azotobacter chroococcum (fragment)
 C:Species: Azotobacter chroococcum
 C>Date: 19-Mar-1997 #sequence_revision 30-Jan-1998 #text_change 09-Jul-2004
 C:Accession: S17461
 R:Bagby, S.; Barker, P.D.; Hill, H.A.O.; Sanghera, G.S.; Dunbar, B.; Ashby, G.A.; Eady,
 Biochem. J. 277, 313-319, 1991
 A:Title: Direct electrochemistry of two genetically distinct flavodoxins isolated from A
 A:Reference number: S16929; PMID:91315397; PMID:1859358
 A:Accession: S17461
 A:Molecule type: protein
 A:Residues: 1-20 <BAG>
 A:Cross-references: UNIPROT:Q9RSU5, UNIPARC:UPI00000B6F94
 C:Superfamily: Flavodoxin; Flavodoxin homology
 C:Keywords: electron transfer; flavoprotein; FMN
 F:5-20/Domain: flavodoxin homology (fragment) <FLX>
 F:9-14/Region: FMN-phosphate binding #status predicted

Query Match 17.7% Score 22; DB 2; Length 20;
 Best Local Similarity 57.1%; Pred. No. 5.8e+03;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 18 NNGATRO 24
 : | : | : |
 Db 10 NTGKTRK 16

RESULT 24

JA0142
 Proteinase inhibitor DE-3 - coral tree (fragment)
 C:Species: Erythrina corallodendron (coral tree)
 C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
 C:Accession: JA0142
 R:Joubert, F.J.
 Phytochemistry 27, 1297-1300, 1988
 A:Title: Purification and properties of proteinase inhibitors from Erythrina corallodend
 A:Reference number: JA0142
 A:Accession: JA0142
 A:Molecule type: protein
 A:Residues: 1-20 <JOU>
 A:Cross-references: UNIPROT:P07475, UNIPARC:UPI00001763AB
 A:Note: proteinase inhibitor DE-3 has an estimated molecular weight of 20K
 C:Superfamily: Plant Kunitz-type proteinase inhibitor
 C:Keywords: proteinase inhibitor

Query Match 17.7% Score 22; DB 2; Length 20;
 Best Local Similarity 57.1%; Pred. No. 5.8e+03;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 16 VLANGAT 22
 : | : | : |
 Db 9 VVQNGGT 15

RESULT 25

D42842
 antifungal 2S storage albumin large chain - radish (fragment)

C:Species: Raphanus sativus (radish)
 C>Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 31-Dec-2004

C:Accession: D42842
 R:Ritters, F.R.; Schoofs, H.M.; De Bolle, M.F.; Van Leuven, F.; Rees, S.B.; Vanderleyden,
 J. Biol. Chem. 267, 15301-15309, 1992
 A:Title: Analysis of two novel classes of plant antifungal proteins from radish (Raphanus

A:Reference number: A42842; PMID:92348373; PMID:1639777
 A:Accession: D42842
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-20 <TER>
 A:Cross-references: UNIPROT:Q9S8Y7, UNIPARC:UPI00000A93E6
 A:Experimental source: seed
 A:Note: sequence extracted from NCBI backbone (NCBIP:109925)
 C:Superfamily: Alpha amylase inhibitor

Query Match 17.7% Score 22; DB 2; Length 20;
 Best Local Similarity 31.2%; Pred. No. 5.8e+03;
 Matches 5; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

QY 4 QNKKYRQFIQSVLNN 19
 : | : | : | : |
 Db 2 QGPGQRPPLQCCNN 17

Search completed: January 26, 2006, 08:05:01
 Job time : 13 secs

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OM protein - protein search, using sw model

Run on: January 26, 2006, 07:47:56 ; Search time 71.3793 Seconds
(without alignments)
237.221 Million cell updates/sec

Title: US-09-662-293-8

Perfect score: 124

Sequence: 1 DMAQNYKYRQOFIQSVLNGATRQ 24

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 216443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 15779

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Uniprot 05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	25.8	20	2	Q4YK5_PLABE
2	32	25.8	20	2	P81074_BACCE
3	30	24.2	15	2	Q9S8A2_HELAN
4	30	24.2	20	1	PUPK_RHOSH
5	29	23.4	20	2	Q4YB5_PLABE
6	29	23.4	21	2	Q7RBF8_PLAYO
7	29	23.4	21	2	Q7RKZ7_PLAYO
8	28.5	23.0	19	2	Q38371_BPMS2
9	28	22.6	17	2	Q7BVD5_BORBU
10	28	22.6	21	2	Q9R5K0_STRPY
11	27.5	22.2	20	2	Q9R5E1_AERHY
12	27	21.8	16	1	HTPG_ACICA
13	27	21.8	18	2	Q4Z714_PLABE
14	27	21.8	19	2	Q9TWY2_LEIME
15	27	21.8	19	2	Q4X617_PLACH
16	27	21.8	21	2	Q4YB5_PLABE
17	26	21.0	17	2	Q7M2E3_SOLTU
18	26	21.0	18	2	Q9TRD8_RABIT
19	26	21.0	21	2	Q4Y571_PLACH
20	25	20.2	9	2	Q9BYF9_HUMAN
21	25	20.2	16	2	Q5G554_BALMU
22	25	20.2	17	2	Q9UM85_HUMAN
23	25	20.2	17	2	Q7M2E9_LYCES
24	25	20.2	17	2	Q9S8Y3_LUPAR
25	25	20.2	18	2	Q9TW6_APLCA
26	25	20.2	18	2	Q8B133_IATY6
27	25	20.2	19	2	Q60F81_CARCR
28	25	20.2	20	2	Q4XN21_PLACH
29	25	20.2	20	2	Q4XWC8_PLACH
30	25	20.2	20	2	Q64619_RAT
31	25	20.2	21	2	Q5BWH5_SCHUA

32	25	20.2	21	2	Q7RPC3_PLAYO	Q7RPC3 plasmodium
33	24	19.4	10	2	Q9R5N6_CLOBO	Q9R5N6 clostridium
34	24	19.4	15	2	Q5K607_CRAGI	Q5K607 crassostrea
35	24	19.4	15	2	Q9MBU7_VIRIU	Q9MBU7 vibrio phag
36	24	19.4	15	2	Q7BVD9_BORBU	Q7BVD9 borrelia bu
37	24	19.4	16	2	Q7RG27_PLABO	Q7RG27 plasmodium
38	24	19.4	17	2	Q4Y9B8_PLABE	Q4Y9B8 plasmodium
39	24	19.4	18	2	Q8VNJ9_PAPAT	Q8VNJ9 haemophilus
40	24	19.4	19	2	Q4XOC6_PLACH	Q4XOC6 plasmodium
41	24	19.4	19	2	Q9QUN1_SWORI	Q9QUN1 ractus sp.,
42	24	19.4	20	2	Q4Y4K7_PLACH	Q4Y4K7 plasmodium
43	24	19.4	20	2	Q4YQN8_PLABE	Q4YQN8 plasmodium
44	24	19.4	21	2	Q9U400_DROXY	Q9U400 drosophila
45	24	19.4	21	2	Q11811_SHIVI	Q11811 human immun
46	23.5	19.0	9	1	HUTU_KLBAE	P12381 klebsiella
47	23.5	19.0	17	2	Q4XN35_PLACH	Q4XN35 plasmodium
48	23	18.5	13	2	Q7PD99_PLAYO	Q7PD99 plasmodium
49	23	18.5	13	2	Q50L81_9DIPR	Q50L81 drosophila
50	23	18.5	13	2	Q79D25_FREDI	Q79D25 fremyella d
51	23	18.5	14	2	Q50176_DROAN	Q50176 drosophila
52	23	18.5	15	2	Q6LC05_PSEAE	Q6LC05 pseudomonas
53	23	18.5	16	2	Q50L70_9DIPR	Q50L70 drosophila
54	23	18.5	16	2	Q50L82_9DIPR	Q50L82 drosophila
55	23	18.5	17	2	Q7R8F8_PLAYO	Q7R8F8 plasmodium
56	23	18.5	17	2	Q7RAG5_PLAYO	Q7RAG5 plasmodium
57	23	18.5	18	2	Q7SCI4_NEUCR	Q7SCI4 neurospora
58	23	18.5	19	2	Q4X3T4_PLACH	Q4X3T4 plasmodium
59	23	18.5	19	2	Q4X3V6_PLACH	Q4X3V6 plasmodium
60	23	18.5	20	1	HGY2_PANDA	P82312 panulirus j
61	23	18.5	20	2	Q9TWN5_THESE	Q9TWN5 theileria s
62	23	18.5	20	2	Q50L73_DROVA	Q50L73 drosophila
63	23	18.5	20	2	Q4XVG2_PLACH	Q4XVG2 plasmodium
64	23	18.5	20	2	Q4Y9Y2_PLABE	Q4Y9Y2 plasmodium
65	23	18.5	21	2	Q4X4U6_PLACH	Q4X4U6 plasmodium
66	23	18.5	21	2	Q4XJY0_PLACH	Q4XJY0 plasmodium
67	23	18.5	21	2	Q4YQZ6_PLABE	Q4YQZ6 plasmodium
68	23	18.5	21	2	Q4YS28_PLABE	Q4YS28 plasmodium
69	23	18.5	21	2	Q4Z1S7_PLABE	Q4Z1S7 plasmodium
70	23	18.5	21	2	Q4Z540_PLABE	Q4Z540 plasmodium
71	23	18.5	21	2	Q66MQ2_9HIV1	Q66MQ2 human immun
72	22.5	18.1	19	2	Q9F6J8_YERPE	Q9F6J8 yersinia pe
73	22	17.7	9	2	Q7ML51_9BACT	Q7ML51 unidentified
74	22	17.7	9	2	Q765Y9_CHICK	Q765Y9 gallus gall
75	22	17.7	11	2	Q5GUT3_COXBU	Q5GUT3 coxiella bu
76	22	17.7	11	2	Q5GUT3_COXBU	Q5GUT3 coxiella bu
77	22	17.7	12	2	Q5EGT6_ANACL	Q5EGT6 anas crecea
78	22	17.7	12	2	Q5EGT8_ANACL	Q5EGT8 anas clypea
79	22	17.7	12	2	Q5EGT9_ANADI	Q5EGT9 anas discor
80	22	17.7	12	2	Q5EGU0_ANAAC	Q5EGU0 anas discor
81	22	17.7	12	2	Q5EGU1_AIXSP	Q5EGU1 aix spona
82	22	17.7	12	2	Q5EGU6_ANAST	Q5EGU6 anas eutep
83	22	17.7	12	2	Q5EGU9_ANAPA	Q5EGU9 anas falc
84	22	17.7	12	2	Q5EGV6_ANAPB	Q5EGV6 anas pemeio
85	22	17.7	12	2	Q5EGW1_ANAAM	Q5EGW1 anas americ
86	22	17.7	12	2	Q5EGW3_ANAST	Q5EGW3 anas sibil
87	22	17.7	14	2	Q6EUU7_CAPHI	Q6EUU7 capra hircu
88	22	17.7	14	2	Q9SM55_BOVIN	Q9SM55 bos taurus
89	22	17.7	15	1	ESTB_SCHGA	P81011 schizaphis
90	22	17.7	15	2	Q4YCG5_PLABE	Q4YCG5 plasmodium
91	22	17.7	16	2	Q96TR0_HUMAN	Q96TR0 homo sapien
92	22	17.7	16	2	Q91923_SHITO	Q91923 shigella bo
93	22	17.7	16	2	Q91925_SHITL	Q91925 shigella fl
94	22	17.7	16	2	Q91927_SHISO	Q91927 shigella so
95	22	17.7	16	2	Q91937_SHISO	Q91937 shigella so
96	22	17.7	17	2	Q9UCF0_HUMAN	Q9UCF0 homo sapien
97	22	17.7	17	2	Q5MBK4_TYMAN	Q5MBK4 tymanoctom
98	22	17.7	17	2	Q76N86_RAT	Q76N86 ractus norv
99	22	17.7	18	2	Q71UR5_HUMAN	Q71UR5 homo sapien
100	22	17.7	18	2	Q9Z178_SHYME	Q9Z178 gryon sp. c

ALIGNMENTS

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RESULT 1
O4YIK5_PLABE PRELIMINARY; PRT; 20 AA.
ID O4YIK5;
AC O4YIK5;
DT 13-SEP-2005 (TRENBLrel. 31, Created)
DT 13-SEP-2005 (TRENBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TRENBLrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=PB40245.00.0;
OS Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5821;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Bertin M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churche C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carnucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrett B., Turner C.M.R., Waters A.P., Sinden R.S.,
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses."
RL Science 307:82-86 (2005).
CC -! CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
KW EMBL; CAI01004758; CAI02160.1; -: Genomic_DNA.
FT NON_TER
SQ SEQUENCE 20 AA; 2282 MW; AF1P9ECC90CFE6FA CRC64;

Query Match 25.8%; Score 32; DB 2; Length 20;
Best Local Similarity 37.5%; Pred. No. 8.2e+02;
Matches 6; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

OY 3 AONYKRYQOFTIOSVLN 18
Db 3 SSGYVFINLFTOKILN 18

RESULT 2
P83074_BACCE PRELIMINARY; PRT; 20 AA.
ID P83074;
AC P83074;
DT 01-OCT-2001 (TRENBLrel. 18, Created)
DT 01-OCT-2001 (TRENBLrel. 18, Last sequence update)
DT 01-OCT-2001 (TRENBLrel. 25, Last annotation update)
DE 60 kDa chaperonin (Protein Cpn60) (groEL protein) (Fragment).
OS Bacillus cereus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1396;
RN [1]
RP PROTEIN SEQUENCE, AND INDUCTION.
RA STRAIN=NCIMB 11796;
RA Browne N., Dowds B.C.A.;
RL Submitted (JUL-2001) to Swiss-Prot.
CC -! FUNCTION: Prevents misfolding and promotes the refolding and
CC proper assembly of unfolded polypeptides generated under stress
CC conditions (By similarity).
CC -! SUBUNIT: Oligomer of 14 subunits composed of two stacked rings of
CC 7 subunits (By similarity).
CC -! INDUCTION: By heat shock.
CC -! SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0051082; F:unfolded protein binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR001844; Chaperin_Cpn60.
DR PROSITE; PS00296; CHAPERONIN_CPN60; PARTIAL.
KW ATP-binding; Chaperone; Heat shock.
FT NON_TER 20

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SQ SEQUENCE 20 AA; 2307 MW; 0AC72E346264AF03 CRC64;

Query Match 25.8%; Score 32; DB 2; Length 20;
Best Local Similarity 46.7%; Pred. No. 8.2e+02;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 3 AONYKRYQOFTIOSVL 17
Db 1 AKNIKFSQARSRSL 15

RESULT 3
O9S8A2_HELAN PRELIMINARY; PRT; 15 AA.
ID O9S8A2_HELAN;
AC O9S8A2;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TRENBLrel. 14, Last annotation update)
DE Oleosin (Fragment).
OS Helianthus annuus (Common sunflower).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Campanulids; Asterales; Asteraceae; Asteroidae; Heliantheae;
OC Helianthus.
OX NCBI_TaxID=4232;
RN [1]
RP PROTEIN SEQUENCE.
RA MEDLINE=96195148; PubMed=8660304;
RA Willrich M., Tacham A.S., Jackson F., Griffiths G., Shewry P.R.,
RA Stobart A.K.;
RT "Purification and characterization of oil-bodies (oleosomes) and oil-
RT body boundary proteins (oleosins) from the developing cotyledons of
RT sunflower (Helianthus annuus L.)."
RL Biochem. J. 314:333-337 (1996).
SQ SEQUENCE 15 AA; 1619 MW; CDC28A062F7F8704 CRC64;

Query Match 24.2%; Score 30; DB 2; Length 15;
Best Local Similarity 54.5%; Pred. No. 1.2e+03;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 13 IQSVLNGATR 23
Db 5 VAGFLNNGAFR 15

RESULT 4
PUFK_RHOSH STANDARD; PRT; 20 AA.
ID PUFK_RHOSH;
AC Q53121; O08033;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Transcriptional regulatory protein pufK.
GN Name=pufK.
OS Rhodospirillum rubrum (Rhodospirillum rubrum).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
OC Rhodospirillaceae; Rhodospirillum.
OX NCBI_TaxID=1063;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA STRAIN=ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158;
RX MEDLINE=96349111; PubMed=8760918;
RA Gong L., Kaplan S.;
RT "Translational control of puf operon expression in Rhodospirillum
RL rubrum 2.4.1."
RN Microbiology 142:2057-2069 (1996).
RP NUCLEOTIDE SEQUENCE.
RA STRAIN=ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158;
RA McIlvinn P.;
RT "R. rubrum genes bchC, bchX, bchY, bchZ and pufQ."
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [3]

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RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158;
 RA MEDLINE=20115911; Pubmed=10648776; DOI=10.1093/nar/28.4.862;
 RT Choudhary M., Kaplan S.;
 RT "DNA sequence analysis of the photosynthesis region of Rhodobacter
 sphaeroides 2.4.1.";
 RL Nucleic Acids Res. 28:862-867(2000).
 CC -!- FUNCTION: Involved in the transcriptional regulation of putB.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR EMBL; S82643; AAB46798.1; -; Genomic DNA.
 DR EMBL; AJ010302; CAB38751.1; -; Genomic DNA.
 DR EMBL; AF195122; AAF24301.1; -; Genomic DNA.
 DR PIR; T50757; T50757.
 KM Transcription; Transcription regulation.
 SQ SEQUENCE 20 AA; 2262 MW; 764DBD64B9DD990C CRC64;
 Query Match 24.2%; Score 30; DB 1; Length 20;
 Best Local Similarity 50.0%; Pred. No. 1.7e+03;
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 Oy 9 RQGFQSVLVNNG 20
 Db 8 RHQHVASVLRSG 19

RESULT 5
 Q4YUE5_PLABE PRELIMINARY; PRT; 20 AA.
 ID Q4YUE5;
 AC Q4YUE5;
 DT 13-SEP-2005 (TREMBlrel. 31, Created)
 DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
 DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
 DE Hypothetical protein (Fragment).
 GN ORFNames=PB105963.00.0;
 OS Plasmodium bershei.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5821;
 RN [1]
 NP NUCLEOTIDE SEQUENCE.
 RA Hall N., Karas M., Raine J.D., Carlton J.M., Kooij T.W.A.,
 RA Berlihan M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
 RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
 RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
 RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
 RA Janse C.J., Barrett B., Turner C.M.R., Waters A.P., Sinden R.S.;
 RT "A comprehensive survey of the Plasmodium life cycle by genomic,
 RT transcriptomic, and proteomic analyses.";
 RL Science 307:82-86(2005).
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC EMBL; CAA101002380; CAH98362.1; -; Genomic DNA.
 KM Hypothetical protein.
 FT NON TER 1
 SQ SEQUENCE 20 AA; 2265 MW; 1322E950F0B057BF CRC64;
 Query Match 23.4%; Score 29; DB 2; Length 20;
 Best Local Similarity 44.4%; Pred. No. 2.5e+03;
 Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
 Oy 7 KYRQGFQSVLVNNGATRG 24
 Db 2 KHMOCITVSNLNGLATNE 19

RESULT 6
 Q7RBF8_PLAYO

ID Q7RBF8_PLAYO PRELIMINARY; PRT; 21 AA.
 AC Q7RBF8;
 DT 01-MAR-2004 (TREMBlrel. 26, Created)
 DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Hypothetical protein (Fragment).
 GN Name=PY06186;
 OS Plasmodium yoelii yoelii.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=73239;
 RN [1]
 NP NUCLEOTIDE SEQUENCE.
 RC STRAIN=17XNL;
 RX MEDLINE=22255706; Pubmed=12368865; DOI=10.1038/nature01099;
 RA Carlton J.M., Angiuoli S.V., Sun B.B., Kooij T.W., Perera M.,
 RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
 RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
 RA Shallom S.J., van Aken S.E., Riedmiller S.B., Feldblyum T.V.,
 RA Cho J.K., Quackenbush J., Sedegah M., Shoabhi A., Cummings L.M.,
 RA Florens L., Yates J.R., Iit, Raine J.D., Sinden R.E., Harris M.A.,
 RA Cunningham D.A., Preiser P.R., Bergman L.W., Valdiva A.B.,
 RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
 RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
 RA Carucci D.J.;
 RT "Genome sequence and comparative analysis of the model rodent malaria
 RT parasite Plasmodium yoelii yoelii.";
 RL Nature 419:512-519(2002).
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AABL01002064; EAA18352.1; -; Genomic DNA.
 KM Hypothetical protein.
 FT NON TER 1
 SQ SEQUENCE 21 AA; 2763 MW; BD4713F274E82473 CRC64;
 Query Match 23.4%; Score 29; DB 2; Length 21;
 Best Local Similarity 35.7%; Pred. No. 2.6e+03;
 Matches 5; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
 Oy 5 NYKYRQGFQSVLVN 18
 Db 4 NYWYRHIMWHIYN 17

RESULT 7
 Q7RZK7_PLAYO PRELIMINARY; PRT; 21 AA.
 ID Q7RZK7;
 AC Q7RZK7;
 DT 01-MAR-2004 (TREMBlrel. 26, Created)
 DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Hypothetical protein (Fragment).
 GN Name=PY02751;
 OS Plasmodium yoelii yoelii.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=73239;
 RN [1]
 NP NUCLEOTIDE SEQUENCE.
 RC STRAIN=17XNL;
 RX MEDLINE=22255706; Pubmed=12368865; DOI=10.1038/nature01099;
 RA Carlton J.M., Angiuoli S.V., Sun B.B., Kooij T.W., Perera M.,
 RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
 RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
 RA Shallom S.J., van Aken S.E., Riedmiller S.B., Feldblyum T.V.,
 RA Cho J.K., Quackenbush J., Sedegah M., Shoabhi A., Cummings L.M.,
 RA Florens L., Yates J.R., Iit, Raine J.D., Sinden R.E., Harris M.A.,
 RA Cunningham D.A., Preiser P.R., Bergman L.W., Valdiva A.B.,
 RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
 RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
 RA Carucci D.J.;
 RT "Genome sequence and comparative analysis of the model rodent malaria
 RT parasite Plasmodium yoelii yoelii.";
 RL Nature 419:512-519(2002).

-1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABJ01000761; EAA22236.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON_TER
SQ SEQUENCE 21 AA; 2533 MW; C7BB3387484628C1 CRC64;
Query Match 23.4%; Score 29; DB 2; Length 21;
Best Local Similarity 55.6%; Pred. No. 2.6e+03;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Qy 11 QFIQSVLNN 19
Db 10 KFIISIINN 16
RESULT 8
Q38371_BPMS2 PRELIMINARY; PRT; 19 AA.
ID Q38371_BPMS2 PRELIMINARY; PRT; 19 AA.
AC Q38371
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Coat protein; NCBI gi: 553004 (Fragment).
OS Bacteriophage MS2.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Levivirus; Levivirus subgroup I.
NCBI_TaxID=12022;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=73163785; PubMed=4512458;
RA Contreras R.R., Ysebaert M., Jou W.M., Fiers W.;
RT "Bacteriophage MS2 RNA: nucleotide sequence of the end of the a
RL Nature New Biol. 241:99-101(1973).
DR EMBL; M25187; AAA32258.1; -; Genomic_RNA.
DR HSSP; P03612; IMSC.
KW Capsid protein.
FT NON_TER 19
SQ SEQUENCE 19 AA; 1972 MW; 71CB7F78026D26C8 CRC64;
Query Match 23.0%; Score 28.5; DB 2; Length 19;
Best Local Similarity 38.1%; Pred. No. 2.8e+03;
Matches 8; Conservative 5; Mismatches 3; Indels 5; Gaps 2;
Qy 2 MAQNKYRQFIQSVLNNCAT 22
Db 1 MASNFF--TQFV--LVNDGGT 16
RESULT 9
Q7BVD5_BORBU PRELIMINARY; PRT; 17 AA.
ID Q7BVD5_BORBU PRELIMINARY; PRT; 17 AA.
AC Q7BVD5;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Borrelia burgdorferi plasmid cp32-7, possible partition proteins,
DE complete cds. (Fragment).
OS Borrelia burgdorferi (Lyme disease spirochete).
OC Plasmid cp32-7.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia;
OC Borrelia burgdorferi group.
NCBI_TaxID=139;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B31;
RX MEDLINE=98361033; PubMed=9695920;
RA Stevenson B., Casjens S., Rosa P.;
RT "Evidence of past recombination events among the genes encoding the
RL Ebp antigens of Borrelia burgdorferi.";
Microbiology 144:1869-1879(1998).

DR EMBL; AF022483; AAC35457.1; -; Genomic_DNA.
KW Plasmid.
FT NON_TER 17
SQ SEQUENCE 17 AA; 2060 MW; 6B5830E468E030E2 CRC64;
Query Match 22.6%; Score 28; DB 2; Length 17;
Best Local Similarity 42.9%; Pred. No. 3e+03;
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
Qy 5 NYKKRQFIQSVLN 18
Db 3 NLAYRTYIESIKN 16
RESULT 10
Q9RSKO_STRPY PRELIMINARY; PRT; 21 AA.
ID Q9RSKO_STRPY PRELIMINARY; PRT; 21 AA.
AC Q9RSKO;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Mitogenic factor (Fragment).
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
NCBI_TaxID=1314;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=92354761; PubMed=1644200; DOI=10.1016/0014-5793(92)81043-L;
RA Yutsudo T., Mural H., Gonzalez J., Takao T., Shimonishi Y., Takeda Y.,
RA Igataashi H., Hinuma Y.;
RT "A new type of mitogenic factor produced by Streptococcus pyogenes.";
RL FEBS Lett. 308:30-34(1992).
FT NON_TER 1
SQ SEQUENCE 21 AA; 2265 MW; 3ADD561319EF8FB5 CRC64;
Query Match 22.6%; Score 28; DB 2; Length 21;
Best Local Similarity 62.5%; Pred. No. 3.8e+03;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
Qy 16 VLNNGATR 23
Db 9 VLNDGASK 16
RESULT 11
Q9RSE1_AERHY PRELIMINARY; PRT; 20 AA.
ID Q9RSE1_AERHY PRELIMINARY; PRT; 20 AA.
AC Q9RSE1;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE Outer-membrane channel-forming protein IV (Fragment).
OS Aeromonas hydrophila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
NCBI_TaxID=644;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=9113115; PubMed=1283000;
RA Jeanneur D., Gleason N., Patrus F., Buckley J.T.;
RT "Purification of Aeromonas hydrophila major outer-membrane proteins:
RT N-terminal sequence analysis and channel-forming properties.";
RL Mol. Microbiol. 6:335-3353 (1992).
SQ SEQUENCE 20 AA; 2458 MW; EEDFCB4EEDC66D00 CRC64;
Query Match 22.2%; Score 27.5; DB 2; Length 20;
Best Local Similarity 53.8%; Pred. No. 4.4e+03;
Matches 7; Conservative 2; Mismatches 3; Indels 1; Gaps 1;
Qy 1 DMAQN-YKVRQOF 12
Db 1 DMAQN-YKVRQOF 12

Db 6 DIHNDYKRRMQF 18

RESULT 12

HTPE_ACICA STANDARD; PRT; 16 AA.

AC P81876;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Chaperone protein htpg (Heat shock protein htpg) (High temperature protein G) (Fragment).

DE Name=htpg;

GN Acinetobacter calcoaceticus.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

OC Moraxellaceae; Acinetobacter.

OX NCBI_TaxID=471;

RN [1]

RP PROTEIN SEQUENCE.

RC STRAIN=69-V;

RX DOI=10.1002/(STRT)1522-2663(19990101)20:4/5<781::AID-ELPS781>3.0.CO;2-A;

RA Beandorf D., Lofthagen N., Babel W.;

RT "Induction of heat shock proteins in response to primary alcohols in Acinetobacter calcoaceticus."

RL Electrophoresis 20:781-789(1999).

CC -1- FUNCTION: Molecular chaperone. Has ATPase activity (By similarity).

CC -1- SUBUNIT: Homodimer (By similarity).

CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

CC -1- INDUCTION: By heat shock and primary alcohols.

CC -1- SIMILARITY: Belongs to the heat shock protein 90 family.

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CC -----

DR HAMAP: MF_00505; -; 1.

DR InterPro: IPR001404; Hep90.

DR PROSITE: PS00298; HSP90; PARTIAL.

KW ATP-binding; Chaperone; Direct protein sequencing; Heat shock;

KW Nucleotide-binding.

FT NON_TER 16

FT SEQUENCE 16 AA; 1770 MW; 316C70D8928CB482 CRC64;

SO

Query Match 21.8%; Score 27; DB 1; Length 16;

Best Local Similarity 33.3%; Pred. No. 4.1e+03;

Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 3 AQNYKYRQFIQ 14

Db 5 SQNYSFQAEVAQ 16

RESULT 13

Q42714_PLABE PRELIMINARY; PRT; 18 AA.

AC Q42714;

DT 13-SEP-2005 (T-EMBLrel. 31, Created)

DT 13-SEP-2005 (T-EMBLrel. 31, Last sequence update)

DT 13-SEP-2005 (T-EMBLrel. 31, Last annotation update)

DE Hypothetical protein (Fragment).

DE ORFNames=PB100192.00.0;

GN Plasmodium berghei.

OS Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

OC NCBI_TaxID=5821;

OX [1]

RP NUCLEOTIDE SEQUENCE.

RA Hall N., Karrae M., Raine J.D., Carlton J.M., Kooij T.W.A.,

RA Bertrman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,

RA James K., Rutherford K., Harris B., Harris D., Churcher C.,

RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,

RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,

RA Jansse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;

RT "A comprehensive survey of the Plasmodium life cycle by genomic, transcriptomic, and proteomic analyses."

RL Science 307:82-86(2005).

CC -1- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.

CC EMBL; CAI0100075; CAH93662.1; -; Genomic_DNA.

DR EMBL; CAI0100075; CAH93662.1; -; Genomic_DNA.

KW Hypothetical protein.

FT NON_TER 1

FT SEQUENCE 18 AA; 2291 MW; 3C53320CDAF8CF29 CRC64;

SO

Query Match 21.8%; Score 27; DB 2; Length 18;

Best Local Similarity 33.3%; Pred. No. 4.7e+03;

Matches 6; Conservative 3; Mismatches 7; Indels 2; Gaps 1;

OY 6 YKRRQFIQSVLNGAT 23

Db 3 YKRR--FFLSIFKNVWK 18

RESULT 14

Q9TWY2_LEIME PRELIMINARY; PRT; 19 AA.

AC Q9TWY2;

DT 01-MAY-2000 (T-EMBLrel. 13, Created)

DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)

DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)

DE Membrane-bound acid phosphatase (Fragment).

DE Leishmania mexicana.

OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.

OX NCBI_TaxID=5665;

RN [1]

RP PROTEIN SEQUENCE.

RX MEDLINE=91312388; PubMed=1857378; DOI=10.1016/0166-6851(91)90152-V;

RA Menz B., Winter G., Ifig T., Lottspeich F., Overath P.;

RT "Purification and characterization of a membrane-bound acid phosphatase of Leishmania mexicana."

RL Mol. Biochem. Parasitol. 47:101-108(1991).

DR InterPro: IPR000560; HisAc phosphatase.

DR Pfam: PF00328; Acid_phosphat_A; 1.

FT NON_TER 1

FT NON_TER 19

FT SEQUENCE 19 AA; 2178 MW; EC44360F28A7D71B CRC64;

SO

Query Match 21.8%; Score 27; DB 2; Length 19;

Best Local Similarity 35.7%; Pred. No. 5e+03;

Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

OY 8 YROQFIQSVLNGA 21

Db 4 YKVELVQVVRHGA 17

RESULT 15

Q4X617_PLACH PRELIMINARY; PRT; 19 AA.

AC Q4X617;

DT 13-SEP-2005 (T-EMBLrel. 31, Created)

DT 13-SEP-2005 (T-EMBLrel. 31, Last sequence update)

DT 13-SEP-2005 (T-EMBLrel. 31, Last annotation update)

DE Hypothetical protein (Fragment).

DE ORFNames=PC405777.00.0;

GN Plasmodium chabaudi.

OS Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

OC NCBI_TaxID=5825;

OX [1]

RP NUCLEOTIDE SEQUENCE.

RA Hall N., Karrae M., Raine J.D., Carlton J.M., Kooij T.W.A.,

RA Bertrman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,

RA James K., Rutherford K., Harris B., Harris D., Churcher C.,

RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
 RA Bidwell S.L., Rajandream M.A., Carnucci D.J., Yates J.R., Kafatos F.C.,
 RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.,
 RT "A comprehensive survey of the Plasmodium life cycle by genomic,
 RL transcriptomic, and proteomic analyses.";
 Science 307:82-86(2005).
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC EMBL; CA01009496; CA87489.1; -; Genomic_DNA.
 KW Hypothetical protein.
 DR NON TER 1
 FT SEQUENCE 19 AA; 2278 MW; FA6AC117648F8A9 CRC64;
 SQ
 Query Match 21.8%; Score 27; DB 2; Length 19;
 Best Local Similarity 30.8%; Pred. No. 5e+03;
 Matches 4; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
 Oy 2 MAQNYKRYQRFIQ 14
 Db 5 ITQNYQIKQDMAE 17

RESULT 16
 Q4YBES_PLABE PRELIMINARY; PRT; 21 AA.
 ID Q4YBES_PLABE PRELIMINARY;
 AC Q4YBES_PLABE PRELIMINARY;
 DT 13-SEP-2005 (TReMBLrel. 31, Created)
 DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)
 DE Hypothetical protein (Fragment).
 GN ORFNames=PB106774.00.0;
 OS Plasmodium berghei;
 CC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 CC NCBI_TaxID=5821;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
 RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
 RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
 RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
 RA Bidwell S.L., Rajandream M.A., Carnucci D.J., Yates J.R., Kafatos F.C.,
 RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.,
 RT "A comprehensive survey of the Plasmodium life cycle by genomic,
 RL transcriptomic, and proteomic analyses.";
 Science 307:82-86(2005).
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC EMBL; CA01006816; CA104804.1; -; Genomic_DNA.
 KW Hypothetical protein.
 DR NON TER 1
 FT SEQUENCE 21 AA; 2501 MW; F4140B6CCFA1E386 CRC64;
 SQ
 Query Match 21.8%; Score 27; DB 2; Length 21;
 Best Local Similarity 55.6%; Pred. No. 5.6e+03;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 Oy 2 MAQNYKRYQ 10
 Db 6 LVQNYKCSQ 14

RESULT 17
 Q7M2E3_SOLTU PRELIMINARY; PRT; 17 AA.
 ID Q7M2E3_SOLTU PRELIMINARY;
 AC Q7M2E3;
 DT 01-MAR-2004 (TReMBLrel. 26, Created)
 DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
 DE Hypothetical 2.1K protein.
 OS Solanum tuberosum (Potato).
 OG Chloroplast.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamids; Solanales; Solanaceae; Solanum.
 CC NCBI_TaxID=4113;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Kwaage Y., Kikuta Y.,
 RT "Chloroplast DNA evolution in potato (Solanum tuberosum L.).";
 RL Theor. Appl. Genet. 81:13-20(1991).
 DR PIR; JQ2320; JQ2320.
 SQ SEQUENCE 17 AA; 2089 MW; 02326E0F9569C176 CRC64;
 SQ
 Query Match 21.0%; Score 26; DB 2; Length 17;
 Best Local Similarity 50.0%; Pred. No. 6.4e+03;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 Oy 2 MAQNYKRY 9
 Db 1 MKSNYSYK 8

RESULT 18
 Q9TRD8_RABIT PRELIMINARY; PRT; 18 AA.
 ID Q9TRD8_RABIT PRELIMINARY;
 AC Q9TRD8;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
 DE Chapteronin (Fragment).
 OS Oryctolagus cuniculus (Rabbit).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
 CC Oryctolagus.
 CC NCBI_TaxID=9986;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=94089752; PubMed=7903455;
 RA Rommelaere H., Van Troys M., Gao Y., Melki R., Cowan N.J.,
 RA Vandekerckhove J., Ampe C.,
 RT "Eukaryotic cytosolic chapteronin contains t-complex polypeptide 1 and
 RL seven related subunits.";
 P roc. Natl. Acad. Sci. U.S.A. 90:11975-11979(1993).
 SQ SEQUENCE 18 AA; 1884 MW; B608F6EB5A8A2A6 CRC64;
 SQ
 Query Match 21.0%; Score 26; DB 2; Length 18;
 Best Local Similarity 62.5%; Pred. No. 6.8e+03;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Oy 15 SVLNGAT 22
 Db 10 TVTNDGAT 17

RESULT 19
 Q4Y571_PLACH PRELIMINARY; PRT; 21 AA.
 ID Q4Y571_PLACH PRELIMINARY;
 AC Q4Y571;
 DT 13-SEP-2005 (TReMBLrel. 31, Created)
 DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)
 DE Hypothetical protein (Fragment).
 GN ORFNames=PC101630.00.0;
 OS Plasmodium chabaudi.
 CC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 CC NCBI_TaxID=5825;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
 RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
 RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
 RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
 RA Bidwell S.L., Rajandream M.A., Carnucci D.J., Yates J.R., Kafatos F.C.,
 RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.,

RT "A comprehensive survey of the Plasmodium life cycle by genomic, transactipomic, and proteomic analyses.";
 RL Science 307:82-86 (2005).
 CC -1- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.
 CC EMBL; CAJ01000943; CAH75689.1; -; Genomic_DNA.
 DR EMBL; CAJ01000943; CAH75689.1; -; Genomic_DNA.
 KW Hypothetical protein.
 FT NON TER 1
 SQ SEQUENCE 21 AA; 2792 MW; 56BBD6970F8923FE CRC64;

Query Match 21.0%; Score 26; DB 2; Length 21;
 Best Local Similarity 57.1%; Pred. No. 8.1e+03;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 MAONYKY 8
 DB 6 ICNNYKY 12

RESULT 20

09BYF9_HUMAN PRELIMINARY; PRT; 9 AA.
 AC 09BYF9;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Cytochrome 19 (Fragment).
 GN Name=K19;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=21539745; PubMed=11682035; DOI=10.1016/S0168-8278(01)00167-2;
 RA Kagawa M., Kaneo S., Ohno H., Inamura K., Kobayashi K.;
 RT "Cloning and characterization of the 5'-flanking region of human cytochrome 19 gene in human cholangiocarcinoma cell line."
 RL J. Hepatol. 35:504-511(2001).
 DR EMBL; AB045973; BAB40770.1; -; Genomic_DNA.
 DR GO; GO:0005882; C:Intermediate filament; IEA.
 KM Keratin.
 FT NON TER 9
 SQ SEQUENCE 9 AA; 1122 MW; 9E9FC41B45AB45A1 CRC64;

Query Match 20.2%; Score 25; DB 2; Length 9;
 Best Local Similarity 66.7%; Pred. No. 2.2e+06;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 NYKXKQ 10
 DB 3 SYSYKQ 8

RESULT 21

05G554_BALMU PRELIMINARY; PRT; 16 AA.
 AC 05G554;
 DT 10-MAY-2005 (TREMBlrel. 30, Created)
 DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)
 DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)
 DE DNA polymerase beta (Fragment).
 GN Name=POLB;
 OS Balaeoptera musculus (Blue whale).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;
 OC Mysticeti; Balaeopteridae; Balaeoptera.
 OX NCBI_TaxID=9771;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Conway C.A., May B.P.;

RT "Global Population Structure of Blue Whales Balaeoptera musculus ssp
 RT Based on Nuclear Genetic Variation";
 RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY851160; AAW65802.1; -; Genomic_DNA.
 FT NON TER 1
 FT NON TER 1
 SQ SEQUENCE 16 AA; 1732 MW; 06E7C60F1ACB84B0 CRC64;

Query Match 20.2%; Score 25; DB 2; Length 16;
 Best Local Similarity 55.6%; Pred. No. 8.6e+03;
 Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 14 QSVANGAT 22
 DB 2 QETLNGIT 10

RESULT 22

09UM85_HUMAN PRELIMINARY; PRT; 17 AA.
 AC 09UM85;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Beta-globin protein (Fragment).
 GN Name=beta-globin;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=96352914; PubMed=8718696;
 RA Rahbar S., Nozari G., Forrest G., Gelbart T., Forman S.J., Beutler E.;
 RT "A novel intrachromosomal rearrangement in the beta-globin gene found in an African-American family."
 RL Hemoglobin 19:375-388(1995).
 DR EMBL; S82767; AAD14420.1; -; Genomic_DNA.
 DR HSSP; P02023; IC7C.
 FT NON TER 17
 SQ SEQUENCE 17 AA; 2104 MW; 4197E5B5E5260504 CRC64;

Query Match 20.2%; Score 25; DB 2; Length 17;
 Best Local Similarity 40.0%; Pred. No. 9.2e+03;
 Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 YKXROQFIQS 15
 DB 5 YPWTRPFES 14

RESULT 23

07M2E9_LYCES PRELIMINARY; PRT; 17 AA.
 AC 07M2E9;
 DT 01-MAR-2004 (TREMBlrel. 26, Created)
 DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Hypothetical 2.1K protein.
 OS Lycopersicon esculentum (Tomato).
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.
 OX NCBI_TaxID=4081;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Kawagoe Y., Kikuta Y.;
 RT "Chloroplast DNA evolution in potato (Solanum tuberosum L.).";
 RL Theor. Appl. Genet. 81:13-20(1991).
 DR PIR; J02310; J02310.
 SQ SEQUENCE 17 AA; 2099 MW; 02326E0F9569C2B9 CRC64;

Query Match 20.2%; Score 25; DB 2; Length 17;
 Best Local Similarity 50.0%; Pred. No. 9.2e+03;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 MAQNYKYR 9
 | | | | |
 Db 1 MKPNYSYK 8

RESULT 24

09S8Y3 LUPAR PRELIMINARY; PRT; 17 AA.
 AC 09S8Y3 LUPAR PRELIMINARY; PRT; 17 AA.
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE L-asparaginase isoform A (EC 3.5.1.1) (Fragment).
 OS Lupinus arboreus (Tree lupin).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids 1; Fabales; Fabaceae; Papilionoideae; Genisteae; Lupinus.
 OX NCBI_TaxID=3872;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=92344803; PubMed=1368361; DOI=10.1016/0031-9422(92)83098-J;
 RA Lough T.J., Chang K.S., Carne A., Monk B.C., Reynolds P.H.,
 RA Farnden K.J.;
 RL Phytochemistry 31:1519-1527(1992).
 DR GO; GO:0004067; F:asparaginase activity; IEA.
 SQ SEQUENCE 17 AA; 1703 MW; 9AEDD9691F7F0807 CRC64;

Query Match 20.2%; Score 25; DB 2; Length 17;
 Best Local Similarity 60.0%; Pred. No. 9.2e+03;
 Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 13 IOSVLNNGAT 22
 | | | | |
 Db 6 IGSVLNNGT 15

RESULT 25

09TWV6 APLCA PRELIMINARY; PRT; 18 AA.
 AC 09TWV6 APLCA PRELIMINARY; PRT; 18 AA.
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
 DE APLYSIA gonad lectin (Fragment).
 OS Aplysia californica (California sea hare).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Apogastropoda; Heterobranchia; Euthyneura; Opisthobranchia; Anaspiidea;
 OC Aplysioidea; Aplysiidae; Aplysia.
 OX NCBI_TaxID=6500;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=8957436; PubMed=1431843;
 RA Wilson M.P., Carrow G.W., Levitan I.B.;
 RT "Modulation of growth of Aplysia neurons by an endogenous lectin."
 RL J. Neurobiol. 23:739-750(1992).
 SQ SEQUENCE 18 AA; 2105 MW; 5652840B573057D8 CRC64;

Query Match 20.2%; Score 25; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 9.8e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 NYXY 8
 | | | | |
 Db 15 NYXY 18

Search completed: January 26, 2006, 08:03:54
 Job time : 74.3793 secs

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OM protein - protein search, using sw model

Run on: January 26, 2006, 07:47:09 ; Search time 78.1207 Seconds
(without alignments)
129.360 Million cell updates/sec

Title: US-09-662-293-9

Perfect score: 118
Sequence: 1 DEKNVKKYVLYTMHYLNLNGATR 23

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 897420

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database :

A_Geneseq_21: *
1: geneseqp1980s: *
2: geneseqp1990s: *
3: geneseqp2000s: *
4: geneseqp2001s: *
5: geneseqp2002s: *
6: geneseqp2003as: *
7: geneseqp2003bs: *
8: geneseqp2004s: *
9: geneseqp2005s: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44.5	37.7	20	2	AAR15535 Immunop
2	35	29.7	16	5	ABP46205 Human Bly
3	35	29.7	16	7	ADG97032 scFV VHCD
4	34	28.8	12	6	AAE30892 Human Bly
5	34	28.8	16	5	ABP46248 Human Bly
6	34	28.8	16	7	ADG97075 scFV VHCD
7	34	28.8	20	2	AAR15580 Immunop
8	33.5	28.4	14	8	ADR88216 Human Bly
9	33.5	28.4	14	8	ADR78183 Functiona
10	33.5	28.4	15	9	AEA42432 Human Bly
11	33.5	28.4	15	9	ADU70841 Human Bly
12	33.5	28.4	15	9	ADU71059 Human Bly
13	33.5	28.4	15	9	ADU71060 Human Bly
14	33.5	28.4	15	9	ADU71272 Human Bly
15	33.5	28.4	15	9	ADU70927 Human Bly
16	33.5	28.4	15	9	ADU70927 Human Bly
17	33	28.0	15	9	ADU70969 Hepatoma
18	33	28.0	15	9	ADU71114 Human Bly
19	33	28.0	17	3	AAB06372 Randomise
20	33	28.0	18	3	AAB06381 Randomise
21	33	28.0	18	3	AAB06379 Randomise
22	33	28.0	18	3	AAB05890 Randomise
23	33	28.0	18	3	AAB06385 Randomise
24	32	27.1	9	5	ABB94872 CTL epit

25	32	27.1	9	9	ADU70797 Human hep
26	32	27.1	9	9	ADU70700 Human hep
27	32	27.1	9	9	ADU70638 Human hep
28	32	27.1	9	9	ADU70662 Human hep
29	32	27.1	9	9	ADU70639 Human hep
30	32	27.1	10	8	ABY00912 SARS coro
31	32	27.1	13	7	ADM75353 Potential
32	32	27.1	13	7	ADM75618 Potential
33	32	27.1	13	7	ADM74824 Potential
34	32	27.1	15	5	ABP46898 Human Bly
35	32	27.1	15	7	ADG97725 scFV VHCD
36	32	27.1	15	7	ADM75913 Human MHC
37	32	27.1	15	7	ADM75938 Human MHC
38	32	27.1	15	7	ADM75962 Human MHC
39	32	27.1	15	7	ADM75981 Human MHC
40	32	27.1	15	8	ADG06417 Human B-d
41	32	27.1	15	9	ADU71058 Human hep
42	32	27.1	15	9	ADU70968 Human hep
43	32	27.1	15	9	ADU71210 Human hep
44	32	27.1	15	9	AEA00411 LaSsa vir
45	32	27.1	16	9	AEA15030 pTfG Lox
46	32	27.1	17	3	AAB06393 Randomise
47	32	27.1	17	3	AAB05887 Randomise
48	32	27.1	18	3	AAB06363 Randomise
49	32	27.1	20	5	ABP46885 Human Bly
50	32	27.1	20	5	ABP46147 Human Bly
51	32	27.1	20	5	ABP46892 Human Bly
52	32	27.1	20	7	ADG97712 scFV VHCD
53	32	27.1	20	7	ADG96974 scFV VHCD
54	32	27.1	20	7	ADG97719 scFV VHCD
55	32	27.1	20	9	ADM52290 Human PL
56	31	26.3	12	7	ADCL4017 Rheumatoid
57	31	26.3	13	1	AAP60378 Antigenic
58	31	26.3	14	2	ADV57777 G protein
59	31	26.3	15	2	AAW49219 Human leu
60	31	26.3	15	7	ADCL7629 Type IV c
61	31	26.3	15	8	ADRL9151 Type IV c
62	31	26.3	16	5	ABP46206 Human Bly
63	31	26.3	16	5	ABP46305 Human Bly
64	31	26.3	16	5	ABP46204 Human Bly
65	31	26.3	16	5	ABP46203 Human Bly
66	31	26.3	16	5	ABP46287 Human Bly
67	31	26.3	16	5	ABP46208 Human Bly
68	31	26.3	16	7	ADG97035 scFV VHCD
69	31	26.3	16	7	ADG97031 scFV VHCD
70	31	26.3	16	7	ADG97132 scFV VHCD
71	31	26.3	16	7	ADG97030 scFV VHCD
72	31	26.3	16	7	ADG97114 scFV VHCD
73	31	26.3	16	7	ADG97033 scFV VHCD
74	31	26.3	17	9	AEA44861 Apolipop
75	31	26.3	18	6	ABJ38660 VH-CDR3 p
76	31	26.3	18	6	ADA89069 Human c10
77	31	26.3	18	7	ADG74321 Human VH-
78	31	26.3	18	9	ADW38809 T-cell me
79	31	26.3	20	3	AAI87760 Potato TH
80	31	26.3	20	3	AAI87761 Potato TH
81	31	26.3	20	3	AAI87765 Potato TH
82	31	26.3	20	3	AAI87764 Potato TH
83	31	26.3	20	9	ADU98711 Lung tumo
84	31	26.3	20	9	AEH10519 Mouse mon
85	30	25.4	9	8	ADM12519 MHC class
86	30	25.4	9	8	ADM12519 MHC class
87	30	25.4	10	2	AAV7636 Human tyr
88	30	25.4	11	4	AAW9163 Vaccine r
89	30	25.4	11	8	ADN17001 GI-alpha
90	30	25.4	13	8	ADM12490 TI-key/hu
91	30	25.4	13	8	ADM12542 TI-key/hu
92	30	25.4	13	8	ADO38773 Tyrosinas
93	30	25.4	13	8	ADO38773 Human tyr
94	30	25.4	15	2	AAW45823 Peptide r
95	30	25.4	15	2	AAW45618 Peptide r
96	30	25.4	16	6	ABO04914 Human col
97	30	25.4	16	7	ADK40554 KDR & VEG

98	30	25.4	16	7	ADK40360 Cyclic pe
99	30	25.4	16	8	Adm12543 Ii-key/hu
100	30	25.4	16	8	Ado38774 Human tyr

ALIGNMENTS

RESULT 1

AARI5535 standard; protein; 20 AA.

AARI5535;

02-MAR-1992 (first entry)

Immunopeptide derived from HPV11 E2 peptide.

cervical cancer; cervical intraepithelial neoplasia; CIN; wart;

squamous cell carcinoma; ELISA; HPV.

Synthetic.

WO9118294-A.

28-NOV-1991.

11-MAY-1990; 90SE-00001705.

11-MAY-1990; 90SE-00001705.

(MEDS-) MEDSCAND AB.

Dillner J, Dillner L, Cheng HM;

WPI; 1991-369390/50.

Diagnosis of human papilloma virus infection and PV-carrying tumours -
 using synthetic peptide(s) to detect virus specific antigen-antibody
 complexes by immunoassay.

Disclousure; Page 20; 72pp; English.

This is one of a large number of peptides which have been synthesised on
 the basis of the amino acid sequences for the E2, E4, E7, I1 or I2
 proteins of HPV 1, 5, 6, 8, 11, 16, 18, 31 and 33. The selection of
 peptide sequences was based on the assumption that an immunoreactive
 region might be situated in the same relative region of a protein from
 different HPV types. The peptides were used in diagnostic immunoassays to
 detect HPV-infection. See AARI5523-R15601

SQ Sequence 20 AA;

Query Match 37.7%; Score 44.5; DB 2; Length 20;

Best Local Similarity 62.5%; Pred. No. 2.8;

Matches 10; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

OY 2 EXNVMXYLYLTMHYL 17

Db 5 EDNVMXYVWT-HIYL 19

RESULT 2

ABP46205 standard; peptide; 16 AA.

ABP46205;

19-AUG-2002 (first entry)

Human Blys binding scFv VH CDR3 SEQ ID 2216.

Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;

tumour necrosis factor; B cell proliferation; B cell differentiation;
 immunosuppressive; immunostimulant; immunomodulatory; antineutrotic;
 antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS.

Homo sapiens.

WO200202641-A1.

10-JAN-2002.

15-JUN-2001; 2001WO-US019110.

16-JUN-2000; 2000US-0212210P.

17-OCT-2000; 2000US-0240816P.

16-MAR-2001; 2001US-0276248P.

21-MAR-2001; 2001US-0277379P.

25-MAY-2001; 2001US-0293499P.

(HUMA-) HUMAN GENOME SCI INC.

(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

WPI; 2002-114799/15.

Antibodies against B lymphocyte Stimulating polypeptides, useful for the

diagnosis and treatment of cancers and immune disorders.

Claim 2; Page 2953; 3148pp; English.

This invention describes novel antibodies that immunospecifically bind to
 B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
 tumour necrosis factor (TNF) super family and induces B cell
 proliferation and differentiation. The antibodies of the invention have
 cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 antineutrotic and antiAIDS activity and can be used in vaccines to
 inhibit the expression and activity of Blys. The antibodies bind to Blys
 and so may be used to detect and quantitate the presence of Blys in
 biological samples and may be used in this way to diagnose disease
 associated with aberrant expression of Blys. They may also be
 administered to treat diseases associated with aberrant Blys expression
 and activity such as cancer, immune, and autoimmune disorders and
 diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP47228 represent
 the antibodies and fragments of the antibodies described in the method of
 the invention

SQ Sequence 16 AA;

Query Match 29.7%; Score 35; DB 5; Length 16;

Best Local Similarity 71.4%; Pred. No. 84;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 11 YTMHYL 17

Db 9 YLHYL 15

RESULT 3

ADG97032 standard; peptide; 16 AA.

ADG97032;

11-MAR-2004 (first entry)

scFv VHCDR3 peptide that immunospecifically binds Blys SeqID 2216.

antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;

B cell proliferation; differentiation; scFv; myasthenia gravis;

KM multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
 KM carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective;
 KM antiinflammatory; antiaesthetic; antiallergic; cytostatic.
 OS unidentified.
 XX WO2003055979-A2.
 PN 10-JUL-2003.
 PD 14-NOV-2002; 2002WO-US036496.
 PF 16-NOV-2001; 2001US-0311469P.
 PR 19-DEC-2001; 2001US-0340817P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;
 PI WPI; 2003-505530/47.
 DR Novel antibody that immunospecifically binds to a B lymphocyte stimulator
 PT (Blys), useful for detecting and treating diseases or disorders e.g.
 PT rheumatoid arthritis, asthma and leukemia.
 PS Example 1; SEQ ID NO 2216; 394pp; English.
 XX This invention relates to novel antibodies that immunospecifically bind
 CC to B lymphocyte stimulator (Blys). The Blys gene has been mapped to
 CC chromosome 13q34 and encodes a protein that is a member of the tumour
 CC necrosis factor superfamily and induces both in vivo and in vitro B cell
 CC proliferation and differentiation. Specifically, it refers to single
 CC chain antibody molecules (scFvs) derived, preferably, from the variable
 CC heavy CDR3 region that immunospecifically bind to a polypeptide, or
 CC fragment thereof, of either human, murine, rat or monkey Blys. The
 CC present invention refers to the use of such antibodies in various methods
 CC for the detection, diagnosis and prognosis of diseases related to the
 CC aberrant expression or inappropriate function of Blys or its receptor. As
 CC such, these compositions are useful for identifying immune disorders
 CC including myasthenia gravis and multiple sclerosis, inflammatory
 CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
 CC as AIDS and proliferative disorders including leukaemia, carcinoma and
 CC lymphoma. Accordingly, they can be described as exhibiting various
 CC activities such as antirheumatic, antiarthritic, neuroprotective,
 CC antiinflammatory, antiaesthetic, antiallergic and cytostatic. This
 CC peptide sequence is a single chain antibody variable heavy CDR3 peptide
 CC that immunospecifically binds Blys of the invention.
 CC
 XX
 SQ Sequence 16 AA;
 Query Match 29.7%; Score 35; DB 7; Length 16;
 Best Local Similarity 71.4%; Pred. No. 84;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Oy 11 YTMHYVL 17
 | : |||||
 Db 9 YVLMHYL 15
 RESULT 4
 AAE30892
 ID AAE30892 standard; peptide: 12 AA.
 AC AAE30892;
 XX 24-FEB-2003 (first entry)
 DT MDM2-binding motif #7, identified by phage-peptide display.
 XX p53 polypeptide; p300 polypeptide; cell cycle; cell death; gene therapy;
 KM cancer; ischaemia; cytostatic; vasotropic.
 XX Unidentified.

XX
 PN WO200265134-A2.
 XX 22-AUG-2002.
 PD 13-FEB-2002; 2002WO-GB000640.
 PF 13-FEB-2001; 2001GB-00003508.
 PR (UYDU-) UNIV DUNDEE.
 PA Hupp TR, Dorman D;
 PI WPI; 2003-018623/01.
 DR New peptide for modulating the binding of p53 polypeptide to p300
 PT polypeptide, useful for regulating the mammalian cell cycle for the
 PT treatment of cancer or ischemia.
 XX Example 2; Fig 7B; 87pp; English.
 XX The invention relates to a peptide for use in modulating the binding of a
 CC p53 polypeptide to a p300 polypeptide. The new peptide is useful in
 CC modulating the binding of a p53 polypeptide to a p300 polypeptide. The
 CC peptide may be used to regulate the mammalian cell cycle or to induce or
 CC prevent cell death, for the treatment of cancer or ischemia. The
 CC invention is useful in gene therapy. The present sequence is MDM2-
 CC binding motif, identified by phage-peptide display
 CC
 XX
 SQ Sequence 12 AA;
 Query Match 28.8%; Score 34; DB 6; Length 12;
 Best Local Similarity 50.0%; Pred. No. 88;
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 Oy 11 YTMHYVNNNGAT 22
 | : |||||
 Db 1 FPFHYMDNINT 12
 RESULT 5
 ABP46248
 ID ABP46248 standard; peptide: 16 AA.
 XX ABP46248;
 AC 19-AUG-2002 (first entry)
 DT Human Blys binding scFv VH CDR3 SEQ ID 2259.
 XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 KM tumour necrosis factor; B cell proliferation; B cell differentiation;
 KM immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
 KM antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KM systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KM common variable immunodeficiency; acquired immunodeficiency syndrome.
 XX Homo sapiens.
 OS WO200202641-A1.
 PN 10-JAN-2002.
 PD 15-JUN-2001; 2001WO-US019110.
 PF 16-JUN-2000; 2000US-0212210P.
 PR 17-OCT-2000; 2000US-0240816P.
 PR 16-MAR-2001; 2001US-0276248P.
 PR 21-MAR-2001; 2001US-0277379P.
 PR 25-MAY-2001; 2001US-0293499P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

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XX  Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
PI  WPI; 2002-114799/15.
XX
XX  Antibodies against B lymphocyte Stimulating polypeptides, useful for the
PT  diagnosis and treatment of cancers and immune disorders.
XX
XX  Claim 2; Page 2960; 3148pp; English.
XX
XX  This invention describes novel antibodies that immunospecifically bind to
CC  B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
CC  tumour necrosis factor (TNF) super family and induces B cell
CC  proliferation and differentiation. The antibodies of the invention have
CC  cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC  antirheumatic and antiAIDS activity and can be used in vaccines to
CC  inhibit the expression and activity of Blys. The antibodies bind to Blys
CC  and so may be used to detect and quantitate the presence of Blys in
CC  biological samples and may be used in this way to diagnose disease
CC  associated with aberrant expression of Blys. They may also be
CC  administered to treat diseases associated with aberrant Blys expression
CC  and actively such as cancer, immune, and autoimmune disorders and
CC  diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC  immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC  acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC  the antibodies and fragments of the antibodies described in the method of
CC  the invention
XX
XX  Sequence 16 AA;
SQ
XX
XX  Query Match      28.8%; Score 34; DB 5; Length 16;
XX  Best Local Similarity 83.3%; Pred. No. 1.2e+02;
XX  Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY      11 YTMHY 16
        | | | | |
        9 YVMHY 14
Db
XX
XX  RESULT 6
XX  ADG97075
XX  ID ADG97075 standard; peptide; 16 AA.
XX
XX  AC ADG97075;
XX
XX  DT 11-MAR-2004 (first entry)
XX
XX  DE scFV VHCDR3 peptide that immunospecifically binds Blys SeqID 2259.
XX
XX  KW antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;
XX  B cell proliferation; differentiation; scFv; myasthenia gravis;
XX  multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
XX  carcinoma; lymphoma; antirheumatic; antiallergic; neuroprotective;
XX  antiinflammatory; antiasthmatic; antiallergic; cytostatic.
XX
XX  OS Unidentified.
XX
XX  PN WO2003055979-A2.
XX
XX  PD 10-JUL-2003.
XX
XX  PF 14-NOV-2002; 2002MO-US036496.
XX
XX  PR 16-NOV-2001; 2001US-0331469P.
XX  PR 19-DEC-2001; 2001US-0340817P.
XX
XX  PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX  PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX  WPI; 2003-505530/47.
XX
XX  Novel antibody that immunospecifically binds to a B lymphocyte stimulator
PT

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PT  (Blys), useful for detecting and treating diseases or disorders e.g.
PT  rheumatoid arthritis, asthma and leukemia.
XX
XX  Example 1; SEQ ID NO 2259; 394pp; English.
XX
XX  This invention relates to novel antibodies that immunospecifically bind
CC  to B lymphocyte stimulator (Blys). The Blys gene has been mapped to
CC  chromosome 13q34 and encodes a protein that is a member of the tumour
CC  necrosis factor superfamily and induces both in vivo and in vitro B cell
CC  proliferation and differentiation. Specifically, it refers to single
CC  chain antibody molecules (scFvs) derived, preferably, from the variable
CC  heavy CDR3 region that immunospecifically bind to a polypeptide, or
CC  fragment thereof, of either human, murine, rat or monkey Blys. The
CC  present invention refers to the use of such antibodies in various methods
CC  for the detection, diagnosis and prognosis of diseases related to the
CC  aberrant expression or inappropriate function of Blys or its receptor. As
CC  such, these compositions are useful for identifying immune disorders
CC  including myasthenia gravis and multiple sclerosis, inflammatory
CC  disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
CC  as AIDS and proliferative disorders including leukaemia, carcinoma and
CC  lymphoma. Accordingly, they can be described as exhibiting various
CC  activities such as antirheumatic, antirheumatic, antiallergic, neuroprotective,
CC  antiinflammatory, antiasthmatic, antiallergic and cytostatic. This
CC  peptide sequence is a single chain antibody variable heavy CDR3 peptide
CC  that immunospecifically binds Blys of the invention.
XX
XX  Sequence 16 AA;
SQ
XX
XX  Query Match      28.8%; Score 34; DB 7; Length 16;
XX  Best Local Similarity 83.3%; Pred. No. 1.2e+02;
XX  Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY      11 YTMHY 16
        | | | | |
        9 YVMHY 14
Db
XX
XX  RESULT 7
XX  AAR15580
XX  ID AAR15580 standard; protein; 20 AA.
XX
XX  AC AAR15580;
XX
XX  DT 02-MAR-1992 (first entry)
XX
XX  DE Immunopeptide derived from HPV18 E2 peptide.
XX
XX  KW cervical cancer; cervical intraepithelial neoplasia; CIN; wart;
XX  squamous cell carcinoma; ELISA; HPV 18.
XX
XX  OS Synthetic.
XX
XX  PN WO9118294-A.
XX
XX  PD 28-NOV-1991.
XX
XX  PF 11-MAY-1990; 90SE-00001705.
XX
XX  PR 11-MAY-1990; 90SE-00001705.
XX
XX  PA (MEDS-) MEDSCAND AB.
XX
XX  PI Dillner J, Dillner L, Cheng HM;
XX  WPI; 1991-369390/50.
XX
XX  DR 1991-369390/50.
XX
XX  PT Diagnosis of human papilloma virus infection and PV-carrying tumours -
XX  using synthetic peptide(s) to detect virus specific antigen-antibody
XX  complexes by immunoassay.
XX
XX  Disclosure; Page 39; 72pp; English.
XX
XX  This is one of a large number of peptides which have been synthesised on
CC

```


CC the basis of the amino acid sequences for the E2, E4, E7, I1 or I2
 CC proteins of HPV 1, 5, 6, 8, 11, 16, 18, 31 and 33. The selection of
 CC peptide sequences was based on the assumption that an immunoreactive
 CC region might be situated in the same relative region of a protein from
 CC different HPV types. The peptides were used in diagnostic immunoassays to
 CC detect HPV-infection. See AAR15523-R15601

SO Sequence 20 AA;

Query Match 28.8%; Score 34; DB 2; Length 20;
 Best Local Similarity 35.3%; Pred. No. 1.6e+02;
 Matches 6; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

OY 1 DEXNVMXYVLYTMHYL 17
 DB 4 NKDNCMYTVAMDVYIM 20

RESULT 8
 ADR88216
 ID ADR88216 standard; peptide; 14 AA.

AC ADR88216;
 DT 18-NOV-2004 (first entry)

DE Human heparanase epitope pep10.

XX Targeted drug delivery; inflammatory disorder; wound; scar; vasculopathy;
 KM autoimmune disorder; cancer; angiogenesis; metastatic disease;
 KM atherosclerosis; restenosis; aneurysm; solid cancer; non-solid cancer;
 KM hemangioma; lymphocytic leukaemia; myelogenous leukaemia;
 KM Hodgkin's disease; multiple myeloma; haemangiosarcoma; Kaposi's sarcoma;
 KM human; heparanase; enzyme; epitope.

XX Homo sapiens.

OS US2004170631-A1.

PN 02-SEP-2004.

PF 28-NOV-2003; 2003US-00722502.

PR 02-SEP-1997; 97US-00922170.

PR 01-MAY-1998; 98US-00071739.

PR 04-NOV-1998; 98US-00186200.

PR 19-FEB-2003; 2003US-00368044.

PR 22-AUG-2003; 2003US-00645659.

PA (YACO/) YACOBY-ZEEVI O.

PA (PERE/) PERETZ T.

PA (MIRO/) MIRON D.

PA (SHLO/) SHLOMI Y.

PA (PECK/) PECKER I.

PA (AYAL/) AYAL-HERSHKOVITZ M.

PA (VEIN/) FEINSTEIN E.

PA (VGLD/) VAN GELDER J M.

PA (VLAD/) VLADAVSKY I.

XX (FRIE/) FRIEDMANN Y.

XX VACOBY-ZEEVI O, PERETZ T, MIRON D, SHLOMI Y, PECKER I;

PI AYAL-Herskovitz M, Feinstein E, Van Gelder JM, Vladavsky I;

PI Friedmann Y;

XX WPI; 2004-625084/60.

XX Targeted drug delivery to a heparanase-expressing tissue of a patient,

PT useful for treating heparanase-associated conditions such as inflammation

PT or cancer; comprising administering a drug and an anti-heparanase antibody

PT complex.

PS Claim 7; SEQ ID NO 10; 58pp; English.

CC The invention relates to a method of targeted drug delivery to a tissue
 CC of a patient, the tissue expressing heparanase. The method comprises
 CC providing a complex of a drug directly or indirectly linked to an anti-
 CC heparanase antibody, and administering the complex to the patient. In the
 CC targeted drug delivery, the antibody comprises an antibody or its portion
 CC capable of specifically binding to at least one epitope of a heparanase
 CC protein. The composition and methods of the invention are useful for
 CC diagnosing, preventing or treating conditions associated with heparanase
 CC catalytic activity (e.g. an inflammatory disorder; wound; scar;
 CC vasculopathy; an autoimmune disorder; cancer; angiogenesis; cell
 CC proliferation; invasion of circulating tumour cells and metastatic
 CC disease), for purifying heparanase, or for developing drugs for those
 CC heparanase-associated conditions. The vasculopathy is atherosclerosis,
 CC restenosis or aneurysm. The cancerous condition is a solid cancer or a
 CC non-solid cancer. The non-solid cancer is a hematopoietic malignancy
 CC selected from acute lymphocytic leukaemia (ALL), acute myelogenous
 CC leukaemia, chronic lymphocytic leukaemia (CLL), chronic myelogenous
 CC leukaemia (CML), myelodysplastic syndrome (MDS), mast cell leukaemia,
 CC Hodgkin's disease, non-Hodgkin's lymphomas, Burkitt's lymphoma and
 CC multiple myeloma. The solid cancer is selected from tumours in lip and
 CC oral cavity, pharynx, larynx, paranasal sinuses, major salivary glands,
 CC thyroid gland, oesophagus, stomach, small intestine, colon, colorectum,
 CC anal canal, liver, gallbladder, extrahepatic bile ducts, ampulla of
 CC Vater, exocrine pancreas, lung, pleural mesothelioma, soft tissue
 CC sarcoma, carcinoma and malignant melanoma of the skin, breast, vulva,
 CC vagina, cervix uteri, ovary, fallopian tube, gestational trophoblastic
 CC tumours, penis, prostate, testis, kidney, renal pelvis, ureter, urinary
 CC bladder, urethra, carcinoma of the eyelid, carcinoma of the conjunctiva,
 CC retinoblastoma, carcinoma of the conjunctiva, malignant melanoma of the uvea,
 CC meningioma, carcinoma of the lacrimal gland, sarcoma of the orbit,
 CC brain, spinal cord, vascular system, hemangiosarcoma and Kaposi's
 CC sarcoma. The present sequence is human heparanase epitope.

SO Sequence 14 AA;

Query Match 28.4%; Score 33.5; DB 8; Length 14;
 Best Local Similarity 72.7%; Pred. No. 1.3e+02;
 Matches 8; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

OY 14 HYYLN-NGATR 23
 DB 4 HYYLNGRTATR 14

RESULT 9
 ADR78183
 ID ADR78183 standard; peptide; 14 AA.

AC ADR78183;
 DT 13-JAN-2005 (first entry)

DE Functional peptide epitope of human heparanase, pep10.

XX Antibody; epitope; heparanase; pathological condition; angiogenesis;
 KM cell proliferation; cancerous condition; tumour cell invasion;
 KM metastatic disease; heparanase-related disorder; inflammatory disorder;
 KM wound; scar; vasculopathy; autoimmune condition; renal disease;
 KM cytoskeletal; antiinflammatory; vulnery; antiarteriosclerotic;
 KM vasotropic; immunosuppressive; nephrotropic; antidiabetic; human.

XX Homo sapiens.

OS US2004213789-A1.

PN 28-OCT-2004.

PF 22-AUG-2003; 2003US-00645659.

PR 02-SEP-1997; 97US-00922170.

PR 01-MAY-1998; 98US-00071739.

PR 04-NOV-1998; 98US-00186200.

PR 19-FEB-2003; 2003US-00368044.

XX (YACO/) YACOBY-ZEEVI O.
 PA (PERE/) PERETZ T.
 PA (MIRO/) MIRON D.
 PA (SHLO/) SHLOMI Y.
 PA (PECK/) PECKER I.
 PA (AYAL/) AYAL-HERSHKOVITZ M.
 PA (FEIN/) FEINSTEIN E.
 PA (GELD/) GELDER J M V.
 PA (VLOD/) VLODAVSKY I.
 PA (FRIE/) FRIEDMANN Y.
 XX
 PI Yacoby-Zeevi O, Peretz T, Miron D, Shlomi Y, Pecker I,
 PI Ayal-Hershkovitz M, Feinstein E, Gelder JMV, Vlodavsky I;
 PI Friedmann Y;
 DR WPI; 2004-774790/76.
 XX
 PT New neutralizing monoclonal anti-heparanase antibodies, useful for
 PT detecting, treating or preventing cancer, inflammatory or autoimmune
 PT disorder, wound, atherosclerosis, restenosis, or diabetic nephropathy.
 XX
 PS Claim 67; SEQ ID NO 10; 68bp; English.
 XX
 CC The invention relates to an isolated antibody or antibody portion capable
 CC of specifically binding to or elicited by at least one epitope of a
 CC heparanase protein, where the heparanase protein is at least 60%
 CC homologous to any of the 6 sequences given as SEQ ID NOS:1-5 or 11, and
 CC where at least one epitope comprises a sequence at least 70% homologous
 CC to any of the sequences given as SEQ ID NOS: 6-10. Also disclosed are (a)
 CC a hybridoma cell line comprising a cell line for producing the monoclonal
 CC antibody, (b) a method for detecting, treating or preventing a
 CC pathological condition or a heparanase-related disorder or condition in a
 CC subject, (c) a method for monitoring the state of a heparanase-related
 CC disorder or condition in a subject, and (d) a pharmaceutical composition
 CC comprising the isolated anti-heparanase antibody or antibody portion and
 CC a pharmaceutical carrier. The antibody, method, and composition are
 CC useful for detecting, treating, preventing or monitoring a pathological
 CC condition, e.g. angiogenesis, cell proliferation, a cancerous condition
 CC (blood, breast, bladder, rectum, stomach, cervix, ovarian, colon, renal,
 CC or prostate cancer), tumor cell proliferation, invasion of circulating
 CC tumor cells, or a metastatic disease, or a heparanase-related disorder
 CC or condition, e.g. an inflammatory disorder, wound, scar, vasculopathy
 CC (atherosclerosis, restenosis, or aneurysm), autoimmune condition, or
 CC renal disease or disorder (diabetic nephropathy, glomerulosclerosis,
 CC nephrotic syndrome, minimal change nephrotic syndrome, or a renal cell
 CC carcinoma) in a mammal. This sequence represents a functional peptide
 CC epitope of human heparanase.
 CC
 XX
 SQ Sequence 14 AA;
 Query Match 28.4%; Score 33.5; DB 8; Length 14;
 Best Local Similarity 72.7%; Pred. No. 1.3e+02;
 Matches 8; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
 Oy 14 HYYLN-NGATR 23
 Db 4 HYYLNGRTATR 14
 RESULT 10
 AEA42432
 ID AEA42432 standard; peptide; 14 AA.
 XX
 AC AEA42432;
 XX
 DT 28-JUL-2005 (first entry)
 XX
 DE Human heparanase epitope peptide SEQ ID NO:10.
 XX
 KW antibody; heparanase; antiinflammatory; vulnery; immunosuppressive;
 KW antiangiogenic; cytostatic; antiarteriosclerotic; vasotropic;
 KW inflammation; wound healing; scarring; vasculopathy; autoimmune disease;

KW angiogenesis disorder; cancer; tumor; metastasis; epitope.
 XX
 OS Homo sapiens.
 XX
 PN AU2004201462-A1.
 XX
 PD 06-MAY-2004.
 XX
 PE 08-APR-2004; 2004AU-00201462.
 XX
 PR 08-APR-2004; 2004AU-00201462.
 XX
 PA (INSI-) INSIGHT BIOPHARMACEUTICALS LTD.
 PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV LTD.
 XX
 PI Vlodavsky I, Pecker I, Mimon M, Gilboa A, Miron D, Moskowicz H;
 PI Shlomi Y, Peleg Y, Yacoby-Zeevi O, Ayal-Hershkovitz M, Ben-Artzi H,
 PI Feinstein E;
 XX
 DR WPI; 2005-173343/19.
 XX
 PT Novel isolated antibody capable of specifically binding to epitope of
 PT heparanase protein, useful for preventing and creating heparanase-related
 PT disorder such as inflammatory disorder, scars, autoimmune conditions or
 PT angiogenesis.
 XX
 PS Claim 7; SEQ ID NO 10; 260bp; English.
 XX
 CC The invention relates to an isolated antibody or its portion (I) capable
 CC of specifically binding to an epitope of a heparanase protein. Also
 CC described: (1) a cell line (II) for producing a monoclonal antibody or
 CC its portion, comprising a cell line for producing (I); (2) a
 CC pharmaceutical composition comprising (I) and a carrier; and (3) an
 CC affinity medium (III) for binding human heparanase polypeptides.
 CC comprising (I) immobilized to a chemically inert, insoluble carrier. (I)
 CC useful for treating a subject suffering from a pathological condition,
 CC which involves administering (I) to the subject. (I) is useful for
 CC preventing and treating heparanase-related disorder or condition chosen
 CC from inflammatory disorder, wound, scar, vasculopathy, autoimmune
 CC condition, angiogenesis, cell proliferation, cancerous condition, tumor
 CC cell proliferation, invasion of circulating tumor cells and metastatic
 CC disease. (I) is useful for detecting the presence of heparanase
 CC polypeptide in a sample. (I) is useful for detecting heparanase-related
 CC disease or condition in a subject such as vertebrate, preferably mammal
 CC e.g., human. The heparanase-related disorder or condition further
 CC includes renal disease or disorder chosen from diabetic nephropathy,
 CC glomerulosclerosis, nephrotic syndrome, minimal change nephrotic syndrome
 CC and renal cell carcinoma. The present sequence represents a human
 CC heparanase epitope peptide, which is used in the exemplification of the
 CC present invention.
 CC
 XX
 SQ Sequence 14 AA;
 Query Match 28.4%; Score 33.5; DB 9; Length 14;
 Best Local Similarity 72.7%; Pred. No. 1.3e+02;
 Matches 8; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
 Oy 14 HYYLN-NGATR 23
 Db 4 HYYLNGRTATR 14
 RESULT 11
 ADU70841
 ID ADU70841 standard; peptide; 15 AA.
 XX
 AC ADU70841;
 XX
 DT 10-FEB-2005 (first entry)
 XX
 DE Human heparanase peptide SEQ ID NO:526.
 XX
 KW enzyme; heparinase; vaccine; human leukocyte antigen; HLA;

KM immunostimulant; cytostatic; immune disorder; metastasis.
 XX
 OS Homo sapiens.
 XX
 PN EPI479764-A1.
 XX
 PD 24-NOV-2004.
 XX
 PF 19-MAY-2003; 2003EP-00011038.
 XX
 PR 19-MAY-2003; 2003EP-00011038.
 XX
 PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
 XX (UYHE-) UNIV HEIDELBERG RUPRECHT-KARLS.
 PI Schirmacher V, Beckhove P, Sommerfeldt N;
 DR WPI; 2005-014847/02.
 XX
 PT New heparanase nonapeptide that binds to a human leukocyte antigen (HLA)
 PT molecule or its functional derivative, useful for preparing a medicament
 PT for inducing an immune response or for treating metastatic tumors.
 PS
 PS Disclosure; SEQ ID NO 526; 269pp; English.
 CC
 CC The invention relates to a novel heparanase peptide that binds to a human
 CC leukocyte antigen (HLA) molecule, where the peptide is a nonapeptide, or
 CC its functional derivative. A peptide of the invention has immunostimulant
 CC and cytostatic activity, and is used in a vaccine. The heparinase peptide
 CC is useful for preparing a medicament which induces an immune response or
 CC for treating metastatic tumors. The present sequence represents a
 CC heparinase peptide of the invention.
 CC
 SQ Sequence 15 AA;
 QY
 DB 14 HYYLN-NGATR 23
 3 HYYLNGRTATR 13
 Query Match 28.4%; Score 33.5; DB 9; Length 15;
 Best Local Similarity 72.7%; Pred. No. 1.4e+02;
 Matches 8; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
 RESULT 12
 ADU71059
 ID ADU71059 standard; peptide; 15 AA.
 XX
 AC ADU71059;
 XX
 DT 10-FEB-2005 (first entry)
 XX
 DE Human heparanase peptide SEQ ID NO:744.
 XX
 KM enzyme; heparinase; vaccine; human leukocyte antigen; HLA;
 KM immunostimulant; cytostatic; immune disorder; metastasis.
 OS Homo sapiens.
 XX
 PN EPI479764-A1.
 XX
 PD 24-NOV-2004.
 XX
 PF 19-MAY-2003; 2003EP-00011038.
 XX
 PR 19-MAY-2003; 2003EP-00011038.
 XX
 PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
 XX (UYHE-) UNIV HEIDELBERG RUPRECHT-KARLS.
 PI Schirmacher V, Beckhove P, Sommerfeldt N;
 DR WPI; 2005-014847/02.

XX
 PT New heparanase nonapeptide that binds to a human leukocyte antigen (HLA)
 PT molecule or its functional derivative, useful for preparing a medicament
 PT for inducing an immune response or for treating metastatic tumors.
 PS
 PS Disclosure; SEQ ID NO 744; 269pp; English.
 CC
 CC The invention relates to a novel heparanase peptide that binds to a human
 CC leukocyte antigen (HLA) molecule, where the peptide is a nonapeptide, or
 CC its functional derivative. A peptide of the invention has immunostimulant
 CC and cytostatic activity, and is used in a vaccine. The heparinase peptide
 CC is useful for preparing a medicament which induces an immune response or
 CC for treating metastatic tumors. The present sequence represents a
 CC heparinase peptide of the invention.
 CC
 SQ Sequence 15 AA;
 QY
 DB 14 HYYLN-NGATR 23
 5 HYYLNGRTATR 15
 Query Match 28.4%; Score 33.5; DB 9; Length 15;
 Best Local Similarity 72.7%; Pred. No. 1.4e+02;
 Matches 8; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
 RESULT 13
 ADU71060
 ID ADU71060 standard; peptide; 15 AA.
 XX
 AC ADU71060;
 XX
 DT 10-FEB-2005 (first entry)
 XX
 DE Human heparanase peptide SEQ ID NO:745.
 XX
 KM enzyme; heparinase; vaccine; human leukocyte antigen; HLA;
 KM immunostimulant; cytostatic; immune disorder; metastasis.
 OS Homo sapiens.
 XX
 PN EPI479764-A1.
 XX
 PD 24-NOV-2004.
 XX
 PF 19-MAY-2003; 2003EP-00011038.
 XX
 PR 19-MAY-2003; 2003EP-00011038.
 XX
 PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
 XX (UYHE-) UNIV HEIDELBERG RUPRECHT-KARLS.
 PI Schirmacher V, Beckhove P, Sommerfeldt N;
 DR WPI; 2005-014847/02.
 XX
 PT New heparanase nonapeptide that binds to a human leukocyte antigen (HLA)
 PT molecule or its functional derivative, useful for preparing a medicament
 PT for inducing an immune response or for treating metastatic tumors.
 PS
 PS Disclosure; SEQ ID NO 745; 269pp; English.
 CC
 CC The invention relates to a novel heparanase peptide that binds to a human
 CC leukocyte antigen (HLA) molecule, where the peptide is a nonapeptide, or
 CC its functional derivative. A peptide of the invention has immunostimulant
 CC and cytostatic activity, and is used in a vaccine. The heparinase peptide
 CC is useful for preparing a medicament which induces an immune response or
 CC for treating metastatic tumors. The present sequence represents a
 CC heparinase peptide of the invention.
 CC
 SQ Sequence 15 AA;
 QY
 DB 14 HYYLN-NGATR 23
 5 HYYLNGRTATR 15
 Query Match 28.4%; Score 33.5; DB 9; Length 15;

Best Local Similarity 72.7%; Pred. No. 1.4e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

OY 14 HYYLN-NGATR 23
DB 4 HYYLNGRTATR 14

RESULT 14

ADU71272
ID ADU71272 standard; peptide; 15 AA.

XX AC ADU71272;

XX DT 10-FEB-2005 (first entry)

XX DE Human heparanase peptide SEQ ID NO:957.

XX KW enzyme; heparinase; vaccine; human leukocyte antigen; HLA;
immunostimulant; cytostatic; immune disorder; metastasis.

XX OS Homo sapiens.

XX PN EPI479764-A1.

XX PD 24-NOV-2004.

XX PF 19-MAY-2003; 2003EP-00011038.

XX PR 19-MAY-2003; 2003EP-00011038.

XX PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
(UYHE-) UNIV HEIDELBERG RUPRECHT-KARLS.

XX PI Schirmacher V, Beckhove P, Sommerfeldt N;
WPI; 2005-014847/02.

XX DR WPI; 2005-014847/02.

XX PT New heparanase nonapeptide that binds to a human leukocyte antigen (HLA)
molecule or its functional derivative, useful for preparing a medicament

XX PT for inducing an immune response or for treating metastatic tumors.

XX PS Disclosure; SEQ ID NO 957; 269pp; English.

XX CC The invention relates to a novel heparanase peptide that binds to a human
leukocyte antigen (HLA) molecule, where the peptide is a nonapeptide, or
its functional derivative. A peptide of the invention has immunostimulant
and cytostatic activity, and is used in a vaccine. The heparinase peptide
is useful for preparing a medicament which induces an immune response or
for treating metastatic tumors. The present sequence represents a
heparinase peptide of the invention.

XX SQ Sequence 15 AA:

Query Match 28.4%; Score 33.5; DB 9; Length 15;

Best Local Similarity 72.7%; Pred. No. 1.4e+02;

Matches 8; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

OY 14 HYYLN-NGATR 23
DB 1 HYYLNGRTATR 11

RESULT 15

ADU70927
ID ADU70927 standard; peptide; 15 AA.

XX AC ADU70927;

XX DT 10-FEB-2005 (first entry)

XX DE Human heparanase peptide SEQ ID NO:612.

KW enzyme; heparinase; vaccine; human leukocyte antigen; HLA;
immunostimulant; cytostatic; immune disorder; metastasis.

XX OS Homo sapiens.

XX PN EPI479764-A1.

XX PD 24-NOV-2004.

XX PF 19-MAY-2003; 2003EP-00011038.

XX PR 19-MAY-2003; 2003EP-00011038.

XX PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
(UYHE-) UNIV HEIDELBERG RUPRECHT-KARLS.

XX PI Schirmacher V, Beckhove P, Sommerfeldt N;
WPI; 2005-014847/02.

XX DR WPI; 2005-014847/02.

XX PT New heparanase nonapeptide that binds to a human leukocyte antigen (HLA)
molecule or its functional derivative, useful for preparing a medicament
for inducing an immune response or for treating metastatic tumors.

XX PS Disclosure; SEQ ID NO 612; 269pp; English.

XX CC The invention relates to a novel heparanase peptide that binds to a human
leukocyte antigen (HLA) molecule, where the peptide is a nonapeptide, or
its functional derivative. A peptide of the invention has immunostimulant
and cytostatic activity, and is used in a vaccine. The heparinase peptide
is useful for preparing a medicament which induces an immune response or
for treating metastatic tumors. The present sequence represents a
heparinase peptide of the invention.

XX SQ Sequence 15 AA:

Query Match 28.4%; Score 33.5; DB 9; Length 15;

Best Local Similarity 72.7%; Pred. No. 1.4e+02;

Matches 8; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

OY 14 HYYLN-NGATR 23
DB 2 HYYLNGRTATR 12

RESULT 16

ADY27047
ID ADY27047 standard; peptide; 15 AA.

XX AC ADY27047;

XX DT 05-MAY-2005 (first entry)

XX DE Heparanase inhibitor peptide #6.

XX KW Heparanase; cancer; neoplasm; inflammation; cardiovascular disease;
neurological disease; viral infection; infection; cytostatic;

XX KW antiinflammatory; cardiovascular-gen.; neuroprotective; virucide;
heparanase modulator; enzyme purification.

XX OS Synthetic.

XX PN WO2005016227-A2.

XX PD 24-FEB-2005.

XX PF 12-AUG-2004; 2004WO-IL000744.

XX PR 14-AUG-2003; 2003US-0494800P.

XX PR 12-JAN-2004; 2004US-0535492P.

XX PA (INSI-) INSIGHT BIOPHARMACEUTICALS LTD.

QY 12 TMHYLNNGAT 22
| : | : | : |
Db 3 TMHYLNNGRT 13

RESULT 19

AAB06372 ID AAB06372 standard; peptide: 17 AA.

XX AAB06372;

XX 17-OCT-2000 (first entry)

XX Randomised V13 sequence of anti-VEGF antibody variant Y0229-9.

XX Humanised; antibody variant; phage display; randomised library;
KM cytoskeletal; antiarthritic; antipsoriatic; antidiabetic; antiinflammatory;
KM antiarteriosclerotic; vascular endothelial growth factor; VEGF;
KM breast cancer; lung cancer; retinoblastoma; rheumatoid arthritis;
KM psoriasis; atherosclerosis; diabetic retinopathy;
KM complementarity determining region; CDR.

XX Homo sapiens.
OS Synthetic.

XX WO200029584-A1.

XX 25-MAY-2000.

XX 16-NOV-1999; 99WO-US027153.

XX 18-NOV-1998; 98US-0108945P.

XX (GETH) GENENTECH INC.

XX Chen YM, Lowman HB, Muller Y;

XX WPI: 2000-387797/33.

XX Antibody variants with higher binding affinity than native antibodies
PT useful for diagnosis, prevention and treatment of neoplastic and non-
PT neoplastic diseases comprises amino acid insertion in hypervariable
PT region.

XX Example 1; Page 58; 110pp; English.

XX The present sequence is the randomised V13 region of a variant of anti-
CC vascular endothelial growth factor (VEGF) antibody from phage library YC-
CC 95. A large number of antibody variants containing randomised peptide
CC inserts within the complementarity determining regions (CDRs) were
CC prepared by phage display. Libraries were subjected to eight rounds of
CC selection to isolate variants with an antigen binding affinity at least
CC two-fold stronger than the binding affinity of parent antibody for the
CC target VEGF antibody. The anti-VEGF antibody variants may be useful in
CC diagnostic assays for detecting expression of VEGF in cells, tissue or
CC serum. They may also be used in the prevention and treatment of
CC neoplastic diseases such as breast cancer, lung cancer and
CC retinoblastoma, and non-neoplastic diseases including rheumatoid
CC arthritis, psoriasis, atherosclerosis, and diabetic and other
CC proliferative retinopathies

XX Sequence 17 AA;

QY Query Match 28.0%; Score 33; DB 3; Length 17;
Best Local Similarity 83.3%; Pred. No. 1.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 14 HYIYLN 19
| : | : | : |
Db 3 HYIYLN 8

RESULT 20
AAB06381 ID AAB06381 standard; peptide: 18 AA.

XX AAB06381;

XX 17-OCT-2000 (first entry)

XX Randomised V13 sequence of anti-VEGF antibody variant Y0239-8.

XX Humanised; antibody variant; phage display; randomised library;
KM cytoskeletal; antiarthritic; antipsoriatic; antidiabetic; antiinflammatory;
KM antiarteriosclerotic; vascular endothelial growth factor; VEGF;
KM breast cancer; lung cancer; retinoblastoma; rheumatoid arthritis;
KM psoriasis; atherosclerosis; diabetic retinopathy;
KM complementarity determining region; CDR.

XX Homo sapiens.
OS Synthetic.

XX WO200029584-A1.

XX 25-MAY-2000.

XX 16-NOV-1999; 99WO-US027153.

XX 18-NOV-1998; 98US-0108945P.

XX (GETH) GENENTECH INC.

XX Chen YM, Lowman HB, Muller Y;

XX WPI: 2000-387797/33.

XX Antibody variants with higher binding affinity than native antibodies
PT useful for diagnosis, prevention and treatment of neoplastic and non-
PT neoplastic diseases comprises amino acid insertion in hypervariable
PT region.

XX Claim 19; Page 59; 110pp; English.

XX The present sequence is the randomised V13 region of a variant of anti-
CC vascular endothelial growth factor (VEGF) antibody from phage library YC-
CC 95. A large number of antibody variants containing randomised peptide
CC inserts within the complementarity determining regions (CDRs) were
CC prepared by phage display. Libraries were subjected to eight rounds of
CC selection to isolate variants with an antigen binding affinity at least
CC two-fold stronger than the binding affinity of parent antibody for the
CC target VEGF antibody. The anti-VEGF antibody variants may be useful in
CC diagnostic assays for detecting expression of VEGF in cells, tissue or
CC serum. They may also be used in the prevention and treatment of
CC neoplastic diseases such as breast cancer, lung cancer and
CC retinoblastoma, and non-neoplastic diseases including rheumatoid
CC arthritis, psoriasis, atherosclerosis, and diabetic and other
CC proliferative retinopathies

XX Sequence 18 AA;

QY Query Match 28.0%; Score 33; DB 3; Length 18;
Best Local Similarity 71.4%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 14 HYIYLN 20
| : | : | : |
Db 3 HYIYRD 9

RESULT 21

AAB06379 ID AAB06379 standard; peptide: 18 AA.

XX AAB06379;

```

KM antiarteriosclerotic; vascular endothelial growth factor; VEGF;
KM breast cancer; lung cancer; retinoblastoma; rheumatoid arthritis;
KM psoriasis; atherosclerosis; diabetic retinopathy;
KM complementarity determining region; CDR.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX WO200029584-A1.
XX
XX 25-MAY-2000.
XX
XX 16-NOV-1999; 99WO-US027153.
XX
XX 18-NOV-1998; 98US-0108945P.
XX
XX (GETH ) GENENTECH INC.
XX
XX Chen YM, Lowman HB, Muller Y;
PI WPI; 2000-387797/33.
DR
XX
XX
XX Antibody variants with higher binding affinity than native antibodies
PT useful for diagnosis, prevention and treatment of neoplastic and non-
PT neoplastic diseases comprises amino acid insertion in hypervariable
PT region.
XX
XX
XX Example 1; Page 60; 110pp; English.
XX
CC The present sequence is the randomised VH3 region of a variant of anti-
CC vascular endothelial growth factor (VEGF) antibody from phage library YC-
CC 98. A large number of antibody variants containing randomised peptide
CC inserts within the complementarity determining regions (CDRs) were
CC prepared by phage display. Libraries were subjected to eight rounds of
CC selection to isolate variants with an antigen binding affinity at least
CC two-fold stronger than the binding affinity of parent antibody for the
CC target VEGF antibody. The anti-VEGF antibody variants may be useful in
CC diagnostic assays for detecting expression of VEGF in cells, tissue or
CC serum. They may also be used in the prevention and treatment of
CC neoplastic diseases such as breast cancer, lung cancer and
CC retinoblastoma, and non-neoplastic diseases including rheumatoid
CC arthritis, psoriasis, atherosclerosis, and diabetic and other
CC proliferative retinopathies.
XX
XX Sequence 18 AA;
SQ
Query Match 28.0%; Score 33; DB 3; Length 18;
Best Local Similarity 71.4%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0.
QY 14 HYYLNLNG 20
||| |
| : |
Db 3 HYVLKDG 9
RESULT 23
AAB06385
ID AAB06385 standard; peptide; 18 AA.
AC
XX AAB06385;
XX
XX 17-OCT-2000 (first entry)
DT
XX
XX Randomised VH3 sequence of anti-VEGF antibody variant Y0261-2.
DE
KM Humanised; antibody variant; phage display; randomised library;
KM cytoskeletal; antiarthritic; antipsoriatic; antidiabetic; antiinflammatory;
KM antiarteriosclerotic; vascular endothelial growth factor; VEGF;
KM breast cancer; lung cancer; retinoblastoma; rheumatoid arthritis;
KM psoriasis; atherosclerosis; diabetic retinopathy;
KM complementarity determining region; CDR.
XX
XX Homo sapiens.
OS

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OS	Synthetic.
XX	
PN	WO200029584-A1.
PD	25-MAY-2000.
XX	
PB	16-NOV-1999;
XX	99WO-US027153.
PR	18-NOV-1998;
XX	98US-0108945P.
PA	(GETH) GENENTECH INC.
PI	Chen YM, Lowman HB, Muller Y;
XX	WPI; 2000-387797/33.
DR	
XX	
PT	Antibody variants with higher binding affinity than native antibodies useful for diagnosis, prevention and treatment of neoplastic and non-neoplastic diseases comprises amino acid insertion in hypervariable region.
PS	
XX	Example 1; Page 59; 11opp; English.
CC	The present sequence is the randomised VH3 region of a variant of anti-
CC	vascular endothelial growth factor (VEGF) antibody from phage library YC-
CC	95. A large number of antibody variants containing randomised peptide
CC	inserts within the complementarity determining regions (CDRs) were
CC	prepared by phage display. Libraries were subjected to eight rounds of
CC	selection to isolate variants with an antigen binding affinity at least
CC	two-fold stronger than the binding affinity of parent antibody for the
CC	target VEGF antibody. The anti-VEGF antibody variants may be useful in
CC	diagnostic assays for detecting expression of VEGF in cells, tissue or
CC	serum. They may also be used in the prevention and treatment of
CC	neoplastic diseases such as breast cancer, lung cancer and
CC	retinoblastoma, and non-neoplastic diseases including rheumatoid
CC	arthritis, psoriasis, atherosclerosis, and diabetic and other
CC	proliferative retinopathies
SO	
XX	Sequence 18 AA:
QY	
DB	
14 HYYLNG 20 :! 3 HYYLKDG 9	
RESULT 24	
ID ABB94872	
ID ABB94872 standard; peptide; 9 AA.	
AC ABB94872;	
DT 17-JUN-2002 (first entry)	
DE CTL epitope HLA peptide SEQ ID NO:401.	
XX Human; 15BP1F4; chromosome 8q220q23, 15BP1F4; chromosome 8q23; cancer;	
KW bladder cancer; immune response; cytotoxic T lymphocyte; CTL; HLA;	
KW human leukocyte antigen; helper T lymphocyte; HTL.	
OS Homo sapiens.	
OS Synthetic.	
PN WO200216598-A2.	
PD 28-FEB-2002.	
PF 22-AUG-2001; 2001WO-US026411.	
PR 22-AUG-2000; 2000US-0227098P.	

PR	10-APR-2001; 2001US-0282739P.
XX	(AGEN-) AGENSYS INC.
PA	
PB	Challita-Eid PM, Hubert RS, Raitano AB, Afar DEH, Levin E;
PI	Faris M, Ge W, Jakobovits A;
PL	WPI; 2002-269357/31.
DR	
XX	Monitoring 158P1H4 gene products in biological sample from patient who
PT	has or is suspected of having cancer, useful for treating cancer,
PT	comprises identifying presence of aberrant 158P1H4 gene products in
PT	biological sample.
PS	Claim 64; Page 155; 209pp; English.
XX	
CC	The present invention describes a method for monitoring 158P1H4 gene
CC	products in a biological sample from a patient who has or is suspected of
CC	having cancer. The method comprises determining the status of 158P1H4
CC	gene products in a tissue sample from an individual, comparing the status
CC	to the status of 158P1H4 gene products in a normal sample, and
CC	identifying the presence of aberrant 158P1H4 gene products in the sample.
CC	158P1H4 sequences have cytostatic activity and can be used in vaccine
CC	production. 158P1H4 polynucleotides may be used in monitoring genetic
CC	abnormalities. The 158P1H4 proteins may be used in assessing the status
CC	of 158P1H4 gene products in normal versus cancerous tissues and so
CC	eliciting the malignant phenotype, in generating and characterizing
CC	domain-specific antibodies, for identifying agents or cellular factors
CC	that bind to 158P1H4 or its particular domain, and for generating cancer
CC	vaccines. Antibodies against 158P1H4 are useful in diagnostic and
CC	prognostic assays, in treating patients with cancer, in generating
CC	cytotoxic T lymphocyte (CTL) or helper T lymphocyte (HTL) responses, and
CC	as immunological reagents for detecting 158P1H4-expressing cells. The
CC	antibodies are particularly useful in bladder cancer diagnostic and
CC	prognostic assays, and imaging methodologies. The 158P1H4 gene has been
CC	located to chromosome 8q22-q23, and the 158P1H4 gene also described in
CC	the present invention has been located to chromosome 8q23. ABI50400 to
CC	ABI50429 and AB894468 to AB895188 represent sequences used in the
CC	exemplification of the present invention
XX	
SQ	Sequence 9 AA:
OY	8 YVLYTMH 14 : : 2 VVLTVSH 8
DB	
Query Match	27.1%; Score 32; DB 5; Length 9;
Best Local Similarity	71.4%; Pred. No. 2e+06;
Matches	5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
RESULT 25	
ADU70797	ID ADU70797 standard; peptide: 9 AA.
XX	
AC	ADU70797;
XX	
DT	10-FEB-2005 (first entry)
XX	
DE	Human heparanase peptide SEQ ID NO:482.
XX	
KM	enzyme; heparinase; vaccine; human leukocyte antigen; HLA;
KW	immunostimulant; cytosstatic; immune disorder; metastasis.
OS	Homo sapiens.
XX	
PN	EPI479764-A1.
XX	
PD	24-NOV-2004.
XX	
PF	19-MAY-2003; 2003EP-00011038.
XX	
PR	19-MAY-2003; 2003EP-00011038.

XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
 PA (UYHE-) UNIV HEIDELBERG RUPRECHT-KARLS.
 XX
 XX Schirmacher V, Beckhove P, Sommerfeldt N;
 XX WPL; 2005-014847/02.
 DR
 XX
 PT New heparanase nonapeptide that binds to a human leukocyte antigen (HLA)
 PT molecule or its functional derivative, useful for preparing a medicament
 PT for inducing an immune response or for treating metastatic tumors.
 XX
 PS Claim 3; SEQ ID NO 482; 269pp; English.
 XX
 CC The invention relates to a novel heparanase peptide that binds to a human
 CC leukocyte antigen (HLA) molecule, where the peptide is a nonapeptide, or
 CC its functional derivative. A peptide of the invention has immunostimulant
 CC and cytostatic activity, and is used in a vaccine. The heparinase peptide
 CC is useful for preparing a medicament which induces an immune response or
 CC for treating metastatic tumors. The present sequence represents a
 CC heparinase peptide of the invention.
 XX
 SQ Sequence 9 AA;

Query March 27.1k; Score 32; DB 9; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 HYYLN 18
 |||||
 Db 4 HYYLN 8

Search completed: January 26, 2006, 07:58:01
 Job time : 81.1207 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 26, 2006, 07:50:06 ; Search time 21.6121 Seconds
(without alignments)
87.985 Million cell updates/sec

Title: US-09-662-293-9

Perfect score: 118
Sequence: 1 DEXNMKYYVLYTMHYILNNGATR 23

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 229350

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

1: Issued Patents AA: *
2: /cgn2_6/ptodata/1/1aa/5_COMB.pep: *
3: /cgn2_6/ptodata/1/1aa/6_COMB.pep: *
4: /cgn2_6/ptodata/1/1aa/H_COMB.pep: *
5: /cgn2_6/ptodata/1/1aa/RE_COMB.pep: *
6: /cgn2_6/ptodata/1/1aa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44.5	37.7	20	1	US-08-934-915-13 Sequence 13, Appl
2	34	28.8	20	1	US-08-934-915-58 Sequence 58, Appl
3	33	28.0	17	2	US-09-440-781-44 Sequence 44, Appl
4	33	28.0	18	2	US-09-440-781-51 Sequence 51, Appl
5	33	28.0	18	2	US-09-440-781-53 Sequence 53, Appl
6	33	28.0	18	2	US-09-440-781-57 Sequence 57, Appl
7	33	28.0	18	2	US-09-440-781-87 Sequence 87, Appl
8	32	27.1	17	2	US-09-440-781-65 Sequence 65, Appl
9	32	27.1	17	2	US-09-440-781-84 Sequence 84, Appl
10	32	27.1	18	2	US-09-440-781-35 Sequence 35, Appl
11	31	26.3	12	2	US-10-395-434A-2 Sequence 2, Appl
12	30	25.4	17	2	US-09-440-781-73 Sequence 73, Appl
13	30	25.4	20	1	US-08-934-915-7 Sequence 7, Appl
14	29.5	25.0	20	2	US-09-287-070-9 Sequence 9, Appl
15	29	24.6	9	1	US-08-370-909-10 Sequence 10, Appl
16	29	24.6	9	2	US-08-774-639-201 Sequence 201, Appl
17	29	24.6	12	2	US-09-419-381-13 Sequence 14, Appl
18	29	24.6	15	2	US-08-793-331-13 Sequence 14, Appl
19	29	24.6	17	2	US-09-440-781-59 Sequence 85, Appl
20	29	24.6	17	2	US-09-440-781-85 Sequence 85, Appl
21	29	24.6	17	2	US-09-440-781-92 Sequence 92, Appl
22	29	24.6	18	2	US-09-461-325-579 Sequence 279, Appl
23	29	24.6	18	2	US-10-012-542-579 Sequence 279, Appl
24	29	24.6	18	2	US-10-115-123-579 Sequence 279, Appl
25	29	24.6	21	2	US-09-178-093B-19 Sequence 19, Appl
26	28.5	24.2	19	2	US-09-828-645-6 Sequence 6, Appl
27	28	23.7	6	2	US-09-563-222C-56 Sequence 56, Appl

28	28	23.7	10	1	US-08-077-797A-12 Sequence 12, Appl
29	28	23.7	10	2	US-09-042-428-8 Sequence 8, Appl
30	28	23.7	10	2	US-09-546-013-41 Sequence 41, Appl
31	28	23.7	10	2	US-09-910-706A-8 Sequence 8, Appl
32	28	23.7	10	4	PCT-US94-01238-12 Sequence 12, Appl
33	28	23.7	11	2	US-09-809-517A-21 Sequence 21, Appl
34	28	23.7	16	1	US-08-372-887-15 Sequence 15, Appl
35	28	23.7	17	1	US-08-116-778E-7 Sequence 7, Appl
36	28	23.7	17	1	US-08-438-562-7 Sequence 7, Appl
37	28	23.7	17	1	US-08-483-528B-95 Sequence 95, Appl
38	28	23.7	17	2	US-09-393-385B-106 Sequence 106, Appl
39	28	23.7	17	2	US-09-440-781-56 Sequence 66, Appl
40	28	23.7	17	2	US-09-440-781-90 Sequence 90, Appl
41	28	23.7	17	2	US-09-440-781-91 Sequence 91, Appl
42	28	23.7	17	2	US-10-195-752-106 Sequence 106, Appl
43	27.5	23.3	11	2	US-09-341-982-56 Sequence 56, Appl
44	27.5	23.3	19	2	US-09-828-645-1 Sequence 1, Appl
45	27.5	23.3	20	1	US-08-934-915-28 Sequence 28, Appl
46	27.5	23.3	20	1	US-08-934-915-11 Sequence 31, Appl
47	27	22.9	7	2	US-09-268-992-78 Sequence 78, Appl
48	27	22.9	7	2	US-09-657-474-78 Sequence 78, Appl
49	27	22.9	8	2	US-08-818-555-41 Sequence 41, Appl
50	27	22.9	9	2	US-09-341-982-26 Sequence 26, Appl
51	27	22.9	16	2	US-09-440-781-54 Sequence 54, Appl
52	27	22.9	17	2	US-09-440-781-38 Sequence 38, Appl
53	27	22.9	17	2	US-09-440-781-47 Sequence 47, Appl
54	27	22.9	17	2	US-09-440-781-50 Sequence 50, Appl
55	27	22.9	17	2	US-09-440-781-62 Sequence 62, Appl
56	27	22.9	17	2	US-09-440-781-79 Sequence 79, Appl
57	27	22.9	17	2	US-09-440-781-82 Sequence 82, Appl
58	27	22.9	17	2	US-09-440-781-86 Sequence 86, Appl
59	27	22.9	17	2	US-09-440-781-89 Sequence 89, Appl
60	27	22.9	18	2	US-09-440-781-56 Sequence 56, Appl
61	27	22.9	18	2	US-09-440-781-72 Sequence 72, Appl
62	27	22.9	18	2	US-09-563-222C-55 Sequence 55, Appl
63	27	22.9	19	2	US-09-177-249-142 Sequence 142, Appl
64	27	22.9	19	2	US-09-812-283-142 Sequence 142, Appl
65	26.5	22.5	20	1	US-08-934-915-136 Sequence 136, Appl
66	26.5	22.5	21	2	US-08-652-877-61 Sequence 61, Appl
67	26.5	22.5	21	2	US-08-476-515A-61 Sequence 61, Appl
68	26	22.0	5	2	US-08-981-122-68 Sequence 68, Appl
69	26	22.0	9	2	US-09-935-430-114 Sequence 114, Appl
70	26	22.0	9	2	US-09-935-430-132 Sequence 132, Appl
71	26	22.0	9	2	US-09-935-430-492 Sequence 492, Appl
72	26	22.0	10	2	US-09-462-645C-29 Sequence 29, Appl
73	26	22.0	10	2	US-09-755-330B-119 Sequence 119, Appl
74	26	22.0	10	2	US-09-935-430-157 Sequence 157, Appl
75	26	22.0	10	2	US-09-935-430-621 Sequence 621, Appl
76	26	22.0	10	2	US-10-658-180-119 Sequence 119, Appl
77	26	22.0	17	1	US-08-480-190-168 Sequence 168, Appl
78	26	22.0	17	1	US-08-488-579-168 Sequence 168, Appl
79	26	22.0	17	1	US-08-475-399A-168 Sequence 168, Appl
80	26	22.0	17	2	US-09-440-781-31 Sequence 31, Appl
81	26	22.0	17	2	US-09-440-781-46 Sequence 46, Appl
82	26	22.0	17	2	US-09-440-781-48 Sequence 48, Appl
83	26	22.0	17	2	US-09-440-781-55 Sequence 55, Appl
84	26	22.0	17	2	US-09-440-781-67 Sequence 67, Appl
85	26	22.0	17	2	US-08-077-255A-168 Sequence 168, Appl
86	26	22.0	17	4	PCT-US93-07545-168 Sequence 168, Appl
87	26	22.0	18	1	US-08-480-190-167 Sequence 167, Appl
88	26	22.0	18	1	US-08-488-379-167 Sequence 167, Appl
89	26	22.0	18	2	US-08-475-399A-167 Sequence 167, Appl
90	26	22.0	18	2	US-09-440-781-30 Sequence 30, Appl
91	26	22.0	18	2	US-09-440-781-43 Sequence 43, Appl
92	26	22.0	18	2	US-09-440-781-52 Sequence 52, Appl
93	26	22.0	18	2	US-08-077-255A-167 Sequence 167, Appl
94	26	22.0	18	4	PCT-US93-07545-167 Sequence 167, Appl
95	26	22.0	20	2	US-08-825-852-59 Sequence 59, Appl
96	26	22.0	20	2	US-09-052-888-60 Sequence 60, Appl
97	26	22.0	20	2	US-09-643-597-250 Sequence 250, Appl
98	26	22.0	20	2	US-09-480-884A-250 Sequence 250, Appl
99	26	22.0	20	2	US-09-542-115A-250 Sequence 250, Appl
100	26	22.0	20	2	US-09-606-421B-250 Sequence 250, Appl

ALIGNMENTS

RESULT 1

US-08-934-915-13

Sequence 13, Application US/08934915

Patent No. 5932412

GENERAL INFORMATION:

APPLICANT: DILLNER, JOAKIM

APPLICANT: DILLNER, LENA

APPLICANT: CHENG, HWEI-MING

TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN

TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8

TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR

TITLE OF INVENTION: DIAGNOSTIC PURPOSES

NUMBER OF SEQUENCES: 193

CORRESPONDENCE ADDRESSES:

ADDRESSEE: MASON & ASSOCIATES, P.A.

STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500

CITY: CLEARWATER

STATE: FLORIDA

COUNTRY: U.S.A.

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: Windows 3.0

SOFTWARE: Microsoft Word 6.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/934,915

FILING DATE: 22-SEP-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/949,836

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: LOUISE A. Fouch

REGISTRATION NUMBER: 37,133

REFERENCE/DOCKET NUMBER: 1946.6

TELECOMMUNICATION INFORMATION:

TELEPHONE: 813-538-3800

TELEFAX: 813-538-3820

TELEX:

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-934-915-13

Query Match

Best Local Similarity 37.7%; Score 44.5; DB 1; Length 20;

Matches 10; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY

2 EXNVMXYLYTMHYL 17

Db

5 EDNWEYVWMT-HYLL 19

RESULT 2

US-08-934-915-58

Sequence 58, Application US/08934915

Patent No. 5932412

GENERAL INFORMATION:

APPLICANT: DILLNER, JOAKIM

APPLICANT: DILLNER, LENA

APPLICANT: CHENG, HWEI-MING

TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN

TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8

TITLE OF INVENTION: DIAGNOSTIC PURPOSES

NUMBER OF SEQUENCES: 193

CORRESPONDENCE ADDRESSES:

ADDRESSEE: MASON & ASSOCIATES, P.A.

STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500

CITY: CLEARWATER

STATE: FLORIDA

COUNTRY: U.S.A.

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: Windows 3.0

SOFTWARE: Microsoft Word 6.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/934,915

FILING DATE: 22-SEP-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/949,836

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: LOUISE A. Fouch

REGISTRATION NUMBER: 37,133

REFERENCE/DOCKET NUMBER: 1946.6

TELECOMMUNICATION INFORMATION:

TELEPHONE: 813-538-3800

TELEFAX: 813-538-3820

TELEX:

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-934-915-13

Query Match

Best Local Similarity 62.5%; Pred. No. 0.91;

Matches 10; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY

2 EXNVMXYLYTMHYL 17

Db

5 EDNWEYVWMT-HYLL 19

TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR

TITLE OF INVENTION: DIAGNOSTIC PURPOSES

NUMBER OF SEQUENCES: 193

CORRESPONDENCE ADDRESSES:

ADDRESSEE: MASON & ASSOCIATES, P.A.

STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500

CITY: CLEARWATER

STATE: FLORIDA

COUNTRY: U.S.A.

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: Windows 3.0

SOFTWARE: Microsoft Word 6.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/934,915

FILING DATE: 22-SEP-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/949,836

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: LOUISE A. Fouch

REGISTRATION NUMBER: 37,133

REFERENCE/DOCKET NUMBER: 1946.6

TELECOMMUNICATION INFORMATION:

TELEPHONE: 813-538-3800

TELEFAX: 813-538-3820

TELEX:

INFORMATION FOR SEQ ID NO: 58:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-934-915-58

Query Match

Best Local Similarity 28.8%; Score 34; DB 1; Length 20;

Matches 6; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY

1 DEXNVMXYLYTMHYL 17

Db

4 KDNQMTYVWDSVYVM 20

RESULT 3

US-09-440-781-44

Sequence 44, Application US/09440781

Patent No. 6632926

GENERAL INFORMATION:

APPLICANT: Yvonne Man-yea Chen et al.

TITLE OF INVENTION: ANTIBODY VARIANTS

FILE REFERENCE: P1469R1

CURRENT APPLICATION NUMBER: US/09/440,781

CURRENT FILING DATE: 1999-11-16

NUMBER OF SEQ ID NOS: 99

SEQ ID NO 44

LENGTH: 17

TYPE: PRT

ORGANISM: artificial sequence

FEATURE:

NAME/KEY: artificial

LOCATION: 1-17

OTHER INFORMATION: variant CDR sequence

US-09-440-781-44

Query Match

Best Local Similarity 28.0%; Score 33; DB 2; Length 17;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY

14 HYLLNN 19

Db

|||||:

Db 3 HYLND 8

RESULT 4

US-09-440-781-51
; Sequence 51, Application US/09440781
; Patent No. 6632926
; GENERAL INFORMATION:
; APPLICANT: Yvonne Man-ye Chen et al.
; TITLE OF INVENTION: ANTIBODY VARIANTS
; FILE REFERENCE: P1469R1
; CURRENT APPLICATION NUMBER: US/09/440,781
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 99
; SEQ ID NO 51
; LENGTH: 18
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: artificial
; LOCATION: 1-18
; OTHER INFORMATION: variant CDR sequence
US-09-440-781-51

Query Match 28.0%; Score 33; DB 2; Length 18;

Best Local Similarity 71.4%; Pred. No. 62;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 14 HYLNDG 20
|||:|
Db 3 HYLKDG 9

RESULT 5

US-09-440-781-53
; Sequence 53, Application US/09440781
; Patent No. 6632926
; GENERAL INFORMATION:
; APPLICANT: Yvonne Man-ye Chen et al.
; TITLE OF INVENTION: ANTIBODY VARIANTS
; FILE REFERENCE: P1469R1
; CURRENT APPLICATION NUMBER: US/09/440,781
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 99
; SEQ ID NO 53
; LENGTH: 18
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: artificial
; LOCATION: 1-18
; OTHER INFORMATION: variant CDR sequence
US-09-440-781-53

Query Match 28.0%; Score 33; DB 2; Length 18;

Best Local Similarity 71.4%; Pred. No. 62;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 14 HYLNDG 20
|||:|
Db 3 HYLKDG 9

RESULT 6

US-09-440-781-57
; Sequence 57, Application US/09440781
; Patent No. 6632926
; GENERAL INFORMATION:
; APPLICANT: Yvonne Man-ye Chen et al.
; TITLE OF INVENTION: ANTIBODY VARIANTS
; FILE REFERENCE: P1469R1
; CURRENT APPLICATION NUMBER: US/09/440,781
; CURRENT FILING DATE: 1999-11-16

NUMBER OF SEQ ID NOS: 99

SEQ ID NO 57
; LENGTH: 18
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: artificial
; LOCATION: 1-18
; OTHER INFORMATION: variant CDR sequence
US-09-440-781-57

Query Match 28.0%; Score 33; DB 2; Length 18;
Best Local Similarity 71.4%; Pred. No. 62;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 14 HYLNDG 20
|||:|
Db 3 HYLKDG 9

RESULT 7

US-09-440-781-87
; Sequence 87, Application US/09440781
; Patent No. 6632926
; GENERAL INFORMATION:
; APPLICANT: Yvonne Man-ye Chen et al.
; TITLE OF INVENTION: ANTIBODY VARIANTS
; FILE REFERENCE: P1469R1
; CURRENT APPLICATION NUMBER: US/09/440,781
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 99
; SEQ ID NO 87
; LENGTH: 18
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: artificial
; LOCATION: 1-18
; OTHER INFORMATION: variant CDR sequence
US-09-440-781-87

Query Match 28.0%; Score 33; DB 2; Length 18;
Best Local Similarity 71.4%; Pred. No. 62;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 14 HYLNDG 20
|||:|
Db 3 HYLKDG 9

RESULT 8

US-09-440-781-65
; Sequence 65, Application US/09440781
; Patent No. 6632926
; GENERAL INFORMATION:
; APPLICANT: Yvonne Man-ye Chen et al.
; TITLE OF INVENTION: ANTIBODY VARIANTS
; FILE REFERENCE: P1469R1
; CURRENT APPLICATION NUMBER: US/09/440,781
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 99
; SEQ ID NO 65
; LENGTH: 17
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: artificial
; LOCATION: 1-17
; OTHER INFORMATION: variant CDR sequence
US-09-440-781-65

Query Match 27.1%; Score 32; DB 2; Length 17;
Best Local Similarity 71.4%; Pred. No. 85;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 14 HYYLNG 20
|||
Db 3 HYYORNG 9

RESULT 9

US-09-440-781-84
; Sequence 84, Application US/09440781
; Patent No. 6632926
; GENERAL INFORMATION:
; APPLICANT: Yvonne Man-yea Chen et al.
; TITLE OF INVENTION: ANTIBODY VARIANTS
; FILE REFERENCE: P1469R1
; CURRENT APPLICATION NUMBER: US/09/440,781
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 99
; SEQ ID NO 84
; LENGTH: 17
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: artificial
; LOCATION: 1-17
; OTHER INFORMATION: variant CDR sequence
US-09-440-781-84

Query Match 27.1%; Score 32; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 HYYLN 18
|||
Db 3 HYYLN 7

RESULT 10

US-09-440-781-35
; Sequence 35, Application US/09440781
; Patent No. 6632926
; GENERAL INFORMATION:
; APPLICANT: Yvonne Man-yea Chen et al.
; TITLE OF INVENTION: ANTIBODY VARIANTS
; FILE REFERENCE: P1469R1
; CURRENT APPLICATION NUMBER: US/09/440,781
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 99
; SEQ ID NO 35
; LENGTH: 18
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: artificial
; LOCATION: 1-18
; OTHER INFORMATION: variant CDR sequence
US-09-440-781-35

Query Match 27.1%; Score 32; DB 2; Length 18;
Best Local Similarity 71.4%; Pred. No. 91;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 14 HYYLNG 20
|||
Db 3 HYYORNG 9

RESULT 11

US-10-395-434A-2
; Sequence 2, Application US/10395434A
; Patent No. 6939948
; GENERAL INFORMATION:
; APPLICANT: Ferrone, Soldano

; TITLE OF INVENTION: GD2 Peptide Mimics
; FILE REFERENCE: 0351.0092
; CURRENT APPLICATION NUMBER: US/10/395,434A
; CURRENT FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: US 60/366,558
; PRIOR FILING DATE: 2002-03-22
; NUMBER OF SEQ ID NOS: 9
; SEQ ID NO 2
; LENGTH: 12
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: J8C peptide mimic for GD2
US-10-395-434A-2

Query Match 26.3%; Score 31; DB 2; Length 12;
Best Local Similarity 66.7%; Pred. No. 83;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 11 YTMHY 16
|||
Db 5 YTLHY 10

RESULT 12

US-09-440-781-73
; Sequence 73, Application US/09440781
; Patent No. 6632926
; GENERAL INFORMATION:
; APPLICANT: Yvonne Man-yea Chen et al.
; TITLE OF INVENTION: ANTIBODY VARIANTS
; FILE REFERENCE: P1469R1
; CURRENT APPLICATION NUMBER: US/09/440,781
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 99
; SEQ ID NO 73
; LENGTH: 17
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: artificial
; LOCATION: 1-17
; OTHER INFORMATION: variant CDR sequence
US-09-440-781-73

Query Match 25.4%; Score 30; DB 2; Length 17;
Best Local Similarity 66.7%; Pred. No. 1.8e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 14 HYYLN 19
|||
Db 3 HYYND 8

RESULT 13

US-08-934-915-7
; Sequence 7, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
; APPLICANT: DILNER, JOAKIM
; APPLICANT: DILNER, LENA
; APPLICANT: CHENG, HWEE-MING
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: MASON & ASSOCIATES, P.A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA

COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,915
FILING DATE: 22-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: LOUISE A. Foulch
REGISTRATION NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 1946.6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
TELEFAX: 813-538-3820
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-934-915-7

Query Match 25.4%; Score 30; DB 1; Length 20;
Best Local Similarity 50.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 NWKXYVLYTMHY 15
| | | | | | | | | | | | | | | | | | | | | |
Db 7 NTMDYVWVTDVY 18

RESULT 14
US-09-287-070-9
Sequence 9, Application US/09287070A
Patent No. 6495139
GENERAL INFORMATION:
APPLICANT: Tuomanen, Elaine
APPLICANT: Gosink, Knoosneh
TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF NOVEL
TITLE OF INVENTION: PNEUMOCOCCAL CHOLINE BINDING PROTERINS Cbpg, AND
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC USES THEREOF
FILE REFERENCE: 1340-1-024cid
CURRENT APPLICATION NUMBER: US/09/287,070A
CURRENT FILING DATE: 1999-04-06
EARLIER APPLICATION NUMBER: 09/196,389
EARLIER FILING DATE: 1998-11-19
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9
LENGTH: 20
TYPE: PRT
ORGANISM: Pneumococcus
US-09-287-070-9

Query Match 25.0%; Score 29.5; DB 2; Length 20;
Best Local Similarity 87.5%; Pred. No. 2.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 15 YVLN-NGA 21
| | | | | | | | | | | | | | | | | | | | | |
Db 10 YVLNANGA 17

RESULT 15
US-08-370-909-10

Sequence 10, Application US/08370909
Patent No. 5843648
GENERAL INFORMATION:
APPLICANT: ROBBINS, PAUL F.; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: D15 AND TYROSINASE
TITLE OF INVENTION: MELANOMA ANTIGENS AND THEIR USE IN DIAGNOSTIC
TITLE OF INVENTION: AND THERAPEUTIC METHODS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/370,909
FILING DATE: 10-JAN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPT
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4155
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: AMINO ACID
STRANDEDNESS: UNKNOWN
TOPOLOGY: UNKNOWN
MOLECULE TYPE: PEPTIDE
US-08-370-909-10

Query Match 24.6%; Score 29; DB 1; Length 9;
Best Local Similarity 66.7%; Pred. No. 4.6e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 13 MHYLN 18
| | | | | | | | | | | | | | | | | | | | | |
Db 3 MHYVS 8

RESULT 16
US-09-774-639-201
Sequence 201, Application US/09774639
Patent No. 6806351
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 90 Human Secreted Proteins
FILE REFERENCE: P2013P1
CURRENT APPLICATION NUMBER: US/09/774,639
CURRENT FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/244,112
PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-04
NUMBER OF SEQ ID NOS: 371
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 201
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (9)
OTHER INFORMATION: Xaa equals stop translation

US-09-774-639-201

Query Match 24.6%; Score 29; DB 2; Length 9;
 Best Local Similarity 83.3%; Pred. No. 4.6e+05;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 13 MHYYLN 18
 |||||
 Db 1 MHYYLN 6

RESULT 17

US-09-419-381-14
 ; Sequence 14, Application US/09419381
 ; Patent No. 6747135
 ; GENERAL INFORMATION:
 ; APPLICANT: No. 6747135a1, Garry P.
 ; APPLICANT: Rozinov, Michael N.
 ; TITLE OF INVENTION: Fluorescent Dye Binding Peptides
 ; FILE REFERENCE: A65681-1/DUB/RMS/DSS
 ; CURRENT APPLICATION NUMBER: US/09/419,381
 ; PRIOR FILING DATE: 1999-10-15
 ; PRIOR APPLICATION NUMBER: 60/104,465
 ; PRIOR FILING DATE: 1998-10-16
 ; NUMBER OF SEQ ID NOS: 122
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 14
 ; LENGTH: 12
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic
 US-09-419-381-14

Query Match 24.6%; Score 29; DB 2; Length 12;
 Best Local Similarity 66.7%; Pred. No. 1.8e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 YTMHY 16
 |||||
 Db 4 YSMHY 9

RESULT 18

US-08-793-331-13
 ; Sequence 13, Application US/08793331
 ; Patent No. 6071877
 ; GENERAL INFORMATION:
 ; APPLICANT: DELECLUSE, ARNELLE
 ; APPLICANT: THIERY, ISABELLE
 ; TITLE OF INVENTION: NEW POLYPEPTIDES HAVING A TOXIC ACTIVITY AGAINST
 ; TITLE OF INVENTION: INSECTS OF THE DIPTERA FAMILY
 ; FILE REFERENCE: 0660-0116-0 PCT
 ; CURRENT APPLICATION NUMBER: US/08/793,331
 ; CURRENT FILING DATE: 1997-05-13
 ; EARLIER APPLICATION NUMBER: PCT/FR95/01116
 ; EARLIER FILING DATE: 1995-08-24
 ; EARLIER APPLICATION NUMBER: FR 94/10299
 ; EARLIER FILING DATE: 1994-08-25
 ; NUMBER OF SEQ ID NOS: 15
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 13
 ; LENGTH: 15
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: JEG66
 US-08-793-331-13

Query Match 24.6%; Score 29; DB 2; Length 15;
 Best Local Similarity 83.3%; Pred. No. 2.3e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 13 MHYYLN 18
 |||||
 Db 1 MHYYGN 6

RESULT 19

US-09-440-781-49
 ; Sequence 49, Application US/09440781
 ; Patent No. 6632926
 ; GENERAL INFORMATION:
 ; APPLICANT: Yvonne Man-yea Chen et al.
 ; TITLE OF INVENTION: ANTIBODY VARIANTS
 ; FILE REFERENCE: P1469R1
 ; CURRENT APPLICATION NUMBER: US/09/440,781
 ; CURRENT FILING DATE: 1999-11-16
 ; NUMBER OF SEQ ID NOS: 99
 ; SEQ ID NO 49
 ; LENGTH: 17
 ; TYPE: PRT
 ; ORGANISM: artificial sequence
 ; FEATURE:
 ; NAME/KEY: artificial
 ; LOCATION: 1-17
 ; OTHER INFORMATION: variant CDR sequence
 US-09-440-781-49

Query Match 24.6%; Score 29; DB 2; Length 17;
 Best Local Similarity 80.0%; Pred. No. 2.7e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 14 HYYLN 18
 |||||
 Db 3 HYYVN 7

RESULT 20

US-09-440-781-85
 ; Sequence 85, Application US/09440781
 ; Patent No. 6632926
 ; GENERAL INFORMATION:
 ; APPLICANT: Yvonne Man-yea Chen et al.
 ; TITLE OF INVENTION: ANTIBODY VARIANTS
 ; FILE REFERENCE: P1469R1
 ; CURRENT APPLICATION NUMBER: US/09/440,781
 ; CURRENT FILING DATE: 1999-11-16
 ; NUMBER OF SEQ ID NOS: 99
 ; SEQ ID NO 85
 ; LENGTH: 17
 ; TYPE: PRT
 ; ORGANISM: artificial sequence
 ; FEATURE:
 ; NAME/KEY: artificial
 ; LOCATION: 1-17
 ; OTHER INFORMATION: variant CDR sequence
 US-09-440-781-85

Query Match 24.6%; Score 29; DB 2; Length 17;
 Best Local Similarity 80.0%; Pred. No. 2.7e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 14 HYYLN 18
 |||||
 Db 3 HYYVN 7

RESULT 21

US-09-440-781-92
 ; Sequence 92, Application US/09440781
 ; Patent No. 6632926
 ; GENERAL INFORMATION:
 ; APPLICANT: Yvonne Man-yea Chen et al.
 ; TITLE OF INVENTION: ANTIBODY VARIANTS
 ; FILE REFERENCE: P1469R1


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; CURRENT APPLICATION NUMBER: US/09/440,781
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 99
; SEQ ID NO 92
; LENGTH: 17
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: artificial
; LOCATION: 1-17
; OTHER INFORMATION: variant CDR sequence
US-09-440-781-92

Query Match      24.6% Score 29; DB 2; Length 17;
Best Local Similarity 80.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      14 HYYLN 18
       |||:|
       3 HYYVN 7

Db
; RESULT 22
US-09-461-325-279
; Sequence 279, Application US/09461325A
; Patent No. 6475753
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: P2029P1
; CURRENT APPLICATION NUMBER: US/09/461,325A
; EARLIER FILING DATE: 1999-12-14
; EARLIER APPLICATION NUMBER: PCT/US99/13418
; EARLIER FILING DATE: 1999-06-15
; EARLIER APPLICATION NUMBER: 60/089,507
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,508
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,509
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,510
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/090,112
; EARLIER FILING DATE: 1998-06-22
; EARLIER APPLICATION NUMBER: 60/090,113
; EARLIER FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 279
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-461-325-279

Query Match      24.6% Score 29; DB 2; Length 18;
Best Local Similarity 62.5%; Pred. No. 2.8e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      12 TMHYLYNN 19
       |||:|
       1 TVLFYLYNN 8

Db
; RESULT 23
US-10-012-542-279
; Sequence 279, Application US/10012542
; Patent No. 6627741
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: P2029P1
; CURRENT APPLICATION NUMBER: US/10/012,542
; CURRENT FILING DATE: 2001-12-12
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; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/461,325
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-14
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,507
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,508
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,509
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,510
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,112
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,113
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 279
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-012-542-279

Query Match      24.6% Score 29; DB 2; Length 18;
Best Local Similarity 62.5%; Pred. No. 2.8e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      12 TMHYLYNN 19
       |||:|
       1 TVLFYLYNN 8

Db
; RESULT 24
US-10-115-123-279
; Sequence 279, Application US/10115123
; Patent No. 6774216
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: P2029G30APID2
; CURRENT APPLICATION NUMBER: US/10/115,123
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: PCT/US99/13418
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/089,507
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089,508
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089,509
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089,510
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/090,112
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090,113
; PRIOR FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 279
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-115-123-279

Query Match      24.6% Score 29; DB 2; Length 18;
Best Local Similarity 62.5%; Pred. No. 2.8e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      12 TMHYLYNN 19
       |||:|
       1 TVLFYLYNN 8

Db
; RESULT 25
```

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US-09-178-093B-19
; Sequence 19, Application US/09178093B
; Patent No. 6660846
; GENERAL INFORMATION:
; APPLICANT: Robert H. Edwards
; APPLICANT: Richard J. Reimer
; APPLICANT: Steve L. McIntire
; APPLICANT: Erik M. Jorgenson
; APPLICANT: Kim Schuke
; TITLE OF INVENTION: Vesicular Amino Acid Transported
; FILE REFERENCE: 2002-0005.30
; CURRENT APPLICATION NUMBER: US/09/178, 093B
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/063, 012
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO: 19
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-178-093B-19

```

```

Query Match      24.6%; Score 29; DB 2; Length 21;
Best Local Similarity 55.6%; Pred. No. 3.4e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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```

QY      11 YTMHYVYLN 19
          |||:|
Db      12 YTSHIFLPN 20

```

Search completed: January 26, 2006, 08:07:01
 Job time : 22.7787 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 26, 2006, 08:04:12 ; Search time 74.75 Seconds
(without alignments)
128.563 Million cell updates/sec

Title: US-09-662-293-9

Perfect score: 118
Sequence: 1 DEXVMKKYVLYTMHYLNGATR 23

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 369445

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published Applications AA Main.*

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3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	30.5	20	4	US-10-346-198-43 Sequence 43, Appl
2	35	29.7	16	3	US-09-880-748-2216 Sequence 2216, Ap
3	35	29.7	16	4	US-10-293-418-2216 Sequence 2216, Ap
4	34	28.8	12	4	US-10-467-758-35 Sequence 35, Appl
5	34	28.8	16	3	US-09-880-748-2259 Sequence 2259, Ap
6	34	28.8	16	4	US-10-293-418-2259 Sequence 2259, Ap
7	34	28.8	21	4	US-10-086-814-30 Sequence 30, Appl
8	34	28.8	21	4	US-10-086-814-36 Sequence 36, Appl
9	34	28.8	21	4	US-10-424-599-147622 Sequence 147622, Ap
10	33.5	28.4	14	4	US-10-723-502-10 Sequence 10, Appl
11	33.5	28.4	14	4	US-10-645-659-10 Sequence 10, Appl
12	33.5	28.4	15	5	US-10-916-598-21 Sequence 21, Appl
13	33	28.0	17	4	US-10-624-153-44 Sequence 44, Appl
14	33	28.0	18	4	US-10-624-153-51 Sequence 51, Appl
15	33	28.0	18	4	US-10-624-153-53 Sequence 53, Appl
16	33	28.0	18	4	US-10-624-153-57 Sequence 57, Appl
17	33	28.0	18	4	US-10-624-153-87 Sequence 87, Appl
18	33	28.0	18	4	US-10-624-153-87 Sequence 87, Appl
19	32	27.1	15	3	US-09-935-384-901 Sequence 401, Appl
20	32	27.1	15	3	US-09-880-748-2909 Sequence 2909, Ap
21	32	27.1	15	6	US-10-293-418-2909 Sequence 2909, Ap
22	32	27.1	15	6	US-11-009-460-104 Sequence 104, Appl
23	32	27.1	17	4	US-10-624-153-65 Sequence 65, Appl
24	32	27.1	17	4	US-10-624-153-84 Sequence 84, Appl
25	32	27.1	18	4	US-10-624-153-35 Sequence 35, Appl
26	32	27.1	20	3	US-09-880-748-2158 Sequence 2158, Ap
27	32	27.1	20	3	US-09-880-748-2896 Sequence 2896, Ap
			20	3	US-09-880-748-2903 Sequence 2903, Ap

28	32	27.1	20	4	US-10-293-418-2158 Sequence 2158, Ap
29	32	27.1	20	4	US-10-293-418-2896 Sequence 2896, Ap
30	32	27.1	20	4	US-10-293-418-2903 Sequence 2903, Ap
31	31	26.3	15	4	US-10-206-699-234 Sequence 234, Appl
32	31	26.3	16	3	US-09-880-748-2214 Sequence 2214, Ap
33	31	26.3	16	3	US-09-880-748-2215 Sequence 2215, Ap
34	31	26.3	16	3	US-09-880-748-2217 Sequence 2217, Ap
35	31	26.3	16	3	US-09-880-748-2219 Sequence 2219, Ap
36	31	26.3	16	3	US-09-880-748-2298 Sequence 2298, Ap
37	31	26.3	16	3	US-09-880-748-2298 Sequence 2298, Ap
38	31	26.3	16	4	US-10-293-418-2214 Sequence 2214, Ap
39	31	26.3	16	4	US-10-293-418-2215 Sequence 2215, Ap
40	31	26.3	16	4	US-10-293-418-2217 Sequence 2217, Ap
41	31	26.3	16	4	US-10-293-418-2219 Sequence 2219, Ap
42	31	26.3	16	4	US-10-293-418-2298 Sequence 2298, Ap
43	31	26.3	16	4	US-10-293-418-2316 Sequence 2316, Ap
44	31	26.3	18	5	US-10-724-661A-20 Sequence 20, Appl
45	31	26.3	20	5	US-10-775-972-562 Sequence 562, Appl
46	31	26.3	20	5	US-10-922-124-562 Sequence 562, Appl
47	30.5	25.8	19	3	US-09-748-875-23 Sequence 23, Appl
48	30.5	25.8	19	3	US-09-298-523B-23 Sequence 23, Appl
49	30.5	25.8	19	5	US-10-341-201-23 Sequence 23, Appl
50	30	25.4	9	4	US-10-245-871-489 Sequence 489, Appl
51	30	25.4	11	4	US-10-253-286-489 Sequence 489, Appl
52	30	25.4	11	4	US-10-239-313A-266 Sequence 266, Appl
53	30	25.4	14	4	US-10-245-871-512 Sequence 512, Appl
54	30	25.4	14	4	US-10-253-286-512 Sequence 512, Appl
55	30	25.4	14	5	US-10-342-896-1 Sequence 1, Appl1
56	30	25.4	16	4	US-10-001-883-128 Sequence 128, Appl
57	30	25.4	16	5	US-10-661-156-11 Sequence 11, Appl
58	30	25.4	16	5	US-10-661-156-205 Sequence 205, Appl
59	30	25.4	17	4	US-10-245-871-513 Sequence 513, Appl
60	30	25.4	17	4	US-10-253-286-513 Sequence 513, Appl
61	30	25.4	17	4	US-10-624-153-73 Sequence 73, Appl
62	30	25.4	19	3	US-09-880-748-2811 Sequence 2811, Ap
63	30	25.4	19	4	US-10-293-418-2811 Sequence 2811, Ap
64	30	25.4	19	4	US-10-413-943-53 Sequence 53, Appl
65	30	25.4	20	4	US-10-396-073-22 Sequence 22, Appl
66	29.5	25.0	20	3	US-09-748-875-18 Sequence 18, Appl
67	29.5	25.0	20	3	US-09-748-875-18 Sequence 18, Appl
68	29.5	25.0	20	3	US-09-748-875-27 Sequence 27, Appl
69	29.5	25.0	20	3	US-09-748-875-28 Sequence 28, Appl
70	29.5	25.0	20	3	US-09-748-875-31 Sequence 31, Appl
71	29.5	25.0	20	3	US-09-748-875-32 Sequence 32, Appl
72	29.5	25.0	20	3	US-09-748-875-33 Sequence 33, Appl
73	29.5	25.0	20	3	US-09-287-070-9 Sequence 9, Appl1
74	29.5	25.0	20	3	US-09-298-523B-18 Sequence 18, Appl
75	29.5	25.0	20	3	US-09-298-523B-20 Sequence 20, Appl
76	29.5	25.0	20	3	US-09-298-523B-27 Sequence 27, Appl
77	29.5	25.0	20	3	US-09-298-523B-28 Sequence 28, Appl
78	29.5	25.0	20	3	US-09-298-523B-32 Sequence 32, Appl
79	29.5	25.0	20	3	US-09-298-523B-32 Sequence 32, Appl
80	29.5	25.0	20	3	US-09-298-523B-33 Sequence 33, Appl
81	29.5	25.0	20	4	US-10-243-977-9 Sequence 9, Appl1
82	29.5	25.0	20	5	US-10-341-201-18 Sequence 18, Appl
83	29.5	25.0	20	5	US-10-341-201-27 Sequence 27, Appl
84	29.5	25.0	20	5	US-10-341-201-28 Sequence 28, Appl
85	29.5	25.0	20	5	US-10-341-201-31 Sequence 31, Appl
86	29.5	25.0	20	5	US-10-341-201-32 Sequence 32, Appl
87	29.5	25.0	20	5	US-10-341-201-33 Sequence 33, Appl
88	29.5	25.0	20	5	US-10-341-201-33 Sequence 33, Appl
89	29.5	25.0	20	5	US-09-969-730-203 Sequence 203, Appl
90	29.5	25.0	8	4	US-10-621-363-203 Sequence 203, Appl
91	29.5	25.0	8	5	US-10-715-610-69 Sequence 69, Appl
92	29.5	25.0	9	3	US-09-774-339-101 Sequence 101, Appl
93	29.5	25.0	9	4	US-10-105-232-169 Sequence 169, Appl
94	29.5	25.0	9	4	US-10-189-437-156 Sequence 156, Appl
95	29.5	25.0	9	5	US-10-860-050-169 Sequence 169, Appl
96	29.5	25.0	12	4	US-10-652-151-14 Sequence 14, Appl
97	29.5	25.0	13	4	US-10-080-948-18 Sequence 18, Appl
98	29.5	25.0	16	3	US-09-880-748-2258 Sequence 2258, Ap
99	29.5	25.0	16	3	US-09-880-748-2260 Sequence 2260, Ap
100	29.5	25.0	16	4	US-10-293-418-2258 Sequence 2258, Ap

ALIGNMENTS

RESULT 1

US-10-346-198-43
; Sequence 43, Application US/10346198
; Publication No. US20040043485A1
; GENERAL INFORMATION:
; APPLICANT: WESSLER, SUSAN R.
; APPLICANT: JIANG, NING
; APPLICANT: BAO, ZHIRONG
; APPLICANT: ZHANG, XIAOYU
; APPLICANT: EDY, SEAN R.
; TITLE OF INVENTION: TRANSPOSABLE ELEMENTS IN RICE AND METHODS OF USE
; FILE REFERENCE: 18465-0018
; CURRENT APPLICATION NUMBER: US/10/346,198
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: 60/337,409
; PRIOR FILING DATE: 2002-05-01
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-346-198-43

Query Match

Best Local Similarity 30.5%; Score 36; DB 4; Length 20;
Best Local Similarity 63.6%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 10 YTMHYLYLNG 20
| | | | |
Db 7 LYNTGYLYLNG 17

RESULT 2

US-09-880-748-2216
; Sequence 2216, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2216
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2216

Query Match

Best Local Similarity 29.7%; Score 35; DB 3; Length 16;
Best Local Similarity 71.4%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 11 YTMHYLYL 17
| : | | | |
Db 9 YVLHYLYL 15

RESULT 3

US-10-293-418-2216
; Sequence 2216, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2216
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-2216

Query Match

Best Local Similarity 29.7%; Score 35; DB 4; Length 16;
Best Local Similarity 71.4%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 11 YTMHYLYL 17
| : | | | |
Db 9 YVLHYLYL 15

RESULT 4

US-10-467-758-35
; Sequence 35, Application US/10467758
; Publication No. US20040132108A1
; GENERAL INFORMATION:
; APPLICANT: Hupp, Theodore
; APPLICANT: Dornan, David
; TITLE OF INVENTION: Screening Method and Agents
; FILE REFERENCE: 9013.54
; CURRENT APPLICATION NUMBER: US/10/467,758
; CURRENT FILING DATE: 2003-08-13
; PRIOR APPLICATION NUMBER: PCT/GB02/00640
; PRIOR FILING DATE: 2002-02-13
; PRIOR APPLICATION NUMBER: GB 0103508.8
; PRIOR FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-467-758-35

Query Match

Best Local Similarity 28.8%; Score 34; DB 4; Length 12;
Best Local Similarity 50.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 11 YTMHYLYLNGAT 22
| : | | | : | | |

Db 1 PFPHYWDNIAT 12

RESULT 5

US-09-880-748-2259
; Sequence 2259, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: P523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2259
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2259

Query Match 28.8%; Score 34; DB 3; Length 16;

Best Local Similarity 83.3%; Pred. No. 2.1e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 YTMHY 16
| | | | |
Db 9 YVMHY 14

RESULT 6

US-10-293-418-2259
; Sequence 2259, Application US/10293418
; Publication No. US2003022396A1
; GENERAL INFORMATION:; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: P523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2259
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-2259

Query Match 28.8%; Score 34; DB 4; Length 16;

Best Local Similarity 83.3%; Pred. No. 2.1e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 YTMHY 16
| | | | |
Db 9 YVMHY 14

RESULT 7

US-10-086-814-30
; Sequence 30, Application US/10086814
; Publication No. US20030092632A1
; GENERAL INFORMATION:; APPLICANT: Dragic, Tatjana
; APPLICANT: Olson, William C.
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 61010-AB-1
; CURRENT APPLICATION NUMBER: US/10/086,814
; CURRENT FILING DATE: 2002-02-28
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (9)..(9)
; OTHER INFORMATION: SULFATATION
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (13)..(13)
; OTHER INFORMATION: SULFATATION
; FEATURE:
; NAME/KEY: BINDING
; LOCATION: (21)..(21)
; OTHER INFORMATION: BIOTIN
US-10-086-814-30

Query Match 28.8%; Score 34; DB 4; Length 21;

Best Local Similarity 41.7%; Pred. No. 2.8e+02;

Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 10 LYTMHYLLNNGA 21
.:.:.:.:
Db 8 IYDINYTSEGA 19

RESULT 8

US-10-086-814-36
; Sequence 36, Application US/10086814
; Publication No. US20030092632A1
; GENERAL INFORMATION:; APPLICANT: Dragic, Tatjana
; APPLICANT: Olson, William C.
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 61010-AB-1
; CURRENT APPLICATION NUMBER: US/10/086,814
; CURRENT FILING DATE: 2002-02-28
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (9)..(9)
; OTHER INFORMATION: PHOSPHORYLATION
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (13)..(13)

OTHER INFORMATION: PHOSPHORYLATION
FEATURE:
NAME/KEY: BINDING
LOCATION: (21)..(21)
OTHER INFORMATION: BIOTIN
US-10-086-814-36

Query Match 28.8%; Score 34; DB 4; Length 21;
Best Local Similarity 41.7%; Pred. No. 2.8e+02;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 10 LYTMHYLYLNCA 21
: : : : :
Db 8 IYDINYTSEGA 19

RESULT 9
US-10-424-599-147622
Sequence 147622, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 147622
LENGTH: 21
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_104320C.1.pep
US-10-424-599-147622

Query Match 28.8%; Score 34; DB 4; Length 21;
Best Local Similarity 35.3%; Pred. No. 2.8e+02;
Matches 6; Conservative 5; Mismatches 4; Indels 2; Gaps 1;

OY 4 NVMXYLYTMHY-YLN 18
: : : : :
Db 2 NUNYFINTLHYISYFN 18

RESULT 10
US-10-722-502-10
Sequence 10, Application US/10722502
Publication No. US20040170631A1
GENERAL INFORMATION:
APPLICANT: Yacoby-Zeevi, Oron
APPLICANT: Peretz, Tuvia
APPLICANT: Miron, Daphna
APPLICANT: Shlom, Yinnon
APPLICANT: Pecker, Iris
APPLICANT: Ayal-Hershkovitz, Maty
APPLICANT: Feinstein, Elena
APPLICANT: Van Gelder, Joel M.
APPLICANT: Vlodavsky, Israel
APPLICANT: Friedmann, Yael
TITLE OF INVENTION: HEPARANASE ACTIVITY NEUTRALIZING ANTI- HEPARANASE MONOCLONAL
TITLE OF INVENTION: ANTIBODY AND OTHER ANTI-HEPARANASE ANTIBODIES
FILE REFERENCE: 26872
CURRENT APPLICATION NUMBER: US/10/722,502
CURRENT FILING DATE: 2003-11-28
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.2
SEQ ID NO 10
LENGTH: 14
TYPE: PRT

ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Functional peptide epitope of heparanase
US-10-722-502-10

Query Match 28.4%; Score 33.5; DB 4; Length 14;
Best Local Similarity 72.7%; Pred. No. 2.2e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

OY 14 HYYLN-NGATR 23
: : : : :
Db 4 HYYLNGRTATR 14

RESULT 11
US-10-645-659-10
Sequence 10, Application US/10645659
Publication No. US20040213789A1
GENERAL INFORMATION:
APPLICANT: Yacoby-Zeevi, Oron
APPLICANT: Peretz, Tuvia
APPLICANT: Miron, Daphna
APPLICANT: Shlom, Yinnon
APPLICANT: Pecker, Iris
APPLICANT: Ayal-Hershkovitz, Maty
APPLICANT: Vlodavsky, Israel
APPLICANT: Friedmann, Yael
TITLE OF INVENTION: HEPARANASE ACTIVITY NEUTRALIZING ANTI- HEPARANASE MONOCLONAL
TITLE OF INVENTION: ANTIBODY AND OTHER ANTI-HEPARANASE ANTIBODIES
FILE REFERENCE: 26128
CURRENT APPLICATION NUMBER: US/10/645,659
CURRENT FILING DATE: 2003-08-22
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.2
SEQ ID NO 10
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Functional peptide epitope of heparanase
US-10-645-659-10

Query Match 28.4%; Score 33.5; DB 4; Length 14;
Best Local Similarity 72.7%; Pred. No. 2.2e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

OY 14 HYYLN-NGATR 23
: : : : :
Db 4 HYYLNGRTATR 14

RESULT 12
US-10-916-598-21
Sequence 21, Application US/10916598
Publication No. US20050042213A1
GENERAL INFORMATION:
APPLICANT: Van Gelder, Joel M.
APPLICANT: Miron, Daphna
TITLE OF INVENTION: 27413
FILE REFERENCE: METHODS AND PHARMACEUTICAL COMPOSITIONS FOR MODULATING HEPARANASE
ACTIVATION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/10/916,598
CURRENT FILING DATE: 2004-08-12
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn version 3.2
SEQ ID NO 21
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic peptide
US-10-916-598-21

Query Match 28.4%; Score 33.5; DB 5; Length 15;
Best Local Similarity 72.7%; Pred. No. 2.3e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 14 HYYLNN-NGATR 23
Db 5 HYYLNGRTATR 15

RESULT 13
US-10-624-153-44
; Sequence 44, Application US/10624153
; Publication No. US20040086502A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, YVONNE M.
; APPLICANT: LOWMAN, HENRY B.
; APPLICANT: MULLER, YVES
; TITLE OF INVENTION: ANTIBODY VARIANTS
; FILE REFERENCE: P1469R1C1
; CURRENT APPLICATION NUMBER: US/10/624,153
; CURRENT FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: US 09/440,781
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: US 60/108,945
; PRIOR FILING DATE: 1998-11-18
; NUMBER OF SEQ ID NOS: 99
; SEQ ID NO 44
; LENGTH: 17
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
; NAME/KEY: artificial
; LOCATION: 1-17
; OTHER INFORMATION: variant CDR sequence
US-10-624-153-44

Query Match 28.0%; Score 33; DB 4; Length 17;
Best Local Similarity 83.3%; Pred. No. 3.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 14 HYYLNN 19
Db 3 HYYLND 8

RESULT 14
US-10-624-153-51
; Sequence 51, Application US/10624153
; Publication No. US20040086502A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, YVONNE M.
; APPLICANT: LOWMAN, HENRY B.
; APPLICANT: MULLER, YVES
; TITLE OF INVENTION: ANTIBODY VARIANTS
; FILE REFERENCE: P1469R1C1
; CURRENT APPLICATION NUMBER: US/10/624,153
; CURRENT FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: US 09/440,781
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: US 60/108,945
; PRIOR FILING DATE: 1998-11-18
; NUMBER OF SEQ ID NOS: 99
; SEQ ID NO 51
; LENGTH: 18
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
; NAME/KEY: artificial
; LOCATION: 1-18

OTHER INFORMATION: variant CDR sequence
US-10-624-153-51

Query Match 28.0%; Score 33; DB 4; Length 18;
Best Local Similarity 71.4%; Pred. No. 3.4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 14 HYYLNG 20
Db 3 HYYLKDQ 9

RESULT 15
US-10-624-153-53
; Sequence 53, Application US/10624153
; Publication No. US20040086502A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, YVONNE M.
; APPLICANT: LOWMAN, HENRY B.
; APPLICANT: MULLER, YVES
; TITLE OF INVENTION: ANTIBODY VARIANTS
; FILE REFERENCE: P1469R1C1
; CURRENT APPLICATION NUMBER: US/10/624,153
; CURRENT FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: US 09/440,781
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: US 60/108,945
; PRIOR FILING DATE: 1998-11-18
; NUMBER OF SEQ ID NOS: 99
; SEQ ID NO 53
; LENGTH: 18
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
; NAME/KEY: artificial
; LOCATION: 1-18
; OTHER INFORMATION: variant CDR sequence
US-10-624-153-53

Query Match 28.0%; Score 33; DB 4; Length 18;
Best Local Similarity 71.4%; Pred. No. 3.4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 14 HYYLNG 20
Db 3 HYYLKDQ 9

RESULT 16
US-10-624-153-57
; Sequence 57, Application US/10624153
; Publication No. US20040086502A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, YVONNE M.
; APPLICANT: LOWMAN, HENRY B.
; APPLICANT: MULLER, YVES
; TITLE OF INVENTION: ANTIBODY VARIANTS
; FILE REFERENCE: P1469R1C1
; CURRENT APPLICATION NUMBER: US/10/624,153
; CURRENT FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: US 09/440,781
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: US 60/108,945
; PRIOR FILING DATE: 1998-11-18
; NUMBER OF SEQ ID NOS: 99
; SEQ ID NO 57
; LENGTH: 18
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized

FEATURE:
; NAME/KEY: artificial
; LOCATION: 1-18
; OTHER INFORMATION: variant CDR sequence
US-10-624-153-57

Query Match 28.0%; Score 33; DB 4; Length 18;
Best Local Similarity 71.4%; Pred. No. 3.4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 14 HYYLNG 20
 ||||:|
Db 3 HYYLKDQ 9

RESULT 17
US-10-624-153-87
; Sequence 87, Application US/10624153
; Publication No. US20040086502A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, YVONNE M.
; APPLICANT: LOWMAN, HENRY B.
; APPLICANT: MULLER, YVES
; TITLE OF INVENTION: ANTIBODY VARIANTS
; FILE REFERENCE: P1469R1C1
; CURRENT APPLICATION NUMBER: US/10/624,153
; CURRENT FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: US 09/440,781
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: US 60/108,945
; PRIOR FILING DATE: 1998-11-18
; NUMBER OF SEQ ID NOS: 99
; SEQ ID NO 87
; LENGTH: 18
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
; FEATURE:
; NAME/KEY: artificial
; LOCATION: 1-18
; OTHER INFORMATION: variant CDR sequence
US-10-624-153-87

Query Match 28.0%; Score 33; DB 4; Length 18;
Best Local Similarity 71.4%; Pred. No. 3.4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 14 HYYLNG 20
 ||||:|
Db 3 HYYLKDQ 9

RESULT 18
US-09-935-384-401
; Sequence 401, Application US/09935384
; Publication No. US20030166526A1
; GENERAL INFORMATION:
; APPLICANT: CHALLITA-ETD, PIA
; APPLICANT: HUBERT, RENE
; APPLICANT: RAIFANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: PARIS, MARY
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1H4
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20033.00
; CURRENT APPLICATION NUMBER: US/09/935,384
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098

; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 783
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 401
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-384-401

Query Match 27.1%; Score 32; DB 3; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.7e+06;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 8 YVLYTMH 14
 ||||:|
Db 2 YVLYSVH 8

RESULT 19
US-09-880-748-2909
; Sequence 2909, Application US/09880748
; Publication No. US20030058937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2909
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2909

Query Match 27.1%; Score 32; DB 3; Length 15;
Best Local Similarity 33.3%; Pred. No. 4e+02;
Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Oy 8 YVLYTMH 14
 ||||:|
Db 4 YVLYTMH 15

RESULT 20
US-10-293-418-2909
; Sequence 2909, Application US/10293418
; Publication No. US20030229396A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 2909
LENGTH: 15
TYPE: PRT
ORGANISM: Homo sapiens
US-10-293-418-2909

Query Match 27.1%; Score 32; DB 4; Length 15;
Best Local Similarity 33.3%; Pred. No. 4e+02;
Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 8 YVLYTMHYLYNN 19
DB 4 YIMTAHYIDS 15

RESULT 21
US-11-009-460-104
Sequence 104, Application US/11009460
Publication No. US20050181459A1
GENERAL INFORMATION:
APPLICANT: BAKER, Matthew
APPLICANT: CARTER, Francis J.
APPLICANT: GRAHAM
TITLE OF INVENTION: METHOD FOR MAPPING AND ELIMINATING
TITLE OF INVENTION: T-CELL EPITOPES
FILE REFERENCE: MER-135
CURRENT APPLICATION NUMBER: US/11/009,460
CURRENT FILING DATE: 2004-12-10
PRIOR APPLICATION NUMBER: PCT/EP03/06110
PRIOR FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: EP02012919.3
PRIOR FILING DATE: 2002-06-11
NUMBER OF SEQ ID NOS: 127
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 104
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Potential T-cell Epitopes
US-11-009-460-104

Query Match 27.1%; Score 32; DB 6; Length 15;
Best Local Similarity 75.0%; Pred. No. 4e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 16 YLNGAIR 23
DB 6 YLNGPQR 13

RESULT 22
US-10-624-153-65
Sequence 65, Application US/10624153
Publication No. US20040086502A1
GENERAL INFORMATION:
APPLICANT: CHEN, YVONNE M.
APPLICANT: LOWMAN, HENRY B.
APPLICANT: MULLER, YVES
TITLE OF INVENTION: ANTIBODY VARIANTS
FILE REFERENCE: P1469R1C1
CURRENT APPLICATION NUMBER: US/10/624,153
CURRENT FILING DATE: 2003-07-21
PRIOR APPLICATION NUMBER: US 09/440,781

PRIOR FILING DATE: 1999-11-16
PRIOR APPLICATION NUMBER: US 60/108,945
PRIOR FILING DATE: 1998-11-18
NUMBER OF SEQ ID NOS: 99
SEQ ID NO 65
LENGTH: 17
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: sequence is synthesized
NAME/KEY: artificial
LOCATION: 1-17
OTHER INFORMATION: variant CDR sequence
US-10-624-153-65

Query Match 27.1%; Score 32; DB 4; Length 17;
Best Local Similarity 71.4%; Pred. No. 4.6e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 14 HYLYNG 20
DB 3 HYQNG 9

RESULT 23
US-10-624-153-84
Sequence 84, Application US/10624153
Publication No. US20040086502A1
GENERAL INFORMATION:
APPLICANT: CHEN, YVONNE M.
APPLICANT: LOWMAN, HENRY B.
APPLICANT: MULLER, YVES
TITLE OF INVENTION: ANTIBODY VARIANTS
FILE REFERENCE: P1469R1C1
CURRENT APPLICATION NUMBER: US/10/624,153
CURRENT FILING DATE: 2003-07-21
PRIOR APPLICATION NUMBER: US 09/440,781
PRIOR FILING DATE: 1999-11-16
PRIOR APPLICATION NUMBER: US 60/108,945
PRIOR FILING DATE: 1998-11-18
NUMBER OF SEQ ID NOS: 99
SEQ ID NO 84
LENGTH: 17
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: sequence is synthesized
NAME/KEY: artificial
LOCATION: 1-17
OTHER INFORMATION: variant CDR sequence
US-10-624-153-84

Query Match 27.1%; Score 32; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 HYLYN 18
DB 3 HYLYN 7

RESULT 24
US-10-624-153-35
Sequence 35, Application US/10624153
Publication No. US20040086502A1
GENERAL INFORMATION:
APPLICANT: CHEN, YVONNE M.
APPLICANT: LOWMAN, HENRY B.
APPLICANT: MULLER, YVES
TITLE OF INVENTION: ANTIBODY VARIANTS
FILE REFERENCE: P1469R1C1

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; CURRENT APPLICATION NUMBER: US/10/624,153
; CURRENT FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: US 09/440,781
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: US 60/108,945
; PRIOR FILING DATE: 1998-11-18
; NUMBER OF SEQ ID NOS: 99
; SEQ ID NO 35
; LENGTH: 18
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
; FEATURE:
; NAME/KEY: artificial
; LOCATION: 1-18
; OTHER INFORMATION: variant CDR sequence
US-10-624-153-35

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```

Query March                27.1%; Score 32; DB 4; Length 18;
Best Local Similarity      71.4%; Pred. No. 4.9e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY          14 HYLNNG 20
           ||| |||
Db          3 HYQNEG 9

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RESULT 25
US-09-880-748-2158
; Sequence 2158, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2158
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2158

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Query March                27.1%; Score 32; DB 3; Length 20;
Best Local Similarity      71.4%; Pred. No. 5.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY          15 YYLNNGA 21
           ||: |||
Db          11 YYIGNGA 17

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Search completed: January 26, 2006, 08:38:36
Job time : 75.75 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 26, 2006, 08:05:12 : Search time 4.36207 Seconds
(without alignments)
57.099 Million cell updates/sec

Title: US-09-662-293-9

Perfect score: 118
Sequence: 1 DENKVMKKVLYTMHYLYNNGATR 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 75621 seqs, 10829074 residues

Total number of hits satisfying chosen parameters: 37628

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

Published Applications AA New:*
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2: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
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5: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	29.7	16	7	US-11-054-515-2216 Sequence 2216, Ap
2	34	28.8	16	7	US-11-054-515-2259 Sequence 2259, Ap
3	32	27.1	13	6	US-10-511-559-255 Sequence 255, App
4	32	27.1	13	6	US-10-511-559-256 Sequence 256, App
5	32	27.1	13	6	US-10-511-559-257 Sequence 257, App
6	32	27.1	15	6	US-10-511-559-75 Sequence 75, Appl
7	32	27.1	15	7	US-11-054-515-2309 Sequence 2309, Ap
8	32	27.1	20	7	US-11-054-515-2158 Sequence 2158, Ap
9	32	27.1	20	7	US-11-054-515-2896 Sequence 2896, Ap
10	32	27.1	20	7	US-11-054-515-2903 Sequence 2903, Ap
11	32	27.1	16	7	US-11-054-515-2214 Sequence 2214, Ap
12	31	26.3	16	7	US-11-054-515-2215 Sequence 2215, Ap
13	31	26.3	16	7	US-11-054-515-2217 Sequence 2217, Ap
14	31	26.3	16	7	US-11-054-515-2219 Sequence 2219, Ap
15	31	26.3	16	7	US-11-054-515-2298 Sequence 2298, Ap
16	31	26.3	16	7	US-11-054-515-2316 Sequence 2316, Ap
17	30	25.4	9	7	US-11-033-039-489 Sequence 489, App
18	30	25.4	14	7	US-11-033-039-512 Sequence 512, App
19	30	25.4	16	6	US-10-939-890-111 Sequence 111, Appl
20	30	25.4	16	6	US-10-939-890-205 Sequence 205, App
21	30	25.4	17	7	US-11-033-039-513 Sequence 513, App
22	30	25.4	19	7	US-11-054-515-2811 Sequence 2811, Ap
23	29	24.6	8	6	US-10-986-501-203 Sequence 203, App
24	29	24.6	13	6	US-10-511-559-254 Sequence 254, App
25	29	24.6	16	7	US-11-054-515-2258 Sequence 2258, Ap

26	29	24.6	16	7	US-11-054-515-2260 Sequence 2260, Ap
27	29	24.6	19	7	US-11-054-515-3087 Sequence 3087, Ap
28	28	23.7	16	7	US-11-054-515-2832 Sequence 2832, Ap
29	28	23.7	18	6	US-10-939-890-117 Sequence 117, App
30	28	23.7	20	7	US-11-054-515-2743 Sequence 2743, Ap
31	27	22.9	16	7	US-11-054-515-2257 Sequence 2257, Ap
32	27	22.9	16	7	US-11-054-515-2302 Sequence 2302, Ap
33	27	22.9	16	7	US-11-054-515-2332 Sequence 2332, Ap
34	27	22.9	19	7	US-11-054-515-2928 Sequence 2928, Ap
35	27	22.9	19	7	US-11-148-108-42 Sequence 42, Appl
36	27	22.9	20	6	US-10-485-788A-539 Sequence 539, Appl
37	26	22.0	9	7	US-11-010-748A-78 Sequence 78, Appl
38	26	22.0	9	7	US-11-010-748A-84 Sequence 84, Appl
39	26	22.0	9	7	US-11-010-748A-85 Sequence 85, Appl
40	26	22.0	9	7	US-11-010-748A-127 Sequence 127, App
41	26	22.0	9	7	US-11-010-748A-133 Sequence 133, App
42	26	22.0	9	7	US-11-010-748A-134 Sequence 134, App
43	26	22.0	9	7	US-11-010-748A-193 Sequence 193, App
44	26	22.0	9	7	US-11-010-748A-199 Sequence 199, App
45	26	22.0	9	7	US-11-010-748A-200 Sequence 200, App
46	26	22.0	9	7	US-11-033-039-443 Sequence 443, App
47	26	22.0	14	6	US-10-501-411A-149 Sequence 149, App
48	26	22.0	14	7	US-11-128-440-65 Sequence 65, Appl
49	26	22.0	14	7	US-11-033-039-453 Sequence 453, App
50	26	22.0	15	6	US-10-866-120-4 Sequence 4, Appl
51	26	22.0	16	7	US-11-010-748A-77 Sequence 77, Appl
52	26	22.0	16	7	US-11-010-748A-126 Sequence 126, App
53	26	22.0	16	7	US-11-054-515-2145 Sequence 2145, App
54	26	22.0	16	7	US-11-054-515-2293 Sequence 2293, Ap
55	26	22.0	16	7	US-11-054-515-2336 Sequence 2336, Ap
56	26	22.0	17	7	US-11-010-748A-192 Sequence 192, App
57	26	22.0	20	6	US-10-623-155-250 Sequence 250, App
58	26	21.6	17	7	US-11-054-515-2862 Sequence 2862, App
59	25	21.2	5	7	US-11-093-274-3 Sequence 3, Appl
60	25	21.2	5	7	US-11-223-834-1 Sequence 1, Appl
61	25	21.2	9	7	US-11-010-748A-90 Sequence 90, Appl
62	25	21.2	9	7	US-11-010-748A-95 Sequence 95, Appl
63	25	21.2	9	7	US-11-010-748A-97 Sequence 97, Appl
64	25	21.2	9	7	US-11-010-748A-139 Sequence 139, App
65	25	21.2	9	7	US-11-010-748A-144 Sequence 144, App
66	25	21.2	9	7	US-11-010-748A-146 Sequence 146, App
67	25	21.2	9	7	US-11-010-748A-205 Sequence 205, App
68	25	21.2	9	7	US-11-010-748A-210 Sequence 210, App
69	25	21.2	9	7	US-11-010-748A-212 Sequence 212, App
70	25	21.2	10	6	US-10-507-662-2 Sequence 2, Appl
71	25	21.2	14	7	US-11-033-039-336 Sequence 336, App
72	25	21.2	15	6	US-10-501-411A-329 Sequence 329, App
73	25	21.2	15	7	US-11-054-515-2734 Sequence 2734, App
74	25	21.2	15	7	US-11-106-332-144 Sequence 144, App
75	25	21.2	16	7	US-11-010-748A-89 Sequence 89, Appl
76	25	21.2	16	7	US-11-010-748A-138 Sequence 138, App
77	25	21.2	16	7	US-11-054-515-2218 Sequence 2218, App
78	25	21.2	16	7	US-11-054-515-2251 Sequence 2251, App
79	25	21.2	16	7	US-11-054-515-2255 Sequence 2255, App
80	25	21.2	16	7	US-11-054-515-2255 Sequence 2255, App
81	25	21.2	17	7	US-11-010-748A-204 Sequence 204, App
82	25	21.2	17	7	US-11-054-515-2871 Sequence 2871, App
83	25	21.2	18	7	US-11-054-515-2748 Sequence 2748, App
84	25	21.2	20	7	US-11-058-735-5 Sequence 5, Appl
85	25	21.2	21	7	US-11-054-515-2172 Sequence 2172, App
86	25	21.2	21	7	US-11-054-515-2972 Sequence 2972, App
87	25	21.2	21	7	US-11-058-735-6 Sequence 6, Appl
88	24	20.3	8	7	US-11-045-024-380 Sequence 380, App
89	24	20.3	8	7	US-11-045-024-4925 Sequence 4925, App
90	24	20.3	8	7	US-11-045-024-8046 Sequence 8046, App
91	24	20.3	8	7	US-11-045-024-10543 Sequence 10543, A
92	24	20.3	9	7	US-11-045-024-8039 Sequence 8039, App
93	24	20.3	9	7	US-11-033-039-465 Sequence 465, App
94	24	20.3	9	7	US-11-033-039-492 Sequence 492, App
95	24	20.3	9	7	US-11-136-079-76 Sequence 76, Appl
96	24	20.3	10	7	US-11-105-268-11 Sequence 11, Appl
97	24	20.3	10	7	US-11-045-024-396 Sequence 396, App
98	24	20.3	10	7	US-11-045-024-4977 Sequence 4977, App

99 24 20.3 10 7 US-11-045-024-8057 Sequence 8057, Ap
100 24 20.3 10 7 US-11-045-024-10532 Sequence 10532, A

ALIGNMENTS

RESULT 1

US-11-054-515-2216
; Sequence 2216, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:

; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P3

; CURRENT APPLICATION NUMBER: US/11/054,515

; PRIOR FILING DATE: 2005-02-10

; PRIOR APPLICATION NUMBER: 60/543,296

; PRIOR FILING DATE: 2004-02-11

; PRIOR APPLICATION NUMBER: 60/580,347

; PRIOR FILING DATE: 2004-06-18

; PRIOR APPLICATION NUMBER: 10/293,418

; PRIOR FILING DATE: 2002-11-14

; PRIOR APPLICATION NUMBER: 60/331,469

; PRIOR FILING DATE: 2001-11-16

; PRIOR APPLICATION NUMBER: 60/340,817

; PRIOR FILING DATE: 2001-12-19

; PRIOR APPLICATION NUMBER: 09/880,748

; PRIOR FILING DATE: 2001-06-15

; PRIOR APPLICATION NUMBER: 60/293,499

; PRIOR FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: 60/277,379

; PRIOR FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/276,248

; PRIOR FILING DATE: 2001-03-16

; PRIOR APPLICATION NUMBER: 60/240,816

; PRIOR FILING DATE: 2000-10-17

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 3247

; SEQ ID NO 2216

; LENGTH: 16

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-054-515-2216

Query Match 29.7%; Score 35; DB 7; Length 16;

Best Local Similarity 71.4%; Pred. No. 5.3;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 YTMHYL 17
|:|||||
Db 9 YVLHYL 15

RESULT 2

US-11-054-515-2259
; Sequence 2259, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:

; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P3

; CURRENT APPLICATION NUMBER: US/11/054,515

; CURRENT FILING DATE: 2005-02-10

; PRIOR APPLICATION NUMBER: 60/543,296

; PRIOR FILING DATE: 2004-02-11

; PRIOR APPLICATION NUMBER: 60/580,347

; PRIOR FILING DATE: 2004-06-18

; PRIOR APPLICATION NUMBER: 10/293,418

; PRIOR FILING DATE: 2002-11-14

; PRIOR APPLICATION NUMBER: 60/331,469

; PRIOR FILING DATE: 2001-11-16

; PRIOR APPLICATION NUMBER: 60/340,817

; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2259
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2259

QY 11 YTMHY 16
|:|||||
Db 9 YVMHY 14

RESULT 3

US-10-511-559-255
; Sequence 255, Application US/10511559
; Publication No. US20050256304A1
; GENERAL INFORMATION:

; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis, J.

; TITLE OF INVENTION: MODIFIED FACTOR VIII

; FILE REFERENCE: MER-133

; CURRENT APPLICATION NUMBER: US/10/511,559

; CURRENT FILING DATE: 2004-10-15

; PRIOR APPLICATION NUMBER: PCT/EP03/04063

; PRIOR FILING DATE: 2003-04-17

; PRIOR APPLICATION NUMBER: EP 02008712.8

; PRIOR FILING DATE: 2002-04-18

; PRIOR APPLICATION NUMBER: EP 03006554.4

; PRIOR FILING DATE: 2003-03-24

; NUMBER OF SEQ ID NOS: 1147

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 255

; LENGTH: 13

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Potential Epitope of human Factor VIII

US-10-511-559-255

Query Match 27.1%; Score 32; DB 6; Length 13;

Best Local Similarity 75.0%; Pred. No. 13;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 16 YLNNGATR 23
|:|||||
Db 5 YLNNGPOR 12

RESULT 4

US-10-511-559-256
; Sequence 256, Application US/10511559
; Publication No. US20050256304A1
; GENERAL INFORMATION:

; APPLICANT: JONES, Tim

; APPLICANT: BAKER, Matthew

; APPLICANT: CARR, Francis, J.

```
; TITLE OF INVENTION: MODIFIED FACTOR VIII
; FILE REFERENCE: MER-133
; CURRENT APPLICATION NUMBER: US/10/511,559
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: PCT/EP03/04063
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: EP 02008712.8
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: EP 03006554.4
; PRIOR FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 1147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 256
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Potential Epitope of human Factor VIII
US-10-511-559-256
```

```
Query Match      27.1%; Score 32; DB 6; Length 13;
Best Local Similarity 75.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Oy      16 YLNNGATR 23
        |||||
Db      3 YLNNGPQR 10
```

```
RESULT 5
US-10-511-559-257
; Sequence 257, Application US/10511559
; Publication No. US20050256304A1
; GENERAL INFORMATION:
; APPLICANT: JONES, Tim
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis, J.
; TITLE OF INVENTION: MODIFIED FACTOR VIII
; FILE REFERENCE: MER-133
; CURRENT APPLICATION NUMBER: US/10/511,559
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: PCT/EP03/04063
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: EP 02008712.8
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: EP 03006554.4
; PRIOR FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 1147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 257
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Potential Epitope of human Factor VIII
US-10-511-559-257
```

```
Query Match      27.1%; Score 32; DB 6; Length 13;
Best Local Similarity 75.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Oy      16 YLNNGATR 23
        |||||
Db      2 YLNNGPQR 9
```

```
RESULT 6
US-10-511-559-75
; Sequence 75, Application US/10511559
; Publication No. US20050256304A1
; GENERAL INFORMATION:
; APPLICANT: JONES, Tim
; APPLICANT: BAKER, Matthew
```

```
; APPLICANT: CARR, Francis, J.
; TITLE OF INVENTION: MODIFIED FACTOR VIII
; FILE REFERENCE: MER-133
; CURRENT APPLICATION NUMBER: US/10/511,559
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: PCT/EP03/04063
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: EP 02008712.8
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: EP 03006554.4
; PRIOR FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 1147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 75
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Epitope of human Factor VIII
US-10-511-559-75
```

```
Query Match      27.1%; Score 32; DB 6; Length 15;
Best Local Similarity 75.0%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Oy      16 YLNNGATR 23
        |||||
Db      6 YLNNGPQR 13
```

```
RESULT 7
US-11-054-515-2909
; Sequence 2909, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2909
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2909
```

```
Query Match      27.1%; Score 32; DB 7; Length 15;
Best Local Similarity 33.3%; Pred. No. 15;
Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
```

```
Oy      8 YVLYTMHYIYLN 19
```

Db 4 YIMTAHHYIDS 15

RESULT 8

US-11-054-515-2158
; Sequence 2158, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2158
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2158

Query Match 27.1%; Score 32; DB 7; Length 20;
Best Local Similarity 71.4%; Pred. No. 20;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 15 YLUNGA 21
||: |||
Db 11 YIINGGA 17

RESULT 9

US-11-054-515-2896
; Sequence 2896, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15

; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2896
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2896

Query Match 27.1%; Score 32; DB 7; Length 20;
Best Local Similarity 71.4%; Pred. No. 20;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 15 YLUNGA 21
||: |||
Db 11 YIINGGA 17

RESULT 10

US-11-054-515-2903
; Sequence 2903, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2903
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2903

Query Match 27.1%; Score 32; DB 7; Length 20;
Best Local Similarity 71.4%; Pred. No. 20;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 15 YLUNGA 21
||: |||
Db 11 YIINGGA 17

RESULT 11

```
US-11-054-515-2214
; Sequence 2214, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2214
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2214

Query Match      26.3%; Score 31; DB 7; Length 16;
Best Local Similarity 66.7%; Pred. No. 23;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      11 YTMHY 16
      | : |||
Db      9 YVLHY 14

RESULT 12
US-11-054-515-2215
; Sequence 2215, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
```

```
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2215
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2215

Query Match      26.3%; Score 31; DB 7; Length 16;
Best Local Similarity 66.7%; Pred. No. 23;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      11 YTMHY 16
      | : |||
Db      9 YVLHY 14

RESULT 13
US-11-054-515-2217
; Sequence 2217, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2217
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2217

Query Match      26.3%; Score 31; DB 7; Length 16;
Best Local Similarity 66.7%; Pred. No. 23;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      11 YTMHY 16
      | : |||
Db      9 YVLHY 14

RESULT 14
US-11-054-515-2219
; Sequence 2219, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
```

```
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2219
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2219
```

```
Query Match          26.3%; Score 31; DB 7; Length 16;
Best Local Similarity 66.7%; Pred. No. 23;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      11 YTMHY 16
        | : |||
Db      9 YVLHY 14
```

```
RESULT 15
; Sequence 2298, Application US/11/054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
```

```
; SEQ ID NO 2298
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2298
```

```
Query Match          26.3%; Score 31; DB 7; Length 16;
Best Local Similarity 66.7%; Pred. No. 23;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      11 YTMHY 16
        | : |||
Db      9 YVLHY 14
```

```
RESULT 16
US-11-054-515-2316
; Sequence 2316, Application US/11/054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2316
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2316
```

```
Query Match          26.3%; Score 31; DB 7; Length 16;
Best Local Similarity 66.7%; Pred. No. 23;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      11 YTMHY 16
        | : |||
Db      9 YVLHY 14
```

```
RESULT 17
US-11-033-039-489
; Sequence 489, Application US/11/033039
; Publication No. US20060002947A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPTOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2017US01
; CURRENT APPLICATION NUMBER: US/11/033,039
; CURRENT FILING DATE: 2005-01-11
```



```

; PRIOR APPLICATION NUMBER: 10/245, 871
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197, 000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396, 813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 1452
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 489
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-033-039-489

```

```

Query Match      25.4%; Score 30; DB 7; Length 9;
Best Local Similarity 55.6%; Pred. No. 5.8e+04;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```

```

OY      13 MHYLLNNGA 21
DB      1 MHYVVSMDA 9

```

```

RESULT 18
US-11-033-039-512
; Sequence 512, Application US/11033039
; Publication No. US2006002947A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REF-2017US01
; CURRENT APPLICATION NUMBER: US/11/033, 039
; PRIOR FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 10/245, 871
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197, 000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396, 813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 1452
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 512
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: hybrid peptide
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (5)..(5)
; OTHER INFORMATION: Ava
US-11-033-039-512

```

```

Query Match      25.4%; Score 30; DB 7; Length 14;
Best Local Similarity 55.6%; Pred. No. 29;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```

```

OY      13 MHYLLNNGA 21
DB      6 MHYVVSMDA 14

```

```

RESULT 19
US-10-939-890-11
; Sequence 11, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.

```

```

; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussac, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddi
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939, 890
; PRIOR FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: PasteSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: KDR or VEGF/KDR Binding Polypeptide
US-10-939-890-11

```

```

Query Match      25.4%; Score 30; DB 6; Length 16;
Best Local Similarity 71.4%; Pred. No. 33;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

OY      14 HYLLNNG 20
DB      3 HCYLHNG 9

```

```

RESULT 20
US-10-939-890-205
; Sequence 205, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussac, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddi
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES

```

```
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 205
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Library Isolate
US-10-939-890-205
```

```
Query Match      25.4%; Score 30; DB 6; Length 16;
Best Local Similarity 71.4%; Pred. No. 33;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      14 HYYLNG 20
      |||:|
Db       3 HCYLHNG 9
```

```
RESULT 21
US-11-033-039-513
; Sequence 513, Application US/11033039
; Publication No. US2006002947A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPIOTOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2017US01
; CURRENT APPLICATION NUMBER: US/11/033,039
; CURRENT FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 10/245,871
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 1452
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 513
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: hybrid peptide
; NAME/KEY: MOD_RES
; LOCATION: (5)..(5)
; OTHER INFORMATION: AVA
US-11-033-039-513
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```
Query Match      25.4%; Score 30; DB 7; Length 17;
Best Local Similarity 55.6%; Pred. No. 35;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
OY      13 HYYLNGA 21
      |||:|
Db       6 HMYVSMMDA 14
```

```
RESULT 22
US-11-054-515-2811
; Sequence 2811, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: P5523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2811
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2811
```

```
Query Match      25.4%; Score 30; DB 7; Length 19;
Best Local Similarity 38.5%; Pred. No. 39;
Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
```

```
OY      8 YVLYTHMYLNG 20
      |||:|:|
Db       4 YDLITGYVYHHG 16
```

```
RESULT 23
US-10-986-501-203
; Sequence 203, Application US/10986501
; Publication No. US20050244845A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 90 Human Secreted Proteins
; FILE REFERENCE: P2013P2C1
; CURRENT APPLICATION NUMBER: US/10/986,501
; CURRENT FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: US/10/621,363
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 09/969,730
; PRIOR FILING DATE: 2001-10-06
; PRIOR APPLICATION NUMBER: 09/774,639
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/238,291
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 09/244,112
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: PCT/US98/16235
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/056,371
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,732
; PRIOR FILING DATE: 1997-08-19
```

```

; PRIOR APPLICATION NUMBER: 60/056,366
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,364
; PRIOR FILING DATE: 1997-08-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 373
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 203
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-986-501-203

```

```

Query Match      24.6%; Score 29; DB 6; Length 8;
Best Local Similarity 83.3%; Pred. No. 5.8e+04;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      13 MHVYLN 18
      |||||
Db      1 MHVYLN 6

```

```

RESULT 24
US-10-511-559-254
; Sequence 254, Application US/10511559
; Publication No. US20050255304A1
; GENERAL INFORMATION:
; APPLICANT: JONES, Tim
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis, J.
; TITLE OF INVENTION: MODIFIED FACTOR VIII
; FILE REFERENCE: MER-133
; CURRENT APPLICATION NUMBER: US/10/511,559
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: PCT/EP03/04063
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: EP 02008712.8
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: EP 03006554.4
; PRIOR FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 1147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 254
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Potential Epitope of human Factor VIII
US-10-511-559-254

```

```

Query Match      24.6%; Score 29; DB 6; Length 13;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      16 YLNG 20
      |||||
Db      7 YLNG 11

```

```

RESULT 25
US-11-054-515-2258
; Sequence 2258, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18

```

```

; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2258
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2258

```

```

Query Match      24.6%; Score 29; DB 7; Length 16;
Best Local Similarity 66.7%; Pred. No. 47;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      11 YTMHY 16
      |||||
Db      9 YTMHY 14

```

Search completed: January 26, 2006, 08:39:06
 Job time : 4.36207 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 26, 2006, 07:48:50 : Search time 11.5 Seconds
(without alignments)
192.434 Million cell updates/sec

Title: US-09-662-293-9

Perfect score: 118

Sequence: 1 DENKVMKXVLYTMHYLNGATR 23

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 4071

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

1: PIR.80:*
2: p1r1:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	26.3	15	2	B41868
2	30	25.4	19	1	LFSAP9
3	30	25.4	19	2	B26930
4	30	25.4	21	2	S08590
5	29	24.6	20	2	B60894
6	27	22.9	14	2	PT0254
7	27	22.9	15	2	S12677
8	26	22.0	12	2	G64003
9	26	22.0	14	2	PH1628
10	26	22.0	17	2	S63503
11	25.5	21.6	20	2	S37684
12	25	21.2	10	2	S42282
13	25	21.2	16	2	PH1604
14	24	20.3	14	2	PH1615
15	24	20.3	14	2	S72217
16	24	20.3	14	2	S59495
17	24	20.3	19	2	PT0332
18	24	20.3	20	2	P00544
19	23	19.5	13	2	PT0263
20	23	19.5	14	2	PH1601
21	23	19.5	17	2	PH1607
22	23	19.5	18	2	B24735
23	23	19.5	19	2	PH1307
24	23	19.5	20	2	P00751
25	22	18.6	11	1	S68352
26	22	18.6	12	2	PH1587
27	22	18.6	13	2	PT0256
28	22	18.6	13	2	PH1593
29	22	18.6	14	2	S39930

30	22	18.6	15	2	JN0730	hypothetical 1.7K
31	22	18.6	17	2	S57991	hydroxyproline-ric
32	22	18.6	17	2	B50454	38K protein 3129 -
33	22	18.6	18	2	S74195	epoxide hydrolase
34	22	18.6	18	2	I46653	T-cell receptor de
35	22	18.6	18	2	A30541	F7-1 fibroblast prot
36	22	18.6	19	2	S43960	Ig mu chain V regi
37	22	18.6	19	2	S43657	hsp90 protein homo
38	22	18.6	20	2	PC2248	lambda 112 protein
39	22	18.6	21	2	S23361	protein-tyrosine k
40	22	17.8	11	2	S42587	cellf protein - Bsc
41	21	17.8	11	2	PT0301	Ig heavy chain CRD
42	21	17.8	14	2	S39931	S-allele-associate
43	21	17.8	15	2	S47357	T-cell antigen rec
44	21	17.8	15	2	S55312	TSH protein beta c
45	21	17.8	15	2	PH1613	Ig H chain V-D-J r
46	21	17.8	15	2	S36890	ribosomal protein
47	21	17.8	16	2	PH1622	Ig H chain V-D-J r
48	21	17.8	16	2	T14224	NADH2 dehydrogenas
49	21	17.8	17	2	S48655	glutathione dehydr
50	21	17.8	17	2	PH1820	T cell receptor al
51	21	17.8	18	2	PH1323	Ig heavy chain DJ
52	21	17.8	19	2	PH1304	T cell receptor al
53	21	17.8	19	2	PH1756	Ig H chain V-D-J r
54	21	17.8	19	2	PH1609	Ig H chain V-D-J r
55	21	17.8	20	2	S17451	flavodoxin B - Azo
56	21	17.8	20	2	PS0028	flagellar motor sw
57	21	17.8	20	2	A37988	acid proteinase he
58	20.5	17.4	19	2	S13046	calreticulin - rab
59	20	16.9	9	2	PC7076	spectrin alpha cha
60	20	16.9	10	2	B60589	spem-activating p
61	20	16.9	11	2	S21127	precortin methyltr
62	20	16.9	11	2	PC2330	cyclonucleosidogac
63	20	16.9	12	2	S17869	glutathione transf
64	20	16.9	13	2	H56046	urinary tract ston
65	20	16.9	14	2	PT0232	Ig heavy chain CRD
66	20	16.9	14	2	PT0252	Ig heavy chain CRD
67	20	16.9	14	2	AF0296	phenylalanyl-trna
68	20	16.9	15	2	PH1616	Ig H chain V-D-J r
69	20	16.9	16	2	B44896	heat shock protein
70	20	16.9	17	2	C37520	glutathione transf
71	20	16.9	17	2	S26747	Ig heavy chain J r
72	20	16.9	17	2	S09085	proteasome chain 4
73	20	16.9	19	2	A48354	nonstructural prot
74	20	16.9	20	2	H49034	nuclear antigen EB
75	20	16.9	20	2	A48367	glutaryl-CoA dehyd
76	20	16.9	20	2	A61264	MHC class I histoc
77	20	16.9	21	2	PH1730	Ig heavy chain V r
78	19	16.1	9	2	PT0270	Ig heavy chain CRD
79	19	16.1	11	2	A61575	Trimeasurus serin
80	19	16.1	12	2	I64829	gene HEXA protein
81	19	16.1	12	2	S23168	Z protein - guinea
82	19	16.1	14	2	S39932	S-allele-associate
83	19	16.1	14	2	PH1614	Ig H chain V-D-J r
84	19	16.1	14	2	PH1617	Ig H chain V-D-J r
85	19	16.1	15	2	C37765	hypothetical prote
86	19	16.1	15	2	PA0016	glycine cleavage T
87	19	16.1	15	2	PA0092	protein QP200011 -
88	19	16.1	15	2	C43334	orf33 3' to aadr -
89	19	16.1	15	2	S03955	acidic fibroblast
90	19	16.1	16	2	S17217	ribulose-bisphosph
91	19	16.1	16	2	PH1588	Ig H chain V-D-J r
92	19	16.1	16	2	C90981	his operon leader
93	19	16.1	16	2	S10678	aldehyde dehydroge
94	19	16.1	16	2	A85827	his operon leader
95	19	16.1	16	4	A33171	hypothetical prote
96	19	16.1	17	2	C37396	pollen allergen Fe
97	19	16.1	18	2	PH1368	Ig heavy chain DJ
98	19	16.1	20	2	FX0042	venomabin B (EC 3.4
99	19	16.1	20	2	PT0248	Ig heavy chain CDR
100	19	16.1	20	2	D37396	pollen allergen Fe

ALIGNMENTS

RESULT 1

B41868 hypochemical protein (tracE1 3' region) - Enterococcus faecalis plasmid PAD1

C:Species: Enterococcus faecalis

C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C:Accession: B41868; B37391

R:Pontius, L.T.; Clewell, D.B.

J. Bacteriol. 174, 3152-3160, 1992

A:Title: Conjugative transfer of Enterococcus faecalis plasmid PAD1: nucleotide sequence

A:Reference number: A41868; MUID:92250408; PMID:1315730

A:Contents: plasmid PAD1

A:Accession: B41868

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-15 <PON>

A:Cross-references: UNIPROT:Q52135; UNIPARC:UPI00000B26AA

R:Clewell, D.B.; Pontius, L.T.; An, F.Y.; Ike, Y.; Suzuki, A.; Nakayama, J.

Plasmid 24, 156-161, 1990

A:Title: Nucleotide sequence of the sex pheromone inhibitor (ADI) determinant of Enteroc

A:Reference number: A37391; MUID:91261999; PMID:2128961

A:Accession: B37391

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-15 <CLE>

A:Cross-references: UNIPARC:UPI00000B26AA; GB:M62888; NID:g141853; PIDN:AAA98040.1; PID:

C:Genetics:

A:Genome: plasmid

Query Match 26.3%; Score 31; DB 2; Length 15;

Best Local Similarity 50.0%; Pred. No. 95;

Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 10 LYTWHYYL 17

Db 1 MYTVHVIY 8

RESULT 2

ermC leader peptide - Staphylococcus aureus plasmids

C:Species: Staphylococcus aureus

C:Date: 29-Jul-1981 #sequence_revision 01-Sep-1981 #text_change 09-Jul-2004

C:Accession: B93717; B93866; A46568; S03586; A03599

R:Gryczan, T.J.; Grandi, G.; Hahn, J.; Grandi, R.; Dubnau, D.

Nucleic Acids Res. 8, 6081-6097, 1980

A:Title: Conformational alteration of mRNA structure and the posttranscriptional regulat

A:Reference number: A93717; MUID:81124320; PMID:6162157

A:Accession: B93717

A:Molecule type: DNA

A:Residues: 1-19 <GRY>

A:Cross-references: UNIPROT:P03063; UNIPARC:UPI00000003A9; GB:V01278; GB:J01755; GB:J017

R:Horinouchi, S.; Weisblum, B.

Proc. Natl. Acad. Sci. U.S.A. 77, 7079-7083, 1980

A:Title: Posttranscriptional modification of mRNA conformation: mechanism that regulated

A:Reference number: A93866; MUID:81175093; PMID:6938954

A:Accession: B93866

A:Molecule type: DNA

A:Residues: 1-19 <HOR>

A:Cross-references: UNIPARC:UPI00000003A9; GB:V01278; GB:J01755; GB:J01756; GB:J01757; G

A:Experimental source: plasmid pE194

R:Catchpole, I.; Thomas, C.; Davies, A.; Dyke, K.G.H.

J. Gen. Microbiol. 134, 697-709, 1988

A:Title: The nucleotide sequence of Staphylococcus aureus plasmid pT48 conferring induc

ve resistance.

A:Reference number: A46568; MUID:89036120; PMID:3141573

A:Accession: A46568

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-19 <CAT>

A:Cross-references: UNIPARC:UPI00000003A9; GB:M19652; NID:g153070; PIDN:AAA20193.1; PID:

A:Experimental source: plasmid pT48

R:Mayford, M.; Weisblum, B.

J. Mol. Biol. 206, 69-79, 1989

A:Title: ermC leader peptide. Amino acid sequence critical for induction by translationa

A:Reference number: S03586; MUID:89199652; PMID:2467989

A:Accession: S03586

A:Molecule type: DNA

A:Residues: 1-19 <MAY>

A:Cross-references: UNIPARC:UPI00000003A9

C:Genetics:

A:Genome: Plasmid

C:Superfamily: ermC leader peptide

Query Match 25.4%; Score 30; DB 1; Length 19;

Best Local Similarity 45.5%; Pred. No. 1.8e+02;

Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Oy 8 YVLTYMHYYLN 18

Db 7 FVISTVHYQPN 17

RESULT 3

ermG leader peptide 2 - Bacillus sphaericus

C:Species: Bacillus sphaericus

C:Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 09-Jul-2004

C:Accession: B26930

R:Monod, M.; Mohan, S.; Dubnau, D.

J. Bacteriol. 169, 340-350, 1987

A:Title: Cloning and analysis of ermG, a new macrolide-lincosamide-streptogramin B resist

A:Reference number: A91840; MUID:87083389; PMID:3025178

A:Accession: B26930

A:Molecule type: DNA

A:Residues: 1-19 <MON>

A:Cross-references: UNIPROT:Q45558; UNIPARC:UPI00000B5B8C; GB:M15332; NID:g142881; PIDN:

C:Superfamily: ermC leader peptide

Query Match 25.4%; Score 30; DB 2; Length 19;

Best Local Similarity 45.5%; Pred. No. 1.8e+02;

Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Oy 8 YVLTYMHYYLN 18

Db 7 FVISTVHYQPN 17

RESULT 4

NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - Debnay's tobacco chloroplast (fr

C:Species: chloroplast Nicotiana debneyi (Debnay's tobacco)

C:Date: 25-Feb-1994 #sequence_revision 01-Dec-1995 #text_change 03-Jun-2002

C:Accession: S08590

R:Hayashida, N.; Matsubayashi, T.; Shinozaki, K.; Sugitara, M.; Inoue, K.; Hiyaama, T.

Curr. Genet. 12, 247-250, 1987

A:Title: The gene for the 9 kd polypeptide, a possible apoprotein for the iron-sulfur ce

A:Reference number: S07170; MUID:88210537; PMID:3329576

A:Accession: S08590

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-21 <HAY>

A:Cross-references: UNIPARC:UPI0000000AD9; EMBL:X05881; NID:g11790; PIDN:CAA29305.1; PID

C:Genetics:

A:Gene: ndnd

A:Genome: chloroplast

C:Superfamily: NADH dehydrogenase (ubiquinone) chain 4

C:Keywords: chloroplast; membrane-associated complex; NAD; oxidoreductase

Query Match 25.4%; Score 30; DB 2; Length 21;

Best Local Similarity 33.3%; Pred. No. 2e+02;

Matches 4; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

R/Meyer, M.; Granderath, K.; Andreesen, J.R.

Eur. J. Biochem. 234, 184-191, 1995

A/Title: Purification and characterization of protein P(B) of betaine reductase and its
phylum.

A/Reference number: S63502; MUID:96096737; PMID:8529639

A/Accession: S63503

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-17 <MEY>

A/Cross-references: UNIPARC:UPI000017AD3D

Query Match 22.0%; Score 26; DB 2; Length 17;

Best Local Similarity 44.4%; Pred. No. 6.8e+02;

Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 13 MHYIANGA 21

Db 3 LHKFLEDGA 11

RESULT 11

protein IEF SSP 9125 - human (fragments)

C/Species: Homo sapiens (man)

C/Date: 09-Dec-1993 #sequence_revision 17-Nov-1995 #text_change 17-Nov-1995

C/Accession: S37684

R/Leffers, H.; Madsen, P.; Rasmussen, H.H.; Honore, B.; Andersen, A.H.; Walbum, E.; Vand

J. Mol. Biol. 231, 982-998, 1993

A/Title: Molecular cloning and expression of the transformation sensitive epithelial mar

A/Reference number: S34753; MUID:93294871; PMID:8515476

A/Accession: S37684

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-20 <LEF>

A/Cross-references: UNIPARC:UPI000017C321

Query Match 21.6%; Score 25.5; DB 2; Length 20;

Best Local Similarity 40.0%; Pred. No. 9.7e+02;

Matches 6; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

QY 2 EXNVXXVLYTMHY 16

Db 6 ERNLLS-VAYKVFY 19

RESULT 12

paraoporal crystal protein cryIIIB - *Bacillus thuringiensis* plasmid (fragment)

N/Alterate names: delta-endotoxin

C/Species: *Bacillus thuringiensis*

C/Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 24-Jul-1998

C/Accession: S42282

R/Crickmore, N.; Wheeler, V.C.; Ellar, D.J.

Mol. Gen. Genet. 242, 365-368, 1994

A/Title: Use of an operon fusion to induce expression and crystallisation of a *Bacillus*

A/Reference number: S42282; MUID:94150472; PMID:7906381

A/Accession: S42282

A/Molecule type: protein

A/Residues: 1-10 <CRI>

A/Cross-references: UNIPARC:UPI000017ACD4

A/Experimental source: subsp. *Galleriae* 916

C/Genetics:

A/Genes: cryIIIB

A/Genome: plasmid

C/Keywords: delta-endotoxin

Query Match 21.2%; Score 25; DB 2; Length 10;

Best Local Similarity 62.5%; Pred. No. 5.5e+02;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 13 MHYIANG 20

Db 1 MNTVLNNG 8

RESULT 13

Ig H chain V-D-J region (wild-type clone 327) - mouse (fragment)

C/Species: *Mus musculus* (house mouse)

C/Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999

C/Accession: PH1604

R/Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 317-329, 1993

A/Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice

A/Reference number: PH1580; MUID:9301609; PMID:8315387

A/Accession: PH1604

A/Molecule type: DNA

A/Residues: 1-16 <LEV>

A/Cross-references: UNIPARC:UPI000017C6C0

A/Experimental source: bone marrow pre-B lymphocyte

C/Keywords: immunoglobulin

Query Match 21.2%; Score 25; DB 2; Length 16;

Best Local Similarity 50.0%; Pred. No. 9.1e+02;

Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 11 YTMHY 16

Db 7 WLLHY 12

RESULT 14

Ig H chain V-D-J region (clone B-less 22) - mouse (fragment)

C/Species: *Mus musculus* (house mouse)

C/Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999

C/Accession: PH1615

R/Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 317-329, 1993

A/Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice

A/Reference number: PH1580; MUID:9301609; PMID:8315387

A/Accession: PH1615

A/Molecule type: DNA

A/Residues: 1-14 <LEV>

A/Cross-references: UNIPARC:UPI000017C69E

A/Experimental source: bone marrow pre-B lymphocyte

C/Keywords: immunoglobulin

Query Match 20.3%; Score 24; DB 2; Length 14;

Best Local Similarity 40.0%; Pred. No. 1.1e+03;

Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DEXVXXVYL 10

Db 3 DESNPIRYAM 12

RESULT 15

D-arabinose 1-dehydrogenase [NAD(P)] (EC 1.1.1.117) - yeast (*Candida albicans*) (fragment)

C/Species: *Candida albicans*

C/Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 03-Jun-2002

C/Accession: S72217

R/Kim, S.T.; Huh, W.K.; Kim, J.Y.; Hwang, S.W.; Kang, S.O.

Biochim. Biophys. Acta 1297, 1-8, 1996

A/Title: D-arabinose dehydrogenase and biosynthesis of erythroascorbic acid in *Candida a*

A/Reference number: S72217; MUID:96439039; PMID:8841374

A/Accession: S72217

A/Molecule type: protein

A/Residues: 1-14 <KIM>

A/Cross-references: UNIPARC:UPI000017CDB9

C/Keywords: oxidoreductase

Query Match 20.3%; Score 24; DB 2; Length 14;

Best Local Similarity 66.7%; Pred. No. 1.1e+03;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 15 YLNNNG 20
 : ||||
 Db 9 FXLNNNG 14

RESULT 16

SS9495
 formate dehydrogenase delta chain - Alcaligenes eutrophus (fragment)
 C/Species: Alcaligenes eutrophus
 C/Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
 C/Accession: S59495
 R/Friedelbojd, J.; Mayer, F.; Bill, E.; Trautwein, A.X.; Bowien, B.
 Biol. Chem. Hoppe-Seyler 376, 561-568, 1995
 A/Title: Structural and immunological studies on the soluble formate dehydrogenase from
 A/Reference number: S59492; MUID:96145736; PMID:8561915
 A/Accession: S59495
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-14 <FRI>
 A/Cross-references: UNIPROT:Q7MON7; UNIPARC:UPI000017AA11

Query Match 20.3%; Score 24; DB 2; Length 14;
 Best Local Similarity 80.0%; Pred. No. 1.1e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 16 YLNNNG 20
 : ||||
 Db 9 YANNNG 13

RESULT 17

PT0332
 Ig heavy chain CRD3 region (clone J2-139) - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C/Accession: PT0332
 R/Yamada, M.; Maeserger, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
 J. Exp. Med. 173, 395-407, 1991
 A/Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
 A/Reference number: PT0222; MUID:91108337; PMID:1899102
 A/Accession: PT0332
 A/Molecule type: DNA
 A/Residues: 1-19 <YAM>
 A/Cross-references: UNIPARC:UPI000017C21A
 A/Experimental source: B lymphocyte
 C/Keywords: heterotrimer; immunoglobulin

Query Match 20.3%; Score 24; DB 2; Length 19;
 Best Local Similarity 33.3%; Pred. No. 1.6e+03;
 Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 14 HYLLNNGAT 22
 : || : ||:
 Db 6 YYYGSGSS 14

RESULT 18

PQ0544
 capsid protein VP5 - human herpesvirus 1 (fragments)
 C/Species: human herpesvirus 1
 C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
 C/Accession: PQ0544
 R/Davison, M.D.; Rixon, F.J.; Davison, A.J.
 J. Gen. Virol. 73, 2709-2713, 1992
 A/Title: Identification of genes encoding two capsid proteins (VP24 and VP26) of herpes
 A/Reference number: PQ0544; MUID:93019027; PMID:1338483
 A/Accession: PQ0544
 A/Molecule type: protein
 A/Residues: 1-20 <DAV>
 A/Cross-references: UNIPARC:UPI000017A7CA
 A/Experimental source: strain 17
 C/Genetics:

A/Gene: ULI9
 C/Keywords: capsid protein

Query Match 20.3%; Score 24; DB 2; Length 20;
 Best Local Similarity 80.0%; Pred. No. 1.7e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 16 YLNNNG 20
 : ||||
 Db 3 YLDNG 7

RESULT 19

PT0263
 Ig heavy chain CRD3 region (clone 2-121B) - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C/Accession: PT0263
 R/Yamada, M.; Maeserger, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
 J. Exp. Med. 173, 395-407, 1991
 A/Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
 A/Reference number: PT0222; MUID:91108337; PMID:1899102
 A/Accession: PT0263
 A/Molecule type: DNA
 A/Residues: 1-13 <YAM>
 A/Cross-references: UNIPARC:UPI000017C1F0
 A/Experimental source: B lymphocyte
 C/Keywords: heterotrimer; immunoglobulin

Query Match 19.5%; Score 23; DB 2; Length 13;
 Best Local Similarity 80.0%; Pred. No. 1.5e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 16 YLNNNG 20
 : ||||
 Db 9 YLNGNG 13

RESULT 20

PH1601
 Ig H chain V-D-J region (wild-type clone 311) - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C/Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
 C/Accession: PH1601
 R/Levinson, D.A.; Campos-Torres, J.; Leder, P.
 J. Exp. Med. 178, 317-329, 1993
 A/Title: Molecular characterization of transgene-induced immunodeficiency in B-less mic
 A/Reference number: PH1580; MUID:93301609; PMID:8315387
 A/Accession: PH1601
 A/Molecule type: DNA
 A/Residues: 1-14 <LEV>
 A/Cross-references: UNIPARC:UPI000017C6BE
 A/Experimental source: bone marrow pre-B lymphocyte
 C/Keywords: immunoglobulin

Query Match 19.5%; Score 23; DB 2; Length 14;
 Best Local Similarity 50.0%; Pred. No. 1.6e+03;
 Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 8 YVLYTMHY 15
 : ||||
 Db 7 YYYVANDY 14

RESULT 21

PH1607
 Ig H chain V-D-J region (wild-type clone 333) - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C/Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
 C/Accession: PH1607
 R/Levinson, D.A.; Campos-Torres, J.; Leder, P.
 J. Exp. Med. 178, 317-329, 1993
 A/Title: Molecular characterization of transgene-induced immunodeficiency in B-less mic

A:Reference number: PH1580; MUID:93301609; PMID:8315387
 A:Accession: PH1607
 A:Molecule type: DNA
 A:Residues: 1-17 <LEV>
 A:Cross-references: UNIPARC:UPI0000176DD3
 A:Experimental source: bone marrow pre-B lymphocyte
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: immunoglobulin

Query Match 19.5%; Score 23; DB 2; Length 17;
 Best Local Similarity 50.0%; Pred. No. 2e+03;
 Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 8 YLYTMY 15
 ||||
 Db 10 YYYVAMDY 17

RESULT 22

B24735
 glutathione transferase (EC 2.5.1.18) 1-2 - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 25-Oct-1987 #sequence_revision 25-Oct-1987 #text_change 18-Jun-1993
 C:Accession: B24735
 R:Mannevik, B.; Alin, P.; Guttenberg, C.; Jansson, H.; Tahir, M.K.; Warholm, M.; Jornta
 Proc. Natl. Acad. Sci. U.S.A. 82, 7202-7206, 1985
 A:Title: Identification of three classes of cytosolic glutathione transferase common to
 A:Reference number: A24735; MUID:86042634; PMID:3864155
 A:Accession: B24735
 A:Molecule type: protein
 A:Residues: 1-18 <MAN>
 A:Cross-references: UNIPARC:UPI000017542B
 C:Superfamily: glutathione transferase
 C:Keywords: transferase

Query Match 19.5%; Score 23; DB 2; Length 18;
 Best Local Similarity 37.5%; Pred. No. 2.2e+03;
 Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 13 MHYYLNN 20
 :||:
 Db 6 LHYFNGRG 13

RESULT 23

PH1307
 Ig heavy chain DJ region (clone C96-119) - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
 C:Accession: PH1307
 R:Masserman, R.; Galli, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
 J. Exp. Med. 176, 1577-1581, 1992
 A:Title: Predominance of fetal type DH joining in young children with B precursor lymph
 A:Reference number: PH1302; MUID:93094761; PMID:1460419
 A:Accession: PH1307
 A:Molecule type: DNA
 A:Residues: 1-19 <MAS>
 A:Cross-references: UNIPARC:UPI0000176935
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

Query Match 19.5%; Score 23; DB 2; Length 19;
 Best Local Similarity 50.0%; Pred. No. 2.3e+03;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 11 YTMHY 16
 ||:|
 Db 5 YSYYY 10

RESULT 24
 PQ0751
 self-incompatibility protein S4 - potato (fragment)

C:Species: Solanum tuberosum (potato)
 C>Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 31-Dec-2004
 C:Accession: PQ0751
 R:Kirch, H.H.; Uhrig, H.; Lottepeich, F.; Salami, F.; Thompson, R.D.
 Theor. Appl. Genet. 78, 581-588, 1989
 A:Title: Characterization of proteins associated with self-incompatibility in Solanum tu
 A:Reference number: PQ0749
 A:Accession: PQ0751
 A:Molecule type: protein
 A:Residues: 1-20 <KIR>
 A:Cross-references: UNIPARC:UPI0000175A01
 A:Experimental source: style
 C:Superfamily: RNases
 C:Keywords: glycoprotein

Query Match 19.5%; Score 23; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 YLNN 19
 ||||
 Db 17 YLNN 20

RESULT 25

S68392
 H+-transporting two-sector ATPase (EC 3.6.3.14) chain I - Chlamydomonas reinhardtii chlo
 N:Alternate names: ATP synthase chain I
 C:Species: Chlamydomonas reinhardtii
 C>Date: 04-Dec-1997 #sequence_revision 12-Dec-1997 #text_change 31-Dec-2004
 C:Accession: S68392
 R:Fiedler, H.R.; Schmid, R.; Liu, S.; Shavlt, N.; Strotmann, H.
 FEBS Lett. 377, 163-166, 1995
 A:Title: Isolation of CF(0)CF(1) from Chlamydomonas reinhardtii cw15 and the N-terminal e
 A:Reference number: S68388; MUID:96128220; PMID:8543042
 A:Accession: S68392
 A:Molecule type: protein
 A:Residues: 1-11 <FIR>
 A:Cross-references: UNIPARC:UPI0000175ED3
 A:Experimental source: strain CW15
 C:Genetics:
 A:Genome: Chloroplast
 C:Superfamily: H(+)-transporting ATP synthase protein 6
 C:Keywords: ATP biosynthesis; chloroplast; hydrolase; membrane-associated complex; chyla

Query Match 18.6%; Score 22; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 HYY 16
 |||
 Db 7 HYY 9

Search completed: January 26, 2006, 08:05:02
 Job time : 12.5 secs

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OM protein - protein search, using sw model

Run on: January 26, 2006, 07:47:56 ; Search time 68.4052 Seconds
(without alignments)
237.221 Million cell updates/sec

Title: US-09-662-293-9

Perfect score: 118

Sequence: 1 DEXNMVXVLYTMHYLYNGATR 23

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 15779

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%

Database : Uniprot_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	28.0	19	2	OSDU98_STAP
2	33	28.0	19	2	OGEV48_STANU
3	32	27.1	15	2	O9S8A2_HELAN
4	32	27.1	20	2	O4XS28_PLACH
5	32	27.1	20	2	O4YWP2_PLABE
6	31	26.3	15	2	O52135_9ZZZZ
7	31	26.3	21	2	O4YVW6_PLABE
8	30.5	25.8	18	2	O4Z5U3_PLABE
9	30	25.4	15	2	O4XG09_PLACH
10	30	25.4	19	1	LEPM_STANU
11	30	25.4	19	2	O57313_STAP
12	30	25.4	19	2	O799A5_STANU
13	30	25.4	19	2	O799E4_STAP
14	30	25.4	19	2	O7AVR6_STAP
15	30	25.4	19	2	O4SS58_BACSH
16	30	25.4	19	2	O799W9_STANU
17	30	25.4	19	2	O4JHNS_STANU
18	30	25.4	19	2	O6LBC3_9ZZZZ
19	30	25.4	19	2	O79DR6_9ZZZZ
20	30	25.4	20	2	O7PC06_PLAYO
21	30	25.4	21	2	O4Y2R8_PLACH
22	30	25.4	21	2	O7GEV8_TOBAC
23	29	24.6	20	2	O7M447_9MOLL
24	29	24.6	21	2	O9ZYB7_9HYME
25	29	24.6	21	2	O4X6E8_PLACH
26	29	24.6	21	2	O4Y144_PLACH
27	28.5	24.2	12	2	O4Y9H1_PLABE
28	28	23.7	18	2	O4X1Q2_PLACH
29	28	23.7	19	2	O4X1Z2_PLACH
30	28	23.7	20	2	O4XA28_PLACH
31	28	23.7	21	2	O4X533_PLACH

32	28	23.7	21	2	O4X6E1_PLACH	O4X6E1 plasmodium
33	27.5	23.3	21	2	O4X877_PLACH	O4X877 plasmodium
34	27	22.9	15	1	NIFB1_ANAVA	O44507 anabena va
35	27	22.9	16	2	O7RHS8_PLAYO	O7RHS8 plasmodium
36	27	22.9	18	2	O4XAQ4_PLACH	O4XAQ4 plasmodium
37	27	22.9	19	2	O9L434_SALTY	O9L434 salmoneila
38	27	22.9	21	2	O7RB35_PLAYO	O7RB35 plasmodium
39	27	22.9	21	2	O4XE39_PLACH	O4XE39 plasmodium
40	27	22.9	21	2	O4XK04_PLABE	O4XK04 plasmodium
41	26	22.0	15	1	GST_ASADI	P83246 asaphis dic
42	26	22.0	17	2	O70Y71_9LAMI	O70Y71 thornicrofti
43	26	22.0	18	2	O4YH66_PLABE	O4YH66 plasmodium
44	26	22.0	19	2	O4XJ65_PLACH	O4XJ65 plasmodium
45	26	22.0	19	2	O9F6J8_YERPE	O9F6J8 versinia pe
46	26	22.0	20	2	O5C1Y0_SCHTA	O5C1Y0 echinosoma
47	26	22.0	20	2	O4YR59_PLABE	O4YR59 plasmodium
48	26	22.0	21	2	O5XUW8_HUMAN	O5XUW8 homo sapien
49	26	22.0	21	2	O4XX24_PLACH	O4XX24 plasmodium
50	26	22.0	21	2	O4YDB9_PLABE	O4YDB9 plasmodium
51	25.5	21.6	20	2	O4Z007_PLABE	O4Z007 plasmodium
52	25	21.2	15	2	O7RH22_PLAYO	O7RH22 plasmodium
53	25	21.2	17	2	O19716_HUMAN	O19716 homo sapien
54	25	21.2	18	2	O4X8U6_PLACH	O4X8U6 plasmodium
55	25	21.2	18	2	O4YGB7_PLABE	O4YGB7 plasmodium
56	25	21.2	18	2	O95MB1_HORSE	O95MB1 equus cabal
57	25	21.2	19	2	O60F81_CABCR	O60F81 caretta car
58	25	21.2	21	2	O7RJB6_PLAYO	O7RJB6 plasmodium
59	25	21.2	21	2	O4XMC7_PLACH	O4XMC7 plasmodium
60	25	21.2	21	2	O4YPC6_PLABE	O4YPC6 plasmodium
61	24.5	20.8	19	2	O86DB6_HALBO	O86DB6 halocynthia
62	24.5	20.8	19	2	O4YGY2_PLABE	O4YGY2 plasmodium
63	24.5	20.8	21	2	O7R2U5_PLAYO	O7R2U5 plasmodium
64	24	20.3	11	2	O4XC12_PLACH	O4XC12 plasmodium
65	24	20.3	12	2	O6ITW2_HUMAN	O6ITW2 homo sapien
66	24	20.3	14	2	O7MON7_ALCEU	O7MON7 alcaligenes
67	24	20.3	14	2	P91578_CFEVY	P91578 chortistoneu
68	24	20.3	15	2	O80277_9CAUD	O80277 lactococcus
69	24	20.3	16	2	O4Z674_PLABE	O4Z674 plasmodium
70	24	20.3	16	2	P82444_TOBAC	P82444 nicotiana t
71	24	20.3	16	2	O9KU10_STANA	O9KU10 staphylococ
72	24	20.3	17	2	O4YXY7_PLABE	O4YXY7 plasmodium
73	24	20.3	17	2	O4Z344_PLABE	O4Z344 plasmodium
74	24	20.3	17	2	O9OPC8_TYLCV	O9OPC8 tomato yell
75	24	20.3	18	2	O4Y8A5_PLACH	O4Y8A5 plasmodium
76	24	20.3	18	2	O4YUR7_PLABE	O4YUR7 plasmodium
77	24	20.3	18	2	O4Z6B5_PLABE	O4Z6B5 plasmodium
78	24	20.3	19	2	O7RR06_PLAYO	O7RR06 plasmodium
79	24	20.3	19	2	O4XG21_PLACH	O4XG21 plasmodium
80	24	20.3	19	2	O4YEN3_PLABE	O4YEN3 plasmodium
81	24	20.3	19	2	O4YVW0_PLABE	O4YVW0 plasmodium
82	24	20.3	19	2	O4Z6S8_PLABE	O4Z6S8 plasmodium
83	24	20.3	19	2	O38371_BPMS2	O38371 bacteriopho
84	24	20.3	20	1	O9OV31_9MURI	O9OV31 rattus sp.
85	24	20.3	20	1	HMEC_ARCPR	P84608 archaeoglob
86	24	20.3	20	2	O7RPN2_PLAYO	O7RPN2 plasmodium
87	24	20.3	20	2	O4Y8L0_PLACH	O4Y8L0 plasmodium
88	24	20.3	20	2	O4YH32_PLABE	O4YH32 plasmodium
89	24	20.3	21	2	O9R4G2_VVIBR	O9R4G2 vibrio. bet
90	24	20.3	21	2	O4XKF6_PLACH	O4XKF6 plasmodium
91	24	20.3	21	2	O9RSK0_STREY	O9RSK0 streptococc
92	23	19.5	11	2	O4X942_PLACH	O4X942 plasmodium
93	23	19.5	11	2	O4L8Q1_STANU	O4L8Q1 staphylococ
94	23	19.5	16	2	O7JUN10_DROME	O7JUN10 drosophiila
95	23	19.5	16	2	O4XVQ2_PLACH	O4XVQ2 plasmodium
96	23	19.5	16	2	O4Y227_PLABE	O4Y227 plasmodium
97	23	19.5	17	2	O4XHV2_PLACH	O4XHV2 plasmodium
98	23	19.5	17	2	O4YXZ5_PLABE	O4YXZ5 plasmodium
99	23	19.5	19	2	O4XOC6_PLACH	O4XOC6 plasmodium
100	23	19.5	19	2	O4YER2_PLABE	O4YER2 plasmodium

ALIGNMENTS

```

RESULT 1
Q5DU98_9STAP PRELIMINARY; PRT; 19 AA.
ID Q5DU98_9STAP PRELIMINARY; PRT; 19 AA.
AC Q5DU98;
DT 10-MAY-2005 (TREMBlrel. 30, Created)
DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)
DE Hypothetical protein.
OS Staphylococcus lentus.
OC Plasmid pST2.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=42858;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=44;
RA Hauschild T., Luehje P., Schwarz S.;
RT "The staphylococcal tetracycline macrolide-lincosamide-streptogramin B
RT resistance plasmid pST2 is an RSA mediated in vivo recombination
RT product."
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ888003; CAI59791.1; -; Genomic_DNA.
KW Hypothetical protein; Plasmid.
SQ SEQUENCE 19 AA; 2219 MW; 13FEE3D9897F3A7B CRC64;

Query Match 28.0%; Score 33; DB 2; Length 19;
Best Local Similarity 45.5%; Pred. No. 4.8e+02;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 8 YVLYTMHYLN 18
Db 7 FVISTVHYHN 17

RESULT 2
Q9EV48_STAUV PRELIMINARY; PRT; 19 AA.
ID Q9EV48_STAUV PRELIMINARY; PRT; 19 AA.
AC Q9EV48;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Leader peptide of ErmGM.
GN Name=leader peptide (LP) of ermGM;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21621309; PubMed=11751136; DOI=10.1128/JAC.46.1.211-215.2002;
RA Matsushita M., Inoue M., Nakajima Y., Endo Y.;
RT "New erm Gene in Staphylococcus aureus clinical isolates."
RL Antimicrob. Agents Chemother. 46:211-215 (2002).
DR EMBL; AB014481; BAB20747.1; -; Genomic_DNA.
SQ SEQUENCE 19 AA; 2195 MW; 605CBAD99E4B6B7F CRC64;

Query Match 28.0%; Score 33; DB 2; Length 19;
Best Local Similarity 40.0%; Pred. No. 4.8e+02;
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 4 NVKXYVLYTMHYLN 18
Db 3 NCSLFLVINTVHYQPN 17

RESULT 3
Q9SBA2_HELAN PRELIMINARY; PRT; 15 AA.
ID Q9SBA2_HELAN PRELIMINARY; PRT; 15 AA.
AC Q9SBA2;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE Oleosin (Fragment).
OS Helianthus annuus (Common sunflower).

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OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Campanulids; Asterales; Asteraceae; Asteroideae; Heliantheae;
OC Helianthus.
OX NCBI_TaxID=4232;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=96195148; PubMed=8660304;
RA Millichip M., Tatham A.S., Jackson F., Griffiths G., Shewry P.R.,
RA Scobart A.K.;
RT "Purification and characterization of oil-bodies (oleosomes) and oil-
RT body boundary proteins (oleosins) from the developing cotyledons of
RT sunflower (Helianthus annuus L.)."
RL Biochem. J. 314:333-337 (1996).
SQ SEQUENCE 15 AA; 1619 MW; CDC28A0627F8704 CRC64;

Query Match 27.1%; Score 32; DB 2; Length 15;
Best Local Similarity 75.0%; Pred. No. 5.4e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 16 YLNNGATR 23
Db 8 FLNNGAFR 15

RESULT 4
Q4XSZ8_PLACH PRELIMINARY; PRT; 20 AA.
ID Q4XSZ8_PLACH PRELIMINARY; PRT; 20 AA.
AC Q4XSZ8;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=PC106693.00.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5825;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kool J.T.W.A.,
RA Bettinan M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Jansz C.J., Barrall B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses."
RL Science 307:82-86 (2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAJ01003410; CAH79964.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 20 AA; 2488 MW; C628661F489812F9 CRC64;

Query Match 27.1%; Score 32; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 7.3e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 8 YVLYTMHYVL 17
Db 11 YLYICVYI 20

RESULT 5
Q4YWF2_PLABE PRELIMINARY; PRT; 20 AA.
ID Q4YWF2_PLABE PRELIMINARY; PRT; 20 AA.
AC Q4YWF2;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).

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RESULT 7
ID Q4YVN6_PLABE PRELIMINARY; PRT; 21 AA.
AC Q4YVN6;
DT 13-SEP-2005 (TREMBLrel. 31, Created)
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=PB105419.00.0;
OS Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
NCBI_TaxID=5621;
[1]
RN NUCLEOTIDE SEQUENCE.
RP Hall N., Karras M., Raine J.D., Carlton J.M., Koolif T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Patin A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bitwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Katatos F.C.,
RA Jaise C.J., Barrett B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CA0100238; CAH97920.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 21 AA; 2441 MW; B79B04782E2A5B04 CRC64;

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Oy 4 NMXXVLYTMHYLYN 18
 ||| : |||
 Db 3 NMVYCNF-VHFFN 16

RESULT 9

O4XG09 PLACH PRELIMINARY; PRT; 15 AA.
 ID O4XG09 PLACH PRELIMINARY; PRT; 15 AA.
 AC O4XG09
 DT 13-SEP-2005 (TREMBlrel. 31, Created)
 DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
 DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=PC401954.00.0;
 OS Plasmodium chabaudi.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 NCBI_TaxID=5825;
 OX NCBI_TaxID=5825;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
 RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
 RA Quail M.A., Ormond D., Duggett J., Trueman H.E., Mendoza J.,
 RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
 RA Jansz C.J., Barrett B., Turner C.M.R., Waters A.P., Sinden R.S.;
 RT "A comprehensive survey of the Plasmodium life cycle by genomic,
 RT transcriptomic, and proteomic analyses.";
 RL Science 307:82-86(2005).
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.

DR EMBL; CAA01006563; CAH84159.1; -; Genomic_DNA.
 KM Hypothetical protein.
 SQ SEQUENCE 15 AA; 1776 MW; 05ACF46B687A4482 CRC64;

Query Match 25.4%; Score 30; DB 2; Length 15;
 Best Local Similarity 83.3%; Pred. No. 1.1e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 8 YVLYTM 13
 ||| : |||
 Db 5 YVLYTM 10

RESULT 10

LPRM_STAUP STANDARD; PRT; 19 AA.
 ID LPRM_STAUP STANDARD; PRT; 19 AA.
 AC P03063;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE 23S rRNA methylase leader peptide (Erythromycin resistance leader
 DE peptide).
 GN Name=ermC;
 OS Staphylococcus aureus.
 OC Plasmid pE194, and Plasmid pT48.
 CC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RC PLASMID=PE194;
 RC MEDLINE=81124320; PubMed=6162157;
 RA Gryczan T.J., Grandi G., Hahn J., Grandi R., Dubnau D.;
 RT "Conformational alteration of mRNA structure and the
 RT posttranscriptional regulation of erythromycin-induced drug
 RT resistance.";
 RL Nucleic Acids Res. 8:6081-6097(1980).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.

RC PLASMID=PE194;
 RX MEDLINE=81175093; PubMed=6938954;
 RA Horinouchi S., Weisblum B.;

RT "Posttranscriptional modification of mRNA conformation: mechanism that
 RT regulates erythromycin-induced resistance.";
 RL Proc. Natl. Acad. Sci. U.S.A. 77:7079-7083(1980).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.

RC PLASMID=PE194;
 RA MEDLINE=86037249; PubMed=2414456;
 RX Mayford M., Weisblum B.;
 RT "Messenger RNA from Staphylococcus aureus that specifies macrolide-
 RT lincosamide-streptogramin resistance. Demonstration of its
 RT conformations and of the leader peptide it encodes.";
 RL J. Mol. Biol. 185:769-780(1985).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.

RC PLASMID=PE194;
 RX MEDLINE=8919652; PubMed=2467989;
 RA Mayford M., Weisblum B.;
 RT "ermC leader peptide. Amino acid sequence critical for induction by
 RT translational attenuation.";
 RL J. Mol. Biol. 206:69-79(1989).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.

RC PLASMID=PT48;
 RX MEDLINE=89036120; PubMed=3141573;
 RA Catchpole I., Thomas C., Davies A., Dyke K.G.H.;
 RT "The nucleotide sequence of Staphylococcus aureus plasmid pT48
 RT conferring inducible macrolide-lincosamide-streptogramin B resistance
 RT and comparison with similar plasmids expressing constitutive
 RT resistance.";
 RL J. Gen. Microbiol. 134:697-709(1988).
 CC -1- FUNCTION: This peptide is involved in the control mechanism of the
 CC synthesis of the erythromycin resistance protein.

CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.

DR EMBL; V01278; CAA24592.1; -; Genomic_DNA.
 DR EMBL; M37841; AAA98225.1; -; Genomic_DNA.
 DR EMBL; M19652; AAA20193.1; -; Unassigned_DNA.
 DR PIR; B93717; LPSAP9.
 KM Antibiotic resistance; Leader peptide; Plasmid.
 SQ SEQUENCE 19 AA; 2210 MW; 13FE3D99E4F3A7B CRC64;

Query Match 25.4%; Score 30; DB 1; Length 19;
 Best Local Similarity 45.5%; Pred. No. 1.4e+03;
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Oy 8 YVLYTMHYLYN 18
 ||| : |||
 Db 7 FVISTVHYQPN 17

RESULT 11

O57313_9STAP PRELIMINARY; PRT; 19 AA.
 ID O57313_9STAP PRELIMINARY; PRT; 19 AA.
 AC O57313;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Orf1 protein.
 GN Name=orf1;
 OS Staphylococcus equorum subsp. equorum.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=29383;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RC MEDLINE=96379895; PubMed=8787908;
 RX Lodder G., Schwarz S., Gregory P., Dyke K.;
 RT "Tandem duplication in ermC translational attenuator of the macrolide-

RT lincosamide-streptogramin B resistance plasmid pSES6 from
 RT Staphylococcus equorum";
 RL Antimicrob. Agents Chemother. 40:215-217(1996).
 RN [2]
 RN NUCLEOTIDE SEQUENCE.
 RX MEDLINE=97358486; PubMed=9215582; DOI=10.1016/S0928-8244(97)00016-3;
 RA Loder G., Wercenkenthin C., Schwarz S., Dyke K.;
 RT "Molecular analysis of naturally occurring ermC-encoding plasmids in
 RT staphylococci isolated from animals with and without previous contact
 RT with macrolide / lincosamide antibiotics.";
 RL FEBS Immunol. Med. Microbiol. 18:7-15(1997).
 RN [3]
 RN NUCLEOTIDE SEQUENCE.
 RA Schwarz S.P.;
 RL Submitted (Oct-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; X82668; CAA57984.1; -; Genomic_DNA.
 KW Plasmid.
 SQ SEQUENCE 19 AA; 2237 MW; 13E4CAD99E4F3A7B CRC64;
 QY Query Match 25.4%; Score 30; DB 2; Length 19;
 Best Local Similarity 45.5%; Pred. No. 1.4e+03;
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 Db 8 VVLYTMHYLYN 18
 :|:|:|:|
 7 FVINTVHYQPN 17
 RESULT 12
 ID Q799A5 STAU PRELIMINARY; PRT; 19 AA.
 AC Q799A5;
 DT 05-JUL-2004 (Tremblrel. 27, Created)
 DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
 DE Hypothetical protein.
 OS Staphylococcus aureus.
 OC Plasmid pSES31.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OK NCBI_TaxID=1280;
 RN [1]
 RN NUCLEOTIDE SEQUENCE.
 RC Schwarz S.;
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RN NUCLEOTIDE SEQUENCE.
 RA Schwarz S.P.;
 RC STRAIN=12;
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Y17294; CAB46339.1; -; Genomic_DNA.
 KW Hypothetical protein; Plasmid.
 SQ SEQUENCE 19 AA; 2237 MW; 13E4CAD99E4F3A7B CRC64;
 QY Query Match 25.4%; Score 30; DB 2; Length 19;
 Best Local Similarity 45.5%; Pred. No. 1.4e+03;
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 Db 8 VVLYTMHYLYN 18
 :|:|:|:|
 7 FVINTVHYQPN 17
 RESULT 13
 ID Q799E4 STAP PRELIMINARY; PRT; 19 AA.
 AC Q799E4;
 DT 05-JUL-2004 (Tremblrel. 27, Created)
 DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
 DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
 DE Orl 1 protein.
 RN Name=orf 1;
 OS Staphylococcus epidermidis.

OG Plasmid pSES23.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OK NCBI_TaxID=1282;
 RN [1]
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=DK20;
 RA Schwarz S.P.;
 RL Submitted (Oct-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Y15274; CAA75561.1; -; Genomic_DNA.
 KW Plasmid.
 SQ SEQUENCE 19 AA; 2210 MW; 13FEE3D99E4F3A7B CRC64;
 QY Query Match 25.4%; Score 30; DB 2; Length 19;
 Best Local Similarity 45.5%; Pred. No. 1.4e+03;
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 Db 8 VVLYTMHYLYN 18
 :|:|:|:|
 7 FVISTVHYQPN 17
 RESULT 14
 ID Q7AY86 STAP PRELIMINARY; PRT; 19 AA.
 AC Q7AY86;
 DT 05-JUL-2004 (Tremblrel. 27, Created)
 DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
 DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Staphylococcus sciuri.
 OC Plasmid pSCF31.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OK NCBI_TaxID=1296;
 RN [1]
 RN NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22270974; PubMed=12384375;
 RX DOI=10.1128/AAC.46.11.3621-3623.2002;
 RA Schwarz S., Kehrenberg C., Ojo K.K.;
 RT "Staphylococcus sciuri gene erm(33), encoding inducible resistance to
 RT macrolides, lincosamides, and streptogramin B antibiotics, is a
 RT product of recombination between erm(C) and erm(A).";
 RL Antimicrob. Agents Chemother. 46:3621-3623(2002).
 RN [2]
 RN NUCLEOTIDE SEQUENCE.
 RA Schwarz S.P.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ313523; CAC86409.1; -; Genomic_DNA.
 KW Hypothetical protein; Plasmid.
 SQ SEQUENCE 19 AA; 2237 MW; 13E4CAD99E4F3A7B CRC64;
 QY Query Match 25.4%; Score 30; DB 2; Length 19;
 Best Local Similarity 45.5%; Pred. No. 1.4e+03;
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 Db 8 VVLYTMHYLYN 18
 :|:|:|:|
 7 FVINTVHYQPN 17
 RESULT 15
 ID Q45558 BACSH PRELIMINARY; PRT; 19 AA.
 AC Q45558;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
 DE Second leader peptide.
 OS Bacillus sphaericus.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OK NCBI_TaxID=1421;
 RN [1]
 RN NUCLEOTIDE SEQUENCE.
 RX MEDLINE=87083389; PubMed=3025178;

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RA Monod M., Mohan S., Dubnau D.;
RT "Cloning and analysis of ermG, a new macrolide-lincosamide-";
RT streptogramin B resistance element from Bacillus sphaericus.";
RL J. Bacteriol. 169:340-350(1987).
DR EMBL; M1532; AAA22418.1; -; Genomic_DNA.
DR PIR; B26930; B26930.
SQ SEQUENCE 19 AA; 2269 MW; F983BD99E4F3A7B CRC64;

Query Match 25.4%; Score 30; DB 2; Length 19;
Best Local Similarity 45.5%; Pred. No. 1.4e+03;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Oy 8 VLYTYMHYLYN 18
   :|:|:|:|
Db 7 FVISTVHYQPN 17

RESULT 16
Q799W9 STAH0 PRELIMINARY; PRT; 19 AA.
AC Q799W9_
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Orf1 protein (Leader peptide).
GN Name=orf1;
OS Staphylococcus hominis.
OC Plasmid pSES5.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1290;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=97358486; PubMed=9215582; DOI=10.1016/S0928-8244(97)00016-3;
RA Loder G., Werschenhub C., Schwarz S., Dyke K.;
RT "Molecular analysis of naturally occurring ermC-encoding plasmids in
RT staphylococci isolated from animals with and without previous contact
RT with macrolide / lincosamide antibiotics.";
RL FEWS Immunol. Med. Microbiol. 18:7-15(1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=736153; PLASMID=pSES5;
RA Schwarz S.P.;
RL Submitted (OCT-1996) to the EMBL/Genbank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=96379693; PubMed=8787908;
RA Loder G., Schwarz S., Gregory P., Dyke K.;
RT "Tandem duplication in ermC translational attenuator of the macrolide-
RT lincosamide-streptogramin B resistance plasmid pSES6 from
RT Staphylococcus equorum.";
RL Antimicrob. Agents Chemother. 40:215-217(1996).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Schwarz S.P.;
RL Submitted (NOV-1994) to the EMBL/Genbank/DBJ databases.
DR EMBL; Y09001; CAA70205.1; -; Genomic_DNA.
DR EMBL; X82667; CAA57982.1; -; Genomic_DNA.
KW Plasmid.
SQ SEQUENCE 19 AA; 2210 MW; 13FEE3D99E4F3A7B CRC64;

Query Match 25.4%; Score 30; DB 2; Length 19;
Best Local Similarity 45.5%; Pred. No. 1.4e+03;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Oy 8 VLYTYMHYLYN 18
   :|:|:|:|
Db 7 FVISTVHYQPN 17

RESULT 17
Q4JHH5 STAU0 PRELIMINARY; PRT; 19 AA.
ID Q4JHH5 STAU0 PRELIMINARY;

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AC Q4JHH5;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Leader peptide.
GN Name=lep;
OS Staphylococcus aureus.
OC Plasmid pWB6738.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CMRSA;
RA O'Brien F.G., Zaini Z., Grubb W.B.;
RT "The complete sequence of plasmid pWB6738 from the ST1-MRSA-IV lineage
RT of community methicillin-resistant Staphylococcus aureus.";
RL Submitted (JUN-2005) to the EMBL/Genbank/DBJ databases.
DR EMBL; DQ088624; AAY89964.1; -; Genomic_DNA.
KW Plasmid.
SQ SEQUENCE 19 AA; 2210 MW; 13FEE3D99E4F3A7B CRC64;

Query Match 25.4%; Score 30; DB 2; Length 19;
Best Local Similarity 45.5%; Pred. No. 1.4e+03;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Oy 8 VLYTYMHYLYN 18
   :|:|:|:|
Db 7 FVISTVHYQPN 17

RESULT 18
Q6LEG3 9ZZZZ PRELIMINARY; PRT; 19 AA.
ID Q6LEG3 9ZZZZ PRELIMINARY;
AC Q6LEG3_
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Leader peptide.
OS Plasmid pRJS.
OC other sequences; plasmids.
OX NCBI_TaxID=31885;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=93381457; PubMed=8371109;
RA Oliveira S.S., Murphy B., Gamon M.R., Bastos M.C.;
RT "pRJS: a naturally occurring Staphylococcus aureus plasmid expressing
RT constitutive macrolide-lincosamide-streptogramin B resistance contains
RT a tandem duplication in the leader region of the ermC gene.";
RL J. Gen. Microbiol. 139:1461-1467(1993).
DR EMBL; L04687; AAA92763.1; -; Genomic_DNA.
KW Plasmid.
SQ SEQUENCE 19 AA; 2210 MW; 13FEE3D99E4F3A7B CRC64;

Query Match 25.4%; Score 30; DB 2; Length 19;
Best Local Similarity 45.5%; Pred. No. 1.4e+03;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Oy 8 VLYTYMHYLYN 18
   :|:|:|:|
Db 7 FVISTVHYQPN 17

RESULT 19
Q79DT6 9ZZZZ PRELIMINARY; PRT; 19 AA.
ID Q79DT6 9ZZZZ PRELIMINARY;
AC Q79DT6_
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Leader peptide.
GN Name=ermG;
OS Plasmid pGT633.

```


OG Plasmid pGT633.
 OC other sequences: plasmids.
 OX NCBI_TaxID=28406;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=94224982; PubMed=817126; DOI=10.1006/plas.1994.1007;
 RA Tamok G.W., Luchansky J.B., Miller L.A., Connell H.,
 RA Thode-Andersen S., Mercer A.A., Kleenhammer T.R.;
 RT "Molecular characterization of a plasmid-borne (pGT633) erythromycin
 resistance determinant (ermGT) from *Lactobacillus reuteri* 100-63.";
 RL Plasmid 31:60-71(1994).
 DR EMBL; M64090; AAA98095.1; -; Genomic_DNA.
 KW Plasmid.
 SQ SEQUENCE 19 AA; 2237 MW; 13B4CAD99E4F3A7B CRC64;
 Query Match 25.4%; Score 30; DB 2; Length 19;
 Best Local Similarity 45.5%; Pred. No. 1.4e+03;
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 8 YVLYTMHYLYN 18
 Db 7 FVINTVHQP 17

RESULT 20
 O7PC06 PLAYO PRELIMINARY; PRT; 20 AA.
 ID O7PC06
 AC O7PC06
 DT 01-MAR-2004 (TReMBLrel. 26, Created)
 DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
 DE Hypothetical protein (Fragment).
 GN Name=PY06333; Synonym=PY01707;
 OS Plasmodium yoelii yoelii.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=73239;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=17XNL;
 RX MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
 RA Carlton J.M., Anginoli S.V., Suh B.B., Kooij T.W., Perlea M.,
 RA Salva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
 RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
 RA Shallom S.J., van Aken S.B., Riedmuller S.B., Feldblyum T.V.,
 RA Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,
 RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
 RA Cunningham D.A., Preiser P.R., Bergman L.W., Valdivia A.B.,
 RA van Lin L.H., Jansz C.J., Waters A.P., Smith H.O., White O.R.,
 RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
 RA Carucci D.J.;
 RT "Genome sequence and comparative analysis of the model rodent malaria
 parasite *Plasmodium yoelii yoelii*.";
 RL Nature 419:512-519(2002).
 CC -!- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AABL01002128; EAA18531.1; -; Genomic_DNA.
 KW Hypothetical protein.
 FT NON TER 1
 SQ SEQUENCE 20 AA; 2516 MW; DD48FCB3936EA2 CRC64;
 Query Match 25.4%; Score 30; DB 2; Length 20;
 Best Local Similarity 55.6%; Pred. No. 1.5e+03;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 10 LYTMHYLYN 18
 Db 3 LYKMHLEN 11

RESULT 21
 O4Y2F8 PLACH PRELIMINARY; PRT; 21 AA.
 ID O4Y2F8

AC O4Y2F8;
 DT 13-SEP-2005 (TReMBLrel. 31, Created)
 DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=PC102749.00.0;
 OS Plasmodium chabaudi.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5825;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
 RA Berrian M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
 RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
 RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
 RA Bidwell S.L., Rajadream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
 RA Jansz C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
 RT "A comprehensive survey of the *Plasmodium* life cycle by genomic,
 RT transcriptomic, and proteomic analyses.";
 RL Science 307:82-86(2005).
 CC -!- CAUTION: The sequence shown here is derived from an
 CC preliminary data.
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 DR EMBL; CAAJ01001590; CAH76652.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 21 AA; 2693 MW; FD162F9CAD7A4A46 CRC64;
 Query Match 25.4%; Score 30; DB 2; Length 21;
 Best Local Similarity 40.0%; Pred. No. 1.6e+03;
 Matches 6; Conservative 1; Mismatches 8; Indels 0; Gaps 0;
 QY 4 NVKXVLYTMHYLYN 18
 Db 6 NVFLFHINMHYLYN 20

RESULT 22
 O7GEY8 TOBAC PRELIMINARY; PRT; 21 AA.
 ID O7GEY8
 AC O7GEY8
 DT 05-JUL-2004 (TReMBLrel. 27, Created)
 DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
 DE NdhD gene product (21 AA) (Fragment).
 DE Nicotiana tabacum (Common tobacco).
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC asterids; lamids; Solanales; Solanaceae; Nicotiana.
 OX NCBI_TaxID=4097;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Bright yellow 4; TISSUE=leave;
 RX MEDLINE=88210537; PubMed=3329576;
 RA Hayashida N., Matsubayashi T., Shinozaki K., Sugura M., Inoue K.,
 RA Hyama T.;
 RT "The gene for the 9 kd polypeptide, a possible apoprotein for the
 RT iron-sulfur centers A and B of the photosystem I complex, in tobacco
 RT chloroplast DNA.";
 RL Curr. Genet. 12:247-250(1987).
 DR EMBL; X05881; CAA29305.1; -; Genomic_DNA.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON TER 21
 SQ SEQUENCE 21 AA; 2547 MW; 0A06CB19BB649FB7 CRC64;
 Query Match 25.4%; Score 30; DB 2; Length 21;
 Best Local Similarity 33.3%; Pred. No. 1.6e+03;
 Matches 4; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
 QY 5 VVKXVLYTMHYLYN 16
 Db 2 VQVLYVETNYF 13

RESULT 23
 Q7M447.9MOLL
 ID Q7M447.9MOLL PRELIMINARY; PRT; 20 AA.
 AC Q7M447;
 DT 01-MAR-2004 (TREMBLrel. 26, Created)
 DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Crystallin (Fragment).
 OS Sepia esculenta.
 OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
 CC Decapodiformes; Sepioidae; Sepiidae; Sepia.
 OX NCBI_TaxID=31210;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=89351593; PubMed=3255376;
 RA Chlou S.H.;
 RT "The protein sequence homology of gamma-crystallins among major
 vertebrate classes and their DNA sequence homology to heat-shock
 protein genes."
 RL J. Protein Chem. 7:527-534(1988).
 DR PIR; E60894; E60894.
 FT NON_TER 1
 FT TER 20
 SQ SEQUENCE 20 AA; 2448 MW; 4CD89E874BCB2EB7 CRC64;

Query Match 24.6%; Score 29; DB 2; Length 20;
 Best Local Similarity 40.0%; Pred. No. 2.2e+03;
 Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 11 YTMHYLYLNG 20
 Db 3 YTLVYFNGRG 12

RESULT 24
 Q9ZYB7.9HYME
 ID Q9ZYB7.9HYME PRELIMINARY; PRT; 21 AA.
 AC Q9ZYB7;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Cytochrome oxidase II (Fragment).
 OS Spinaria sp. MD-1998.
 OC Mitochondrion.
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Preygota;
 CC Neoptera; Endopterygota; Hymenoptera; Apocrita; Ichneumonidea;
 CC Braconidae; Rogadinae; Spinaria.
 OX NCBI_TaxID=77908;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=99152621; PubMed=10028295;
 RA Dowton M., Austin A.D.;
 RT "Evolutionary dynamics of a mitochondrial rearrangement 'hot spot' in
 the Hymenoptera."
 RL Mol. Biol. Evol. 16:298-309(1999).
 DR EMBL; AF071212; AAD17665.1; -; Genomic_DNA.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KM Mitochondrion.
 FT NON_TER 1
 SQ SEQUENCE 21 AA; 2691 MW; 9445FCDBA90F8C5 CRC64;

Query Match 24.6%; Score 29; DB 2; Length 21;
 Best Local Similarity 25.0%; Pred. No. 2.3e+03;
 Matches 4; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DEXNVKXVLYTMHY 16
 Db 4 ESDVFLMYLNMVNY 19

RESULT 25

Q4X6E8.PLACH
 ID Q4X6E8.PLACH PRELIMINARY; PRT; 21 AA.
 AC Q4X6E8;
 DT 13-SEP-2005 (TREMBLrel. 31, Created)
 DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
 DE Hypothetical protein (Fragment).
 GN ORFNames=PC405819.00.0;
 OS Plasmodium chabaudi.
 CC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5825;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
 RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
 RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
 RA Quail M.A., Ormond D., Doggett J., Trueman H.B., Mendoza J.,
 RA Bidwell S.L., Rajandream M.A., Carnucci D.J., Yates J.R., Kafatos F.C.,
 RA Jansz C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
 RT "A comprehensive survey of the Plasmodium life cycle by genomic,
 transcriptomic, and proteomic analyses."
 RL Science 307:82-86(2005).
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; CAAJ01009531; CAH87528.1; -; Genomic_DNA.
 KM Hypothetical protein.
 FT NON_TER 1
 SQ SEQUENCE 21 AA; 2608 MW; 803A3B52CC2F369F CRC64;

Query Match 24.6%; Score 29; DB 2; Length 21;
 Best Local Similarity 26.7%; Pred. No. 2.3e+03;
 Matches 4; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 5 VMXVLYTMHYLNN 19
 Db 2 IINILYSVFYIPSN 16

Search completed: January 26, 2006, 08:03:57
 Job time : 71.4052 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 26, 2006, 07:47:09 ; Search time 57.7414 Seconds
(without alignments)
129.360 Million cell updates/sec

Title: US-09-662-293-10

Perfect score: 83
Sequence: 1 DKLVMGVIFYGRAXSIE 17

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378761 residues

Total number of hits satisfying chosen parameters: 897420

Minimum DB seq length: 0

Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

A_Geneseq_21: *
1: geneseqp1980s: *
2: geneseqp1980s: *
3: geneseqp2000s: *
4: geneseqp2001s: *
5: geneseqp2002s: *
6: geneseqp2003as: *
7: geneseqp2003bs: *
8: geneseqp2004s: *
9: geneseqp2005s: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	81	97.6	17	5	AAY52519 House dms
2	81	97.6	17	3	AAU96323 Der HMW-m
3	47	56.6	16	2	AAW45138 Human car
4	42	50.6	15	8	ADL26336 Synthetic
5	42	50.6	20	8	ADM29133 Hepatitis
6	41	49.4	10	4	ABBS5898 Vascular
7	41	49.4	10	4	ABBS6114 Vascular
8	41	49.4	10	4	ABBS5939 Vascular
9	41	49.4	10	4	AAU28751 DPI trypt
10	41	49.4	10	4	AAU28791 DPI trypt
11	41	49.4	10	4	AAU28539 DPI trypt
12	41	49.4	10	4	AAU25095 Schizophr
13	41	49.4	10	4	AAU25399 Depressio
14	41	49.4	10	4	AAU26439 Depressio
15	41	49.4	10	4	AAU26186 Depressio
16	41	49.4	10	4	AAU15439 Schizophr
17	41	49.4	10	4	ABBS52306 Human API
18	41	49.4	10	6	ABBS59112 Alzheimer
19	41	49.4	10	8	ADN13951 Human Alz
20	41	49.4	10	8	ADN13951 Human Alz
21	41	49.4	10	8	ADN13951 Human Alz
22	41	49.4	10	8	ADN13951 Human Alz
23	40	48.2	18	9	ADV22957 HCV H77 i
24	40	48.2	18	9	ADV22958 HCV H77 i

25	39	47.0	10	6	ABBS9057 Alzheimer
26	39	47.0	10	8	ADN13952 Human Alz
27	39	47.0	12	7	ADN13988 TRPI deri
28	39	47.0	12	7	ADN13988 TRPI deri
29	36	43.4	16	2	AAW45139 Human car
30	35	42.2	8	2	AAW44471 Human car
31	35	42.2	8	3	AAW73124 Hepatitis
32	35	42.2	8	4	AAU00049 Hepatitis
33	35	42.2	8	4	AAU03907 Hepatitis
34	35	42.2	8	4	AAU01621 Hepatitis
35	35	42.2	8	4	AAU01643 Hepatitis
36	35	42.2	8	4	AAU01110 Hepatitis
37	35	42.2	8	4	AAU00256 Hepatitis
38	35	42.2	8	4	AAU04104 Hepatitis
39	35	42.2	8	4	AAU02138 Hepatitis
40	35	42.2	8	5	ABJ00088 HCV deriv
41	35	42.2	8	6	ABO00953 B7-like s
42	35	42.2	8	8	ADJ79584 CTL epit
43	35	42.2	9	4	AAJ00257 Hepatitis
44	35	42.2	9	4	AAJ00873 Hepatitis
45	35	42.2	9	4	AAJ01752 Hepatitis
46	35	42.2	9	7	ADW32956 HLA bindi
47	35	42.2	9	8	ADV98608 MHC-B40-a
48	35	42.2	9	9	ADZ86801 Cytotoxic
49	35	42.2	10	4	AAJ02500 Hepatitis
50	35	42.2	10	7	ADM32957 HLA bindi
51	35	42.2	15	4	AAE02910 Tryptic p
52	35	42.2	21	8	ADH35147 Plasma se
53	35	42.2	21	9	ADM07132 Isoleupe-1
54	34	41.0	13	4	AAE02857 Tryptic p
55	34	41.0	15	6	AAO29829 hTRT MHC
56	34	41.0	15	2	AAK45137 Human car
57	32	38.6	15	9	AECl1322 Escherich
58	32	38.6	18	4	AAW22037 Peptide #
59	32	38.6	18	4	ABBA4423 Peptide #
60	32	38.6	18	4	AAW38410 Peptide #
61	32	38.6	18	4	ABB27270 Protein #
62	32	38.6	18	4	AAW78165 Human bon
63	32	38.6	18	4	AAW65503 Human bra
64	32	38.6	18	4	ABBS5911 Human liv
65	31	37.3	9	2	AAW35936 Hepatitis
66	31	37.3	9	4	AAJ02866 Hepatitis
67	31	37.3	9	4	AAJ02499 Hepatitis
68	31	37.3	9	6	ABBS6104 E. coli g
69	31	37.3	11	5	AAU98969 Peptide #
70	31	37.3	20	4	ABBA2376 Peptide #
71	31	37.3	20	4	AAW36185 Peptide #
72	31	37.3	20	4	ABB25849 Protein #
73	31	37.3	20	4	AAW76076 Human bon
74	31	37.3	20	4	AAW63264 Human bra
75	31	37.3	20	4	ABBS7800 Human liv
76	31	37.3	20	5	ABBS45459 Human pep
77	31	37.3	20	8	ADM29132 Hepatitis
78	30	36.1	10	8	ADK12127 Maize DUL
79	30	36.1	15	9	ADZ69770 Botulinum
80	30	36.1	19	3	ABBI0670 L. mesent
81	30	36.1	19	4	AAW47234 hMfi Mit
82	30	36.1	19	6	ABU64950 Human Mfn
83	29	34.9	10	5	AAU80236 Unique pe
84	29	34.9	10	5	AAU80237 Unique pe
85	29	34.9	14	2	AAW82998 M. prolif
86	29	34.9	15	1	AAW80518 Synthetic
87	29	34.9	15	5	ABP46746 Human Bly
88	29	34.9	15	7	ADG97573 scFV VHCD
89	29	34.9	15	8	ADDE80945 Caehew nu
90	29	34.9	16	4	AAW89458 Streptoco
91	29	34.9	16	4	AAW84518 Streptoco
92	29	34.9	16	4	AAW89707 Streptoco
93	29	34.9	16	4	AAW88270 Streptoco
94	29	34.9	16	4	AAW62429 Streptoco
95	29	34.9	16	4	AAW63367 Streptoco
96	29	34.9	16	4	AAJ04119 Streptoco
97	29	34.9	16	5	ABBS94470 Streptoco

98	29	34.9	16	5	ABJ11373
99	29	34.9	16	5	ABJ05782
100	29	34.9	16	5	AAU95434

ALIGNMENTS

RESULT 1

AAV52519 ID AAV52519 standard; peptide; 17 AA.

AAV52519;

22-FEB-2000 (first entry)

House dust mite allergen protein (map) A/B fragment map(9).

Mite allergen protein; map; high molecular weight; HMW-map; allergy;

house dust mite; IgE; immunoglobulin E; allergen; mapA; mapB;

hypersensitivity reaction; therapy; treatment; diagnosis; human; feline;

canine; veterinary; antibody; vaccine; immunisation.

Dermatophagoides farinae.

Key location/Qualifiers

Misc-difference 14 /label= Xaa

/note= "Xaa = any amino acid"

MO9954349-A2.

28-OCT-1999.

16-APR-1999; 99WO-US008524.

17-APR-1998; 98US-00062013.

13-MAY-1998; 98US-0085295P.

02-SEP-1998; 98US-0098909P.

(HESK-) HESKA CORP.

Mccall CA, Hunter SM, Weber ER;

WPI; 2000-052700/04.

Novel high molecular weight Dermatophagoides nucleic acid polypeptides

used to modify an animals' hypersensitivity to mite allergens.

Claim 3; Page 70; 154pp; English.

Sequences AAV52510-Y5252 represent proteolytic fragments of

Dermatophagoides farinae high molecular weight mite allergen protein (HMW-

map) composition. The HMW-map composition was isolated from a D. farinae

homogenate by gel filtration, with each fraction being analysed for the

presence of proteins that bound to IgE present in mite-allergic dog

antisera. The HMW-map composition comprises mapA (a 109 kD protein) and

mapB (98 kD). Mite allergenic proteins and peptides, and nucleic acids

encoding them, may be used in therapeutic compositions to modify an

animal's hypersensitivity reaction to mite allergens. Animals that may be

treated include mammals and birds, especially felines, canines, equines,

humans, other pets, and work or domestic animals. The proteins or

fragments may also be used to diagnose allergies via a skin test. The

proteins and peptides can also be used to raise antibodies, which have a

variety of potential uses. For example, they can be used as vaccines to

passively immunise animals against dust mite hypersensitivity, as

positive controls in test kits and as tools to recover desired dust mite

allergens from a mixture of proteins

Sequence 17 AA;

Query Match 97.6%; Score 81; DB 3; Length 17;

Best Local Similarity 100.0%; Pred. No. 4.1e-08;

Matches	17;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	DKLVMGVFFYGRAXSIE	17						
DB	1	DKLVMGVFFYGRAXSIE	17						

RESULT 2

AAU96323 ID AAU96323 standard; peptide; 17 AA.

AAU96323;

15-JUL-2002 (first entry)

Der HMW-map polypeptide #10.

Der HMW-map; American house dust mite; antiallergic; mite; IgE;

mite allergenic protein; immunoglobulin E; hypersensitivity;

immunocomplex formation.

Dermatophagoides farinae.

MO200222807-A2.

21-MAR-2002.

14-SEP-2001; 2001WO-US028730.

14-SEP-2000; 2000US-00662293.

(HESK-) HESKA CORP.

Mccall CA, Hunter SM, Weber ER;

WPI; 2002-351888/38.

New mite allergenic protein isolated from Dermatophagoides, designated

Der HMW-map protein, useful as a vaccine for treating mite allergy.

Claim 12; Page 71; 161pp; English.

The invention relates to an isolated mite allergenic protein of

Dermatophagoides, designated Der HMW-map protein, and its related nucleic

acid. The Der HMW-map protein is useful for eliciting an immune response

against Der HMW-map protein. The protein or a reagent comprising a non-

proteinaceous epitope is useful for identifying an animal (e.g., dog,

cat) susceptible to or having an allergic response to a mite. A

therapeutic composition is useful for desensitising a host animal to an

allergic response to a mite. The DNA and protein can be used in the

detection of anti-Der HMW-map antibodies in animal fluids, and inhibition

of immunoglobulin (Ig)E or Der HMW-map protein activity associated with a

disease. Antibodies that bind to Der HMW-map are useful for inhibiting a

binding of proteins to IgE, to prevent immunocomplex formation, thus

reducing hypersensitivity responses to mite allergens, and as vaccines

against mite allergen hypersensitivity. Sequences AAU96314-AAU96342

represent Der HMW-map polypeptides of the invention

Sequence 17 AA;

Query Match 97.6%; Score 81; DB 5; Length 17;

Best Local Similarity 100.0%; Pred. No. 4.1e-08;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKLVMGVFFYGRAXSIE 17

DB 1 DKLVMGVFFYGRAXSIE 17

RESULT 3

AAW45138 ID AAW45138 standard; peptide; 16 AA.

AC AAW45138;
 XX
 DT 28-APR-1998 (first entry)
 XX
 DE Human cartilage glycoprotein 39 derived peptide #39.
 XX
 KM Articular cartilage; immunosuppressive therapy; antigen; autoantigen;
 KW immunological tolerance; T-cell; human cartilage glycoprotein 39;
 KM HC gp-39; rheumatoid arthritis; epitope.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN W09740068-A1.
 PD 30-OCT-1997.
 XX
 PF 22-APR-1997; 97WO-EP002051.
 XX
 PR 24-APR-1996; 96EP-00201106.
 XX
 PA (ALKU) AKZO NOBEL NV.
 XX
 PI Boehr AMH, Verheijden GFM;
 XX
 DR WPI; 1997-535775/49.
 XX
 PT Peptide suitable for use in antigen specific immunosuppressive therapy -
 PT resembles or mimics epitope present on HC gp-39, so inducing systemic
 PT immunological tolerance to rheumatoid arthritis auto-antigen.
 XX
 PS Claim 2; Page 76; 82pp; English.
 XX
 CC The present sequence represents a peptide which resembles or mimics an
 CC epitope present on human cartilage glycoprotein 39 (HC gp-39), an
 CC autoantigen in rheumatoid arthritis. The invention relates to peptides
 CC consisting of 16-55 amino acid residues comprising at least one of the
 CC following 19 sequences: LVCYTSMS; FLCTHITS; IIVFANIS; LKTLISVGG;
 CC FTKSVPEFL; FDGLDLML; LYGRRKQ; YDIKTSQH; LDISTMT; FLKMTYDF;
 CC FPGQEDAS; YAVGMLRL; LRLGAPAS; LAYEIDCF; LRGATVHT; FLKQRLAG;
 CC LAGAWMAL; VALDLDDF; or LDLDPFQS. They can be used medically in antigen
 CC specific immunosuppressive therapy, particularly the treatment of T-cell
 CC mediated destruction of articular cartilage in autoimmune diseases (e.g.
 CC rheumatoid arthritis). They can also be used to detect activated
 CC autoreactive T cells in an individual. The peptides have a specific
 CC effect on the autoreactive T cells, thus leaving the other components of
 CC the immune system intact, unlike the non-specific suppressive effect of
 CC immunosuppressive drugs, and do not cause toxic side effects. The
 CC peptides are predominantly recognised by autoreactive T cells from
 CC rheumatoid arthritis patients, but rarely by those from healthy donors
 XX
 SQ Sequence 16 AA;
 XX
 Query Match 56.6%; Score 47; DB 2; Length 16;
 Best Local Similarity 66.7%; Pred. No. 0.12;
 Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 2 KLVNMGVFPYGRA 13
 :|||:|:
 Db 4 KLVNMGVFPGRS 15
 RESULT 4
 ID ADL26336 standard; peptide; 15 AA.
 XX
 AC ADL26336;
 XX
 DT 17-JUN-2004 (first entry)
 XX
 DE Synthetic peptide C127 derived from a conserved region of HCV.
 XX
 KM HCV; hepatitis C virus; virucide; vaccine; MHC; HLA;

KW Major histocompatibility complex; human leukocyte antigen.
 XX
 OS Synthetic.
 XX
 PN W02004024182-A2.
 XX
 PD 25-MAR-2004.
 XX
 PF 27-AUG-2003; 2003WO-EP009482.
 XX
 PR 13-SEP-2002; 2002AT-00001376.
 PR 27-FEB-2003; 2003WO-EP002005.
 PR 11-JUL-2003; 2003EP-00450171.
 XX
 PA (INTE-) INTERCELL AG.
 XX
 PI Buschle M, Habel A, Klade C, Matner F, Otava O, Vytvytska O;
 PI Zauner W, Zinke S, Kiriappos H;
 XX
 DR WPI; 2004-269899/25.
 XX
 PT Isolating Hepatitis C Virus peptides (HVs) which have a binding capacity
 PT to a MHC/HLA molecule or a complex comprising the HCV-peptide and the
 PT molecule by separating the complex from the HCV-peptides which do not
 PT bind to the molecule.
 XX
 PS Example 1; Page 31; 73pp; English.
 XX
 CC The invention relates to a novel method for isolating Hepatitis C Virus
 CC (HCV) peptides (HVs). The method of the invention has virucide activity,
 CC and may be useful in producing a vaccine. The method is useful for
 CC isolating Hepatitis C Virus peptides (HVs) which have a binding capacity
 CC to a MHC/HLA molecule or a complex comprising the HCV-peptide and the
 CC MHC/HLA molecule for preparing a vaccine against HCV infection. The T
 CC cells, a T cell clone or a T cell population or preparation is useful for
 CC identifying heteroclitic epitopes or for preparing a composition for
 CC treating HCV infection. The present sequence represents a synthetic
 CC peptide derived from a conserved region of HCV.
 XX
 SQ Sequence 15 AA;
 XX
 Query Match 50.6%; Score 42; DB 8; Length 15;
 Best Local Similarity 63.6%; Pred. No. 1;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 7 VPFYGRXSIE 17
 :|||:|:
 Db 4 IPFYKALPIE 14
 RESULT 5
 ID ADM29133 standard; peptide; 20 AA.
 XX
 AC ADM29133;
 XX
 DT 01-JUL-2004 (first entry)
 XX
 DE Hepatitis C virus cellular immune response related peptide.
 XX
 KM DNA vaccine; vaccine; antigen gene; antigen; hepatitis C virus; HCV;
 KM recombinant adenovirus vaccine; adenovirus; HCV infection;
 KM hepatitis C virus infection; infection; virucide.
 XX
 OS Hepatitis C virus.
 OS Synthetic.
 XX
 PN W02004028563-A1.
 PD 08-APR-2004.
 XX
 PF 24-SEP-2003; 2003WO-KR001951.
 XX

PR 27-SEP-2002; 2002KR-00058712.
PR 06-NOV-2002; 2002KR-00068496.
XX
PA (GENE-) GENEXINE INC.
PA (POST-) POSTECH FOUND.
PA (DONG-) DONG-A PHARM CO LTD.
PA (DAEW-) DAEWONG CO LTD.
PA (POSC-) POSCO.
XX
PI Sung YC, Youn J, Yang S, Park S, Lee CG;
XX
DR WPI; 2004-305120/28.
XX
XX
PT New DNA vaccine comprising plasmid containing 2-6 kb of the total antigen
PT gene of hepatitis C virus (HCV), useful in treating or preventing HCV
PT infection.
XX
XX
PS Disclosure; Fig 20d; 165pp; English.
XX
CC The present invention describes a DNA vaccine which comprises a plasmid
CC containing 2-6 kb of the total antigen gene of hepatitis C virus (HCV).
CC Also described: (1) a recombinant adenovirus vaccine including an
CC adenovirus containing 2-6 kb of total antigen gene of HCV; (2) a vaccine
CC administering method; and (3) a method for treating or preventing HCV
CC infection. The DNA vaccine has virucide activity. The DNA vaccine is
CC useful in treating or preventing HCV infection. The present sequence
CC represents a peptide from the HCV peptide pool used for the investigation
CC of cellular immune response in the exemplification of the present
CC invention.
XX
XX
SQ Sequence 20 AA;

Query Match 50.6%; Score 42; DB 8; Length 20;
Best Local Similarity 63.6%; Pred. No. 1.4;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 7 VPFYGRAXSIE 17
Db :||||:|
5 IPFYGAIRPIE 15

RESULT 6
ABB55898
ID ABB55898 standard; peptide; 10 AA.
XX
AC ABB55898;
XX
DT 15-FEB-2002 (first entry)
XX
DE Vascular dementia-associated protein isoform (VPI) 98.
XX
KM Vascular Dementia; VD; VD-associated protein isoform; VPI; screening;
KM diagnosis; prognosis; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200169261-A2.
XX
PD 20-SEP-2001.
XX
PF 14-MAR-2001; 2001WO-GB001106.
XX
PR 15-MAR-2000; 2000GB-00006285.
PR 24-NOV-2000; 2000GB-00028734.
PR 28-NOV-2000; 2000US-00724391.
XX
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX
PI Herath HMAc, Parekh RB, Rohlf C;
XX
DR WPI; 2001-557937/62.
XX
PT Screening, diagnosis or prognosis of vascular dementia (VD), useful for

PT determining stage of VD and monitoring the effect of VD therapy,
PT comprises analyzing body fluid by 2-dimensional electrophoresis for
PT features correlated with VD.
XX
XX
PS Claim 6; Page 31; 151pp; English.
XX
CC The invention relates to screening, diagnosis or prognosis of Vascular
CC Dementia (VD) in a subject comprising analysing body fluid from the
CC subject by 2-dimensional (2-D) electrophoresis to generate a 2-D array of
CC features containing at least one chosen feature whose relative abundance
CC correlates with the presence, absence, stage or severity of VD or
CC predicts the onset or course of VD, especially detecting in a sample of
CC cerebrospinal fluid (CSF) from the subject one of 223 VD-associated
CC protein isoforms (VPIs) (ABB55801-ABB56295) as fully defined in the
CC specification. Detecting VD-associated features and VPI is useful for the
CC screening, diagnosis or prognosis of VD, for determining the stage or
CC severity of VD, for identifying a subject at risk of VD or for monitoring
CC the effect of therapy administered to a subject having VD. Nucleic acids
CC encoding a VPI or inhibiting the function of a VPI are useful for the
CC treatment of VD and for gene therapy
XX
XX
SQ Sequence 10 AA;

Query Match 49.4%; Score 41; DB 4; Length 10;
Best Local Similarity 70.0%; Pred. No. 0.99;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 LVMGVPPYGR 12
Db :||||:|
1 LVMGIPTFGR 10

RESULT 7
ABB56114
ID ABB56114 standard; peptide; 10 AA.
XX
AC ABB56114;
XX
DT 15-FEB-2002 (first entry)
XX
DE Vascular dementia-associated protein isoform (VPI) 314.
XX
KM Vascular Dementia; VD; VD-associated protein isoform; VPI; screening;
KM diagnosis; prognosis; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200169261-A2.
XX
PD 20-SEP-2001.
XX
PF 14-MAR-2001; 2001WO-GB001106.
XX
PR 15-MAR-2000; 2000GB-00006285.
PR 24-NOV-2000; 2000GB-00028734.
PR 28-NOV-2000; 2000US-00724391.
XX
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX
PI Herath HMAc, Parekh RB, Rohlf C;
XX
DR WPI; 2001-557937/62.
XX
XX
PT Screening, diagnosis or prognosis of vascular dementia (VD), useful for
PT determining stage of VD and monitoring the effect of VD therapy, for
PT comprises analyzing body fluid by 2-dimensional electrophoresis for
PT features correlated with VD.
XX
XX
PS Claim 6; Page 36; 151pp; English.
XX
CC The invention relates to screening, diagnosis or prognosis of Vascular
CC Dementia (VD) in a subject comprising analysing body fluid from the
CC subject by 2-dimensional (2-D) electrophoresis to generate a 2-D array of

CC features containing at least one chosen feature whose relative abundance
CC correlates with the presence, absence, stage or severity of VD or
CC predicts the onset or course of VD, especially detecting in a sample of
CC cerebrospinal fluid (CSF) from the subject one of 223 VD-associated
CC protein isoforms (VPis) (ABBS5801-ABBS6295) as fully defined in the
CC specification. Detecting VD-associated features and VPI is useful for the
CC screening, diagnosis or prognosis of VD, for determining the stage or
CC severity of VD, for identifying a subject at risk of VD or for monitoring
CC the effect of therapy administered to a subject having VD. Nucleic acids
CC encoding a VPI or inhibiting the function of a VPI are useful for the
CC treatment of VD and for gene therapy

SO Sequence 10 AA;

Query Match 49.4%; Score 41; DB 4; Length 10;
Best Local Similarity 70.0%; Pred. No. 0.99;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 LVMGVFPYGR 12
||||:|:
DB 1 LVMGIPTRGR 10

RESULT 8
ABBS5939
ID ABBS5939 standard; peptide; 10 AA.
AC ABBS5939;
XX
XX 15-FEB-2002 (first entry)
DT
XX
DE Vascular dementia-associated protein isoform (VPI) 139.
XX
KM Vascular Dementia; VD; VD-associated protein isoform; VPI; screening;
KM diagnosis; prognosis; gene therapy.
XX
XX Homo sapiens.
XX
XX WO200169261-A2.
XX
XX 20-SEP-2001.
PD
XX
XX 14-MAR-2001; 2001WO-GB001106.
PF
XX 15-MAR-2000; 2000GB-00006285.
PR 24-NOV-2000; 2000GB-00028734.
PR 28-NOV-2000; 2000US-00724391.
XX
XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
PA
XX Herath HMAc, Parekh RB, Rohlf C;
PI
XX WPI; 2001-557937/62.
DR
XX
PT Screening, diagnosis or prognosis of vascular dementia (VD), useful for
PT determining stage of VD and monitoring the effect of VD therapy,
PT comprises analyzing body fluid by 2-dimensional electrophoresis for
PT features correlated with VD.
XX
XX
PS Claim 6; Page 32; 151p; English.

CC The invention relates to screening, diagnosis or prognosis of Vascular
CC Dementia (VD) in a subject comprising analysing body fluid from the
CC subject by 2-dimensional (2-D) electrophoresis to generate a 2-D array of
CC features containing at least one chosen feature whose relative abundance
CC correlates with the presence, absence, stage or severity of VD or
CC predicts the onset or course of VD, especially detecting in a sample of
CC cerebrospinal fluid (CSF) from the subject one of 223 VD-associated
CC protein isoforms (VPis) (ABBS5801-ABBS6295) as fully defined in the
CC specification. Detecting VD-associated features and VPI is useful for the
CC screening, diagnosis or prognosis of VD, for determining the stage or
CC severity of VD, for identifying a subject at risk of VD or for monitoring
CC the effect of therapy administered to a subject having VD. Nucleic acids

CC encoding a VPI or inhibiting the function of a VPI are useful for the
CC treatment of VD and for gene therapy

SO Sequence 10 AA;

Query Match 49.4%; Score 41; DB 4; Length 10;
Best Local Similarity 70.0%; Pred. No. 0.99;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 LVMGVFPYGR 12
||||:|:
DB 1 LVMGIPTRGR 10

RESULT 9
AAU28751
ID AAU28751 standard; peptide; 10 AA.
AC AAU28751;
XX
XX 03-JAN-2002 (first entry)
DT
XX
DE DPI tryptic digest peptide #348.
XX
XX
XX Human; depression associated protein isoform; tryptic digest peptide;
XX DPI; cerebrospinal fluid; CSF; BAD; bipolar affective disorder;
XX neuropsychiatric disorder; bipolar mood disorder; neuroleptic;
XX maniac-depressive illness; schizoaffective disorder.
XX
XX Homo sapiens.
XX
XX WO200162787-A1.
XX
XX 30-AUG-2001.
PD
XX
XX 23-FEB-2001; 2001WO-GB000786.
PF
XX 24-FEB-2000; 2000GB-00004412.
PR 08-DEC-2000; 2000GB-00030050.
PR 12-DEC-2000; 2000US-0254830P.
XX
XX
XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
PA
XX Herath HMAc, Parekh RB, Rohlf C, Terrett JA, Tyson KL;
PI
XX WPI; 2001-570626/64.
DR
XX
XX
PT Novel nucleic acid encoding a protein associated with bipolar affective
PT disorder, which is used for diagnosis, prophylaxis and therapy of
PT neuropsychiatric disorders, such as bipolar affective disorder.
PT
XX
XX Disclosure; Page 38; 153p; English.

CC The present invention relates to the identification of depression
CC associated protein isoforms (DPis), particularly the tryptic digest
CC peptides of these proteins. Some of the DPis (AAU28404-AAU28625)
CC described are decreased in the cerebrospinal fluid (CSF) of BAD (bipolar
CC affective disorder) subjects, whilst other DPis (AAU28626-AAU28887) are
CC increased in BAD subjects. Also described are peptide sequences
CC identified from DPI-45 and DPI-213 and the nucleic acid sequences they are
CC encoded by. The sequences of the invention are useful for clinical
CC screening, diagnosis, prognosis, therapy and prophylaxis of
CC neuropsychiatric disorders e.g. BAD (also known as bipolar mood
CC BP), maniac-depressive illnesses, attention deficit disorders,
CC schizoaffective disorders, and unipolar affective disorders. The present
CC sequence represents one of the DPI tryptic digest peptides of the present
CC invention

SO Sequence 10 AA;

Query Match 49.4%; Score 41; DB 4; Length 10;
Best Local Similarity 70.0%; Pred. No. 0.99;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 LVMGVPPYGR 12
 |||||:|:|
 DB 1 LVMGIPTFGR 10

RESULT 10

AAU28791
 ID AAU28791 standard; peptide; 10 AA.

AC AAU28791;

DT 03-JAN-2002 (first entry)

DE DPI tryptic digest peptide #388.

XX Human; depression associated protein isoform; tryptic digest peptide;
 KW DPI; cerebrospinal fluid; CSF; BAD; bipolar affective disorder;
 KW neuropsychiatric disorder; bipolar mood disorder; neuroleptic;
 KW manic-depressive illness; schizoaffective disorder.

XX Homo sapiens.

PN MO200162787-A1.

PD 30-AUG-2001.

PF 23-FEB-2001; 2001WO-GB000786.

PR 24-FEB-2000; 2000GB-00004412.

PR 08-DEC-2000; 2000GB-00030050.

PR 12-DEC-2000; 2000US-0254830P.

XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

PI Herath HMAc, Parekh RB, Rohlf C, Terrett JA, Tyson KL;

XX WPI; 2001-570626/64.

PT Novel nucleic acid encoding a protein associated with bipolar affective
 disorder, which is used for diagnosis, prophylaxis and therapy of
 neuropsychiatric disorders, such as bipolar affective disorder.

XX Disclosure; Page 38; 153pp; English.

CC The present invention relates to the identification of depression
 associated protein isoforms (DPIs), particularly the tryptic digest
 peptides of these proteins. Some of the DPIs (AAU28404-AAU28625)
 described are decreased in the cerebrospinal fluid (CSF) of BAD (bipolar
 affective disorder) subjects, whilst other DPIs (AAU28626-AAU28887) are
 increased in BAD subjects. Also described are peptide sequences
 identified from DPI-45 and DPI-213 and the nucleic acid sequences they are
 encoded by. The sequences of the invention are useful for clinical
 screening, diagnosis, prognosis, therapy and prophylaxis of
 CC neuropsychiatric disorders e.g. BAD (also known as bipolar mood disorder,
 CC BP), manic-depressive illnesses, attention deficit disorders,
 CC schizoaffective disorders, and unipolar affective disorders. The present
 CC sequence represents one of the DPI tryptic digest peptides of the present
 CC invention

XX Sequence 10 AA;

Query Match 49.4%; Score 41; DB 4; Length 10;

Best Local Similarity 70.0%; Pred. No. 0.99; Mismatches 1; Indels 0; Gaps 0;

QY 3 LVMGVPPYGR 12
 |||||:|:|

DB 1 LVMGIPTFGR 10

RESULT 11

AAU28539

ID AAU28539 standard; peptide; 10 AA.

XX AAU28539;

DT 03-JAN-2002 (first entry)

DE DPI tryptic digest peptide #136.

XX Human; depression associated protein isoform; tryptic digest peptide;
 KW DPI; cerebrospinal fluid; CSF; BAD; bipolar affective disorder;
 KW neuropsychiatric disorder; bipolar mood disorder; neuroleptic;
 KW manic-depressive illness; schizoaffective disorder.

XX Homo sapiens.

PN MO200162787-A1.

PD 30-AUG-2001.

PF 23-FEB-2001; 2001WO-GB000786.

PR 24-FEB-2000; 2000GB-00004412.

PR 08-DEC-2000; 2000GB-00030050.

PR 12-DEC-2000; 2000US-0254830P.

XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

PI Herath HMAc, Parekh RB, Rohlf C, Terrett JA, Tyson KL;

XX WPI; 2001-570626/64.

PT Novel nucleic acid encoding a protein associated with bipolar affective
 disorder, which is used for diagnosis, prophylaxis and therapy of
 neuropsychiatric disorders, such as bipolar affective disorder.

XX Disclosure; Page 33; 153pp; English.

CC The present invention relates to the identification of depression
 associated protein isoforms (DPIs), particularly the tryptic digest
 peptides of these proteins. Some of the DPIs (AAU28404-AAU28625)
 described are decreased in the cerebrospinal fluid (CSF) of BAD (bipolar
 affective disorder) subjects, whilst other DPIs (AAU28626-AAU28887) are
 increased in BAD subjects. Also described are peptide sequences
 identified from DPI-45 and DPI-213 and the nucleic acid sequences they are
 encoded by. The sequences of the invention are useful for clinical
 screening, diagnosis, prognosis, therapy and prophylaxis of
 CC neuropsychiatric disorders e.g. BAD (also known as bipolar mood disorder,
 CC BP), manic-depressive illnesses, attention deficit disorders,
 CC schizoaffective disorders, and unipolar affective disorders. The present
 CC sequence represents one of the DPI tryptic digest peptides of the present
 CC invention

XX Sequence 10 AA;

Query Match 49.4%; Score 41; DB 4; Length 10;

Best Local Similarity 70.0%; Pred. No. 0.99; Mismatches 1; Indels 0; Gaps 0;

QY 3 LVMGVPPYGR 12
 |||||:|:|

DB 1 LVMGIPTFGR 10

RESULT 12

AAU25095

AC AAU25095;

DT 18-DEC-2001 (first entry)

DE Schizophrenia-Associated Protein Isoform (SPI) peptide #324.

KW	Schizophrenia-associated protein isoform; SPI-206; SPI-238; SPI-240; neuroleptic; gene therapy; cerebrospinal fluid; serum; plasma.
XX	
OS	Homo sapiens.
PN	WO200162785-A2.
XX	
PD	30-AUG-2001.
XX	
PF	23-FEB-2001; 2001WO-GB000792.
XX	
PR	24-FEB-2000; 2000GB-00004415.
XX	
PR	28-DEC-2000; 2000US-00750395.
XX	
PA	(OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX	
PI	Herath HMC, Parekh RB, Rohlf C, Terrett JA, Tyson KL;
XX	
DR	WPI; 2001-570624/64.
XX	
PT	New schizophrenia associated protein isoforms and encoding nucleic acid molecules, useful for treatment, diagnosis and prognosis of schizophrenia and screening for potential drugs for treatment and new drug targets.
XX	
PS	Disclosure; Page 35; 148pp; English.
XX	
CC	The sequence represents a schizophrenia-associated protein isoform (SPI-206). These protein isoforms, e.g. SPI-206, SPI-238 and SPI-240 are detectable in cerebrospinal fluid, serum or plasma and are useful markers of schizophrenia. The sequences can be used for treatment and diagnosis of schizophrenia, screening, prognosis, monitoring the results of therapy, identifying patients most likely to respond to a particular therapy and identification of new targets for drug treatment. SPI DNA is useful as a nucleic acid probe to detect the presence of nucleic acids or SPIs
XX	
SO	Sequence 10 AA;
QY	3 LVMGVPFYGR 12
DB	1 LVMGIPYFGR 10
XX	
RESULT 3	
AAU26399	
ID	AAU26399 standard; peptide; 10 AA.
XX	
AC	AAU26399;
XX	
DT	18-DEC-2001 (first entry)
XX	
DE	Depression-Associated Protein isoform DPI-184 #2.
XX	
KW	Human; Bipolar Affective Disorder; BAD; Depression-Associated feature; DF; Depression-Associated protein isoform; DPI; Cerebro-spinal fluid; CSF; antidepressant; antianemic; nootropic; tranquiliser; neuroleptic; attention deficit disorder; schizoaffective disorder;
KM	unipolar affective disorder.
XX	
OS	Homo sapiens.
XX	
PN	WO200163294-A2.
XX	
PD	30-AUG-2001.
XX	
PF	23-FEB-2001; 2001WO-GB000791.
XX	
PR	24-FEB-2000; 2000GB-00004412.
XX	
PR	08-DEC-2000; 2000GB-00030050.
XX	
PR	12-DEC-2000; 2000US-0254830P.
XX	

XX	(OXFO-) OXFORD GLYCOSCIENCES UK LTD.
PA	
XX	
PI	Heřařh HMAĆ, Parekh RB, Rohlf C;
XX	
DR	WPI; 2001-582081/65.
XX	
PT	Preparation for diagnosing or treating bipolar affected disorder (BAD) or
PT	unipolar depression, or for screening for modulators, comprises a BAD-
PT	associated protein isoform.
XX	
PS	Claim 8; Page 38; 163pp; English.
XX	
CC	The invention relates to a preparation comprising an isolated Bipolar
CC	Affected Disorder (BAD)-Associated Protein Isoform (DPIs). The DPI's are
CC	used to screen, diagnose or prognosis of BAD or unipolar depression,
CC	determine the stage or severity of BAD or unipolar depression, identify a
CC	subject at risk of developing BAD or unipolar depression, or monitor the
CC	effect of therapy in a subject. They are also used to screen for or
CC	identify agents that interact with a DPI. These agents, antibodies
CC	against the DPIs, and nucleic acids encoding the DPIs are used to treat
CC	or prevent BAD or unipolar depression. Diseases that can be treated are
CC	attention deficient disorder, a schizoaffective disorder, a bipolar or a
CC	unipolar affective disorder. The DPIs are used in proteomics. The
CC	proteomic approach of using DPIs for screening, diagnosis or prognosis of
CC	BAD or unipolar depression overcomes the problems of using gene
CC	expression analysis, such as not being able to obtain central nervous
CC	system (CNS) tissue from a living patient under normal circumstances. The
CC	present sequence is a DIP increased in the CSF (cerebro-spinal fluid) of
CC	subjects having BAD
XX	
SQ	Sequence 10 AA;
Query Match	49.4%; Score 41; DB 4; Length 10;
Best Local Similarity	70.0%; Pred. No. 0.99;
Matches	7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Oy	3 LVMGVPPYGR 12
	:
Db	1 LVMGIPFGR 10
RESULT 14	
AAU26439	
ID	AAU26439 standard; peptide; 10 AA.
XX	
AC	AAU26439;
XX	
DT	18-DEC-2001 (first entry)
XX	
DE	Depression-Associated Protein isoform DPI-234.
XX	
KM	Human, Bipolar Affective Disorder; BAD, Depression-Associated feature;
KM	DP; Depression-Associated protein isoform; DPI; Cerebro-spinal fluid;
KM	CSF; antidepressant; antimanic; nootropic; tranquilizer; neuroleptic;
KM	attention deficient disorder; schizoaffective disorder;
XX	unipolar affective disorder.
XX	
OS	Homo sapiens.
XX	
PN	WO200163294-A2.
XX	
PD	30-AUG-2001.
XX	
PF	23-FEB-2001; 2001WO-GB000791.
XX	
PR	24-FEB-2000; 2000GB-00004412.
PR	08-DEC-2000; 2000GB-00030050.
PR	12-DEC-2000; 2000US-0254830P.
XX	
PA	(OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX	
PI	Herath HMAĆ, Parekh RB, Rohlf C;

PT	unipolar depression, or for screening for modulators, comprises a BAD-
PT	associated protein isoform.
XX	
PS	Claim 8; Page 33; 163pp; English.
CC	The invention relates to a preparation comprising an isolated Bipolar
CC	Affected Disorder (BAD)-Associated Protein Isoform (DPIs). The DPI's are
CC	used to screen, diagnose or prognose of BAD or unipolar depression,
CC	determine the stage or severity of BAD or unipolar depression, identify a
CC	subject at risk of developing BAD or unipolar depression, or monitor the
CC	effect of therapy in a subject. They are also used to screen for or
CC	identify agents that interact with a DPI. These agents, antibodies
CC	against the DPIs, and nucleic acids encoding the DPIs are used to treat
CC	or prevent BAD or unipolar depression. Diseases that can be treated are
CC	attention deficient disorder, a schizoaffective disorder, a bipolar or a
CC	unipolar affective disorder. The DPIs are used in proteomics. The
CC	proteomic approach of using DPIs for screening, diagnosis or prognosis of
CC	BAD or unipolar depression overcomes the problems of using gene
CC	expression analysis, such as not being able to obtain central nervous
CC	system (CNS) tissue from a living patient under normal circumstances. The
CC	present sequence is a DIP decreased in the CSF (cerebro-spinal fluid) of
CC	subjects having BAD
SQ	
	Sequence 10 AA;
QY	Query Match 49.4%; Score 41; DB 4; Length 10;
	Best Local Similarity 70.0%; Pred. No. 0.99;
Matches	7; Conservative 2; Mismatches 1; Indels 0; Gaps 0
DB	
	3 LVNGVPPYGR 12 : : 1 LVMGIPFRGR 10
RESULT 16	
ID	AAU15439
	AAU15439 standard; peptide; 10 AA.
AC	AAU15439;
XX	
DT	24-OCT-2001 (first entry)
XX	
DE	Schizophrenia-associated isoform peptide #324.
XX	
KW	Schizophrenia; neuroleptic; diagnostic; neuropsychiatric disorder;
KW	neurological disorder; neuropathy.
XX	
OS	Homo sapiens.
XX	
PN	WO200163293-A2.
PD	
PF	30-AUG-2001.
XX	
PR	23-FEB-2001; 2001MO-GB000783.
XX	
PR	24-FEB-2000; 2000GB-00004415.
XX	
PR	28-DEC-2000; 2000US-00750395.
PA	(OXFO-) OXFORD GLYCOSCENCES UK LTD.
XX	
PI	Herath HMAc, Parekh RB, Rohlf C;
XX	
DR	WPI; 2001-502868/55.
XX	
PT	Diagnosing and monitoring Schizophrenia by detecting the presence of
PT	Schizophrenia Associated Features and Schizophrenia Associated Protein
PT	Isoforms in samples of cerebrospinal fluid.
XX	
PS	Claim 6; Page 35; 160pp; English.
CC	The invention relates to methods and compositions for screening,
CC	diagnosis and prognosis of Schizophrenia. The method involves detecting
CC	the presence of Schizophrenia (SCH) Associated Features (Sfs) and SCH

CC Associated Protein Isoforms (SPIs) in samples, e.g. by electrophoresis,
CC immunosay or hybridisation assay, for diagnosing and monitoring SCH
CC studying the effectiveness of treatments and for identifying potential
CC therapeutic agents. The method is used for (1) screening or diagnosis of
CC SCH and the relative abundance of at least 1 chosen feature correlates
CC with the presence or absence of SCH; and (2) monitoring the effect of
CC therapy administered to a subject with SCH and the relative abundance of
CC at least 1 chosen feature which correlates with the severity of SCH. The
CC expression and activity of the SPIs and related molecules (e.g.
CC secondary messengers) are studied to diagnose SCH, monitor the progress
CC of the disorder and the effectiveness of treatment and as targets to
CC identify and produce potential therapeutic agents for the treatment of
CC SCH. The paucity of detectable neuronal defects distinguishes
CC neuropsychiatric disorders such as SCH from neurological disorders, where
CC manifestations of anatomical and biochemical changes have been identified
CC in many cases. Consequently the identification and characterisation of
CC cellular and/or molecular causative defects and neuropathies are
CC necessary for improved treatment of neuropsychiatric disorders. AAU15114-
CC AAU15762 represent the amino acid sequences of schizophrenia-associated
CC isoforms used in the method of the invention
CC
XX
SQ Sequence 10 AA;

Query Match 49.4%; Score 41; DB 4; Length 10;
Best Local Similarity 70.0%; Pred. No. 0.99;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 3 LVMGVPFYGR 12
|||:|:|
Db 1 LVMGIPFGR 10

RESULT 17
ABBS2306
ID ABBS2306 standard; peptide: 10 AA.

XX ABB52306;

DT 08-FEB-2002 (first entry)

XX Human API-41 cryptic digest peptide #1.

XX Human; neuroprotective; nootropic; gene therapy; vaccine;

KM Alzheimer's disease; Alzheimer's Disease-Associated Feature; AP;

KM Alzheimer's Disease-Associated Protein Isoform; API; cryptic digest;

XX Expression Reference Protein Isoform; ERPI; proteolysis.

XX Homo sapiens.

PN WO200175454-A2.

PD 11-OCT-2001.

XX 03-APR-2001; 2001WO-US010908.

PR 03-APR-2000; 2000US-0194504P.

XX 28-NOV-2000; 2000US-0253647P.

PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

PI (PFIZ) PFIZER INC.

XX Durham UK, Friedman DL, Herath HMC, Kimmel LH, Parekh RB;

PI Potter DM, Rohlf C, Silber BM, Stiger TR, Sunderland PT;

XX Townsend RR, White F, Williams SA;

XX WPI; 2001-639384/73.

XX Screening for Alzheimer's disease in a mammal, by making two-dimensional

PT array of a feature whose relative abundance correlates with disease, and

XX comparing with abundance of the feature in samples of healthy persons.

CC The invention relates to methods for the screening, diagnosis and
CC prognosis of Alzheimer's disease. The methods involve the detection of
CC Alzheimer's Disease-Associated Features (AFs) and Alzheimer's Disease-
CC Associated Protein Isoforms (APIs) in cerebrospinal fluid, serum or
CC plasma. The abundance of the AFs and APIs is then normalised to an
CC Expression Reference Protein Isoform (ERPI) in order to determine whether
CC a patient is suffering from, or has a predisposition to, Alzheimer's
CC disease. The relative abundance of the AFs and APIs correlates with the
CC severity of Alzheimer's Disease. The present sequence is a peptide
CC produced from an API by proteolysis
CC
XX
SQ Sequence 10 AA;

Query Match 49.4%; Score 41; DB 4; Length 10;
Best Local Similarity 70.0%; Pred. No. 0.99;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 3 LVMGVPFYGR 12
|||:|:|
Db 1 LVMGIPFGR 10

RESULT 18
ABBS9112
ID ABBS9112 standard; peptide: 10 AA.

XX ABR59112;

DT 11-JUL-2003 (first entry)

XX Alzheimer's Disease-associated protein isoform, API-41, SEQ ID 277.

XX Nootropic; Neuroprotective; Alzheimer's disease; API; human;

KM Alzheimer's Disease-associated protein isoform.

XX Homo sapiens.

PN WO2003028543-A2.

PD 10-APR-2003.

XX 03-OCT-2002; 2002WO-US031642.

PR 03-OCT-2001; 2001US-0326708P.

PA (PFIZ) PFIZER PROD INC.

PI (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

XX Durham UK, Friedman DL, Herath HMC, Kimmel LH, Parekh RB;

PI Potter DM, Rohlf C, Silber BM, Snyder PJ, Soares HD, Stiger TR;

XX Sunderland PT, Townsend RR, White WF, Williams SA;

XX WPI; 2003-371957/35.

XX Screening or diagnosing of Alzheimer's disease (AD) determine the stage

PT or severity of AD in a subject, comprises analyzing a test sample of body

PT fluid from the subject by 2-dimensional electrophoresis.

XX Claim 2; Page 51; 179pp; English.

XX The present invention relates to methods for screening or diagnosing

CC Alzheimer's disease (AD) to determine the stage or severity of AD in a

CC subject, to identify subject at risk of developing AD, or to monitor the

CC effect of therapy administered. The methods comprise analysing a test

CC sample of body fluid by 2-dimensional electrophoresis to generate a 2-
CC dimensional array of AD-associated features (AFs). The method
CC alternatively comprises quantitatively detecting in a sample of body
CC fluid from the subject, one or more AD-associated protein isoforms (APIs;
CC ABR58710-ABBS9184)
XX
SQ Sequence 10 AA;

Query Match 49.4%; Score 41; DB 6; Length 10;

Best Local Similarity 70.0%; Pred. No. 0.99;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 LVMGVPPYGR 12
| | | | : | : |
Db 1 LVMGIPTRGR 10

RESULT 19
ADN31951
ID ADN31951 standard; peptide; 10 AA.

XX AC ADN31951;

XX DT 01-JUN-2004 (first entry)

XX DE Human Alzheimer's disease-API tryptic digest peptide - SEQ ID 277.

XX KW Alzheimer's disease; neurotrophic; neuroprotective; cerebrospinal fluid;
XX CSF; Alzheimer's disease-associated protein isoform; API; tryptic digest;
XX human.

XX OS Homo sapiens.

XX PN EP1408333-A2.

XX PD 14-APR-2004.

XX PF 03-OCT-2002; 2002EP-00256893.

XX PR 03-OCT-2002; 2002US-0326708P.

XX PA (PFIZ) PFIZER PROD INC.
(OXFO-) OXFORD GLYCOSCIENCES UK LTD.

XX PI Dutham LK, Friedman DJ, Herath HMA, Kimmel LH, Parekh RB;
PI Poter DM, Rohlf C, Silber BM, Snyder PJ, Soares HD, Stiger TR;

XX PI Sunderland PT, Townsend RR, White WF, Williams SA;

XX DR WPI; 2004-318939/30.

XX PT Screening or diagnosis of Alzheimer's disease (AD) in subject,
XX PT determining stage or severity of AD, identifying subject at risk of
XX PT developing AD, or monitoring effect of therapy, by detecting Alzheimer's
XX PT disease-Associated Features.

XX PS Example; SEQ ID NO 277; 208pp; English.

XX PS The invention relates to a novel method for screening or diagnosis of

XX CC Alzheimer's disease (AD) in a subject, determining the stage or severity

XX CC of AD, identifying a subject at risk of developing AD or monitoring the

XX CC effect of therapy administered to a subject having AD, by analyzing body

XX CC fluid to generate a two-dimensional array of Alzheimer's disease-

XX CC associated features (AFs) such as AF-200, AF-201, AF-202, AF-203, AF-204,

XX CC AF-205, etc., and comparing the abundance of AFs with a control. The

XX CC method of the invention has neurotrophic and neuroprotective applications

XX CC and may be useful for screening or diagnosis of Alzheimer's disease (AD)

XX CC in a subject, determining the stage or severity of AD in a subject

XX CC identifying a subject at risk of developing AD or monitoring the effect

XX CC of therapy administered to a subject having AD. The body fluid is

XX CC cerebrospinal fluid (CSF). The current sequence is that of a human

XX CC Alzheimer's disease-associated protein isoform (API) tryptic digest

XX SQ Sequence 10 AA;

Query Match 49.4%; Score 41; DB 8; Length 10;

Best Local Similarity 70.0%; Pred. No. 0.99;

Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 LVMGVPPYGR 12
| | | | : | : |
Db 1 LVMGIPTRGR 10

RESULT 20

AD078706
ID AD078706 standard; peptide; 10 AA.

XX AC AD078706;

XX DT 26-AUG-2004 (first entry)

XX DE Schizophrenia-Associated Protein Isoform (SPI) seqid 324.

XX KW neuroleptic; Schizophrenia; immunospecific binding;

XX KW Schizophrenia-Associated Protein Isoform; SPI; schizophrenia screening;

XX KW Schizophrenia diagnosis; schizophrenia prognosis;

XX KW Schizophrenia treatment; drug development; cerebrospinal fluid; human.

XX OS Homo sapiens.

XX PN US2004110938-A1.

XX PD 10-JUN-2004.

XX PF 23-FEB-2001; 2001US-00791377.

XX PR 24-FEB-2000; 2000GB-00044156.

XX PR 28-DEC-2000; 2000US-00750395.

XX PA (PAREK) PAREKH R B.

XX PA (HERA/) CHANDRASIRI HERATH H M A.

XX PA (ROHL/) ROHLFF C.

XX PA (TERR/) TERRETT J A.

XX PA (TYSO/) TYSON K L.

XX PI Parekh RB, Chandrasiri Herath HMA, Rohlf C, Terrett JA, Tyson KL;

XX DR WPI; 2004-440403/41.

XX PT New isolated nucleic acid molecule, useful for diagnosing Schizophrenia,

XX PT for monitoring the effectiveness of Schizophrenia treatment or for

XX PT screening agents for treating Schizophrenia.

XX PS Disclosure; SEQ ID NO 324; 170pp; English.

XX CC The invention describes an isolated nucleic acid molecule (I) that

XX CC hybridizes to two short nucleic acid sequences and the 1515 amino acid

XX CC sequence fully defined in the specification. Also described are: a

XX CC preparation comprising an isolated peptide coded for by the nucleic acid

XX CC molecule above, or comprising an isolated human protein comprising one or

XX CC more of the following sequences: Glu-Leu-Asp-Val-Leu-Gln-Gly-Arg, and Gly

XX CC -Ile-Leu-Ile-Leu-Gly-Gln-Gln-Asp-Thr-Leu-Gly-Gly-Arg; methods for

XX CC diagnosing Schizophrenia; antibodies capable of immunospecific binding to

XX CC Schizophrenia-Associated Protein Isoform (SPI); methods of treating

XX CC Schizophrenia; and methods of screening for agents that modulate a

XX CC characteristic (e.g., expression or binding activity) of an SPI, an SPI

XX CC analogue, or an SPI-related polypeptide. The nucleic acid molecule and

XX CC encoded proteins, as well as the methods and compositions are useful for

XX CC screening, diagnosing, and prognosis Schizophrenia, for monitoring the

XX CC effectiveness of Schizophrenia treatment, for identifying patients most

XX CC likely to respond to a particular therapeutic treatment and for

XX CC developing drug. They are also useful for screening modulators of

XX CC Schizophrenia-Associated Protein Isoform useful for treating

XX CC Schizophrenia. This is the amino acid sequence a schizophrenia-associated

XX CC protein isoform increased in the cerebrospinal fluid of schizophrenia

XX CC patients.

XX SQ Sequence 10 AA;

Query Match 49.4%; Score 41; DB 8; Length 10;

Best Local Similarity 70.0%; Pred. No. 0.99;

Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 LVMGVPPYGR 12
| | | | : | : |
Db 1 LVMGIPTRGR 10

Db 1 LVMGIFTRGR 10

RESULT 21

ADRL9350 ADR19350 standard; peptide; 10 AA.

XX ADR19350;

XX 04-NOV-2004 (first entry)

DE TRPI derived human tryptic digest peptide, SEQ ID 12.

XX Tissue damage; chronic; tissue repair-associated protein isoform; TRPI;
XX antiulcer; vulnery; chronic dermal ulcer; human; tryptic digest;
XX proteolysis; trypsin.

OS Homo sapiens.

XX WO2004069795-A2.

XX 19-AUG-2004.

XX 02-FEB-2004; 2004WO-US002881.

XX 03-FEB-2003; 2003US-0444600P.

XX (PRIZ) PEIZER PROD INC.

XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

XX But R, Rumpel K, Williams-Jones BI, Herath HMAC, Rohlf C;

XX Bruce JA, Patel TP;

XX WPI; 2004-604404/58.

PT Diagnosing, or monitoring the effect of therapy of, chronic tissue damage
PT (e.g. chronic dermal ulcer) comprises detecting and/or quantifying tissue
PT Repair-Associated protein isoform in a sample (e.g. wound exudate) from
PT the subject.

XX Claim 7; SEQ ID NO 12; 107pp; English.

XX The invention relates to a novel method for assessing, screening,
XX diagnosing or prognosing chronic tissue damage in a subject, identifying
XX a subject at risk of developing chronic tissue damage, or monitoring the
XX effect of therapy administered to a subject having chronic tissue damage.
XX The method comprises detecting and/or quantifying in a biological sample
XX from the subject a tissue repair-associated protein isoform (TRPI), given
XX in the specification. The invention further comprises: an isolated or
XX recombinant TRPI selected from the proteins listed in the specification;
XX screening for or identifying an agent capable of modulating the
XX expression or activity of the TRPI or a TRPI-related polypeptide; a
XX pharmaceutical composition comprising the TRPI cited above or an active
XX agent that modulates the expression and/or activity of the TRPI or a TRPI
XX -related polypeptide, and a pharmaceutical carrier, vehicle or diluent;
XX and treating chronic tissue damage. The novel compositions have antiulcer
XX and vulnery activity. The composition and methods are useful for
XX diagnosing, preventing, prognosing and treating chronic tissue damage,
XX such as a chronic dermal ulcer. These may also be used for drug screening
XX or drug development, or for screening or identifying agents capable of
XX modulating the activity of TRPI or TRPI-related polypeptides. This
XX sequence represents a TRPI derived human tryptic digest peptide. The
XX peptide was produced by proteolysis using trypsin of a tissue repair-
XX associated protein isoform of the invention.

XX Sequence 10 AA;

Query Match 49.4%; Score 41; DB 8; Length 10;
Best Local Similarity 70.0%; Pred. NO. 0.99;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 LVMGVFPYGR 12

Db 1 LVMGIFTRGR 10

RESULT 22

ADL26337 ADL26337 standard; peptide; 15 AA.

XX ADL26337;

XX 17-JUN-2004 (first entry)

DE Synthetic peptide C128 derived from a conserved region of HCV.

XX HCV, hepatitis C virus; virucide; vaccine; MHC, HLA;
XX major histocompatibility complex; human leukocyte antigen.

XX Synthetic.

XX WO2004024182-A2.

XX 25-MAR-2004.

XX 27-AUG-2003; 2003WO-EP009482.

XX 13-SEP-2002; 2002AT-00001376.

XX 27-FEB-2003; 2003WO-EP002005.

XX 11-JUL-2003; 2003EP-00450171.

XX (INTE-) INTERCELL AG.

XX Buschle M, Habel A, Klade C, Mattner F, Ocava O, Vytvrska O;

XX Zauner W, Zinke S, Kiriappos H;

XX WPI; 2004-269899/25.

PT Isolating Hepatitis C Virus peptides (HPS) which have a binding capacity
PT to a MHC/HLA molecule or a complex comprising the HCV-peptide and the
PT molecule by separating the complex from the HCV-peptides which do not
PT bind to the molecule.

XX Example 1; Page 31; 73pp; English.

XX The invention relates to a novel method for isolating Hepatitis C Virus
XX (HCV) peptides (HPS). The method of the invention has virucide activity,
XX and may be useful in producing a vaccine. The method is useful for
XX isolating Hepatitis C Virus peptides (HPS) which have a binding capacity
XX to a MHC/HLA molecule or a complex comprising the HCV-peptide and the
XX MHC/HLA molecule for preparing a vaccine against HCV infection. The T
XX cells, a T cell clone or a T cell population or preparation is useful for
XX identifying heteroclitic epitopes or for preparing a composition for
XX treating HCV infection. The present sequence represents a synthetic
XX peptide derived from a conserved region of HCV.

XX Sequence 15 AA;

Query Match 48.2%; Score 40; DB 8; Length 15;
Best Local Similarity 54.5%; Pred. NO. 2.4;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 7 VPFYGRAXST 17
Db 4 IPFYGRAXST 14

RESULT 23

ADV22957 ADV22957 standard; peptide; 18 AA.

XX ADV22957;

XX 10-MAR-2005 (first entry)

DE HCV H77 immunogenic peptide #198.
 XX
 KW Vaccine; virucide; antigen; autoimmune disease; infection;
 KW immune modulation; cancer; neoplasm; cytostatic; melanoma; lung tumor;
 KW breast tumor; uterine cervix tumor; prostatic cancer; colon tumor;
 KW pancreas tumor; stomach tumor; bladder tumor; kidney tumor;
 KW hodgekin's lymphoma.
 XX
 OS Hepatitis C virus strain H77.
 XX
 PN WO2004108753-A1.
 XX
 PD 16-DEC-2004.
 XX
 PE 10-JUN-2004; 2004WO-AU000775.
 XX
 PR 10-JUN-2003; 2003AU-00902875.
 PR 25-MAR-2004; 2004AU-00901589.
 XX
 PA (UYME) UNIV MELBOURNE.
 XX
 PI Kent SJ;
 DR WPI; 2005-031657/03.
 PT Use of at least one set of peptides in the preparation of a medicament
 PT for modulating an immune response, and for treating cancer or yeast,
 PT viral, bacterial, protozoal and mycoplasma infections.
 PT
 XX
 PS Disclosure; SEQ ID NO 1377; 645pp; English.
 XX
 CC The invention relates to the use of at least one set of peptides in the
 CC preparation of a medicament for modulating an immune response, where
 CC individual peptides of a respective set comprise different portions of an
 CC amino acid sequence corresponding to a single polypeptide of interest and
 CC display partial sequence identity or similarity to at least one other
 CC peptide of the same set of peptides (i.e. they are overlapping). Also
 CC included are an antigen-presenting cell which has been contacted with the
 CC peptides above and thus presents the peptides, a population of such
 CC antigen-presenting cells, a process for producing antigen-presenting
 CC cells for modulating an immune response to a polypeptide of interest, a
 CC method for producing antigen-specific lymphocytes, a composition
 CC comprising at least one set of the peptides (and a carrier and/or
 CC diluent), a method for modulating an immune response to a polypeptide of
 CC interest comprising administering to a patient in need at least one set
 CC of the peptides, a method for treatment and/or prophylaxis of a disease
 CC or condition associated with the presence of a polypeptide of interest
 CC and a composition of matter for modulating an immune response in a
 CC subject to a target antigen. The polypeptide of interest is also a
 CC disease- or condition-associated polypeptide that is a polypeptide
 CC produced by a pathogenic organism or a cancer, and produced by a
 CC pathogenic organism selected from yeast, viruses, bacteria, helminths,
 CC protozoans and mycoplasmas. The disease- or condition-associated
 CC polypeptide is produced by a cancer selected from melanoma, lung cancer,
 CC breast cancer, cervical cancer, prostate cancer, colon cancer, pancreatic
 CC cancer, stomach cancer, bladder cancer, kidney cancer, post transplant
 CC lymphoproliferative disease (PTLD) or Hodgekin's lymphoma. The uncultured
 CC antigen-presenting cells or their precursors are useful in the
 CC preparation of a medicament for the treatment of a disease or condition
 CC in a subject, which disease or condition is associated with the presence
 CC or aberrant expression of a target antigen, where the antigen-presenting
 CC cells or their precursors have not been subjected to activating
 CC conditions but have been contacted with an antigen that corresponds to
 CC the target antigen to express a processed or modified form of the antigen
 CC for presentation to the subject's immune system. The present sequence is
 CC one of a set of overlapping immunogenic peptides derived from a Hepatitis
 CC C virus protein.
 XX
 SQ Sequence 18 AA;
 Query Match 48.2%; Score 40; DB 9; Length 18;
 Best Local Similarity 54.5%; Pred. No. 3;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 7 VPEYGRAXSIE 17
 :||||:|:|
 Db 8 IPFYKALPLE 18
 RESULT 24
 ADV22958
 ID ADV22958 standard; peptide; 18 AA.
 XX
 AC ADV22958;
 XX
 DT 10-MAR-2005 (first entry)
 XX
 DE HCV H77 immunogenic peptide #199.
 XX
 KW Vaccine; virucide; antigen; autoimmune disease; infection;
 KW immune modulation; cancer; neoplasm; cytostatic; melanoma; lung tumor;
 KW breast tumor; uterine cervix tumor; prostatic cancer; colon tumor;
 KW pancreas tumor; stomach tumor; bladder tumor; kidney tumor;
 KW hodgekin's lymphoma.
 KW
 OS Hepatitis C virus strain H77.
 XX
 PN WO2004108753-A1.
 XX
 PD 16-DEC-2004.
 XX
 PE 10-JUN-2004; 2004WO-AU000775.
 XX
 PR 10-JUN-2003; 2003AU-00902875.
 PR 25-MAR-2004; 2004AU-00901589.
 XX
 PA (UYME) UNIV MELBOURNE.
 XX
 PI Kent SJ;
 DR WPI; 2005-031657/03.
 PT Use of at least one set of peptides in the preparation of a medicament
 PT for modulating an immune response, and for treating cancer or yeast,
 PT viral, bacterial, protozoal and mycoplasma infections.
 PT
 XX
 PS Disclosure; SEQ ID NO 1378; 645pp; English.
 XX
 CC The invention relates to the use of at least one set of peptides in the
 CC preparation of a medicament for modulating an immune response, where
 CC individual peptides of a respective set comprise different portions of an
 CC amino acid sequence corresponding to a single polypeptide of interest and
 CC display partial sequence identity or similarity to at least one other
 CC peptide of the same set of peptides (i.e. they are overlapping). Also
 CC included are an antigen-presenting cell which has been contacted with the
 CC peptides above and thus presents the peptides, a population of such
 CC antigen-presenting cells, a process for producing antigen-presenting
 CC cells for modulating an immune response to a polypeptide of interest, a
 CC method for producing antigen-specific lymphocytes, a composition
 CC comprising at least one set of the peptides (and a carrier and/or
 CC diluent), a method for modulating an immune response to a polypeptide of
 CC interest comprising administering to a patient in need at least one set
 CC of the peptides, a method for treatment and/or prophylaxis of a disease
 CC or condition associated with the presence of a polypeptide of interest
 CC and a composition of matter for modulating an immune response in a
 CC subject to a target antigen. The polypeptide of interest is also a
 CC disease- or condition-associated polypeptide that is a polypeptide
 CC produced by a pathogenic organism or a cancer, and produced by a
 CC pathogenic organism selected from yeast, viruses, bacteria, helminths,
 CC protozoans and mycoplasmas. The disease- or condition-associated
 CC polypeptide is produced by a cancer selected from melanoma, lung cancer,
 CC breast cancer, cervical cancer, prostate cancer, colon cancer, pancreatic
 CC cancer, stomach cancer, bladder cancer, kidney cancer, post transplant
 CC lymphoproliferative disease (PTLD) or Hodgekin's lymphoma. The uncultured
 CC antigen-presenting cells or their precursors are useful in the
 CC preparation of a medicament for the treatment of a disease or condition

CC in a subject, which disease or condition is associated with the presence
 CC or aberrant expression of a target antigen, where the antigen-presenting
 CC cells or their precursors have not been subjected to activating
 CC conditions but have been contacted with an antigen that corresponds to
 CC the target antigen to express a processed or modified form of the antigen
 CC for presentation to the subject's immune system. The present sequence is
 CC one of a set of overlapping immunogenic peptides derived from a Hepatitis
 CC C virus protein.

XX
 XX
 SQ Sequence 18 AA;

Query Match 48.2%; Score 40; DB 9; Length 18;
 Best Local Similarity 54.5%; Pred. No. 3;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 7 VPFYGRAXSIE 17
 :|||:|:
 Db 1 IPFYKALPLE 11

RESULT 25

ABR59057 standard; peptide; 10 AA.

XX
 AC ABR59057;

XX
 DT 11-JUL-2003 (first entry)

XX
 DE Alzheimer's Disease-associated protein isoform, API-406, SEQ ID 278.

XX
 KM Nootropic; Neuroprotective; Alzheimer's disease; API; human;

XX
 KM Alzheimer's Disease-associated protein isoform.

XX
 OS Homo sapiens.

XX
 PN WO2003028543-A2.

XX
 PD 10-APR-2003.

XX
 PF 03-OCT-2002; 2002WO-US031642.

XX
 PR 03-OCT-2001; 2001US-0326708P.

XX
 PA (PEIZ.) PEIZER PROD INC.
 (OXFO.) OXFORD GLYCOSCIENCES UK LTD.

XX
 PI Durham UK, Friedman DL, Herath HMA, Kimmel LH, Parekh RB;

XX
 PI Potter DM, Rolf C, Silber BM, Snyder PJ, Soares HD, Stiger TR;

XX
 PI Sunderland PT, Townsend RR, White WF, Williams SA;

XX
 DR WPI; 2003-371957/35.

XX
 PT Screening or diagnosing of Alzheimer's disease (AD) determine the stage
 PT or severity of AD in a subject, comprises analyzing a test sample of body
 PT fluid from the subject by 2-dimensional electrophoresis.

XX
 PS Claim 2; Page 47; 179pp; English.

XX
 CC The present invention relates to methods for screening or diagnosing
 CC Alzheimer's disease (AD) to determine the stage or severity of AD in a
 CC subject, to identify subject at risk of developing AD, or to monitor the
 CC effect of therapy administered. The methods comprise analyzing a test
 CC sample of body fluid by 2-dimensional electrophoresis to generate a 2-
 CC dimensional array of AD-associated features (AFs). The method
 CC alternatively comprises quantitatively detecting in a sample of body
 CC fluid from the subject, one or more AD-associated protein isoforms (APIs;
 CC ABR58710-ABR59184)

XX
 SQ Sequence 10 AA;

Query Match 47.0%; Score 39; DB 6; Length 10;
 Best Local Similarity 70.0%; Pred. No. 2.4;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 LVMGVPPYGR 12
 :|||:|:
 Db 1 LVMGLPTFR 10

Search completed: January 26, 2006, 07:58:05
 Job time : 61.7414 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 26, 2006, 07:50:06 : Search time 15.9741 Seconds
(without alignments)
87.985 Million cell updates/sec

Title: US-09-662-293-10

Perfect score: 83

Sequence: 1 DKLVGVFVYGRAXSIE 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 229350

Minimum DB seq length: 0

Maximum DB seq length: 21

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Issued Patents AA: *
1: /cgn2_6/ptodata/1/aa/5 COMB.pep: *
2: /cgn2_6/ptodata/1/aa/6 COMB.pep: *
3: /cgn2_6/ptodata/1/aa/H_COMB.pep: *
4: /cgn2_6/ptodata/1/aa/PTUS_COMB.pep: *
5: /cgn2_6/ptodata/1/aa/RE_COMB.pep: *
6: /cgn2_6/ptodata/1/aa/backfiles.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	81	97.6	17	US-09-292-225-10	Sequence 10, Appl
2	47	56.6	16	US-09-171-705-39	Sequence 39, Appl
3	47	56.6	16	US-09-657-757-39	Sequence 39, Appl
4	36	43.4	16	US-09-171-705-40	Sequence 40, Appl
5	36	43.4	16	US-09-657-757-40	Sequence 40, Appl
6	35	42.2	8	US-09-311-784A-273	Sequence 273, Appl
7	35	42.2	8	US-08-635-886C-146	Sequence 146, Appl
8	35	42.2	8	US-08-974-690C-146	Sequence 146, Appl
9	35	42.2	8	US-08-974-685-146	Sequence 146, Appl
10	34	41.0	13	US-09-709-947-1	Sequence 1, Appl
11	34	41.0	13	US-08-851-843A-171	Sequence 171, Appl
12	34	41.0	15	US-08-974-549A-291	Sequence 291, Appl
13	34	41.0	15	US-08-854-050-171	Sequence 171, Appl
14	34	41.0	15	US-09-403-181B-291	Sequence 171, Appl
15	34	41.0	15	US-09-403-181B-291	Sequence 291, Appl
16	34	41.0	15	US-09-721-456-291	Sequence 291, Appl
17	34	41.0	15	US-09-766-253-171	Sequence 171, Appl
18	34	41.0	15	US-10-054-295-171	Sequence 171, Appl
19	34	41.0	15	US-09-438-486A-171	Sequence 171, Appl
20	34	41.0	16	US-09-171-705-38	Sequence 38, Appl
21	34	41.0	16	US-09-657-757-38	Sequence 38, Appl
22	31	37.3	8	US-08-444-818-420	Sequence 420, Appl
23	31	37.3	11	US-10-038-972A-4	Sequence 4, Appl
24	31	37.3	12	5460961-8	Patent No. 5460961
25	30	36.1	10	US-08-968-542C-22	Sequence 22, Appl
26	30	36.1	10	US-09-554-467A-22	Sequence 22, Appl
27	30	36.1	19	US-09-499-203-7	Sequence 7, Appl

28	30	36.1	19	US-10-117-846-33	Sequence 33, Appl
29	30	36.1	20	US-08-564-972-23	Sequence 23, Appl
30	29	34.9	14	US-09-731-092-3	Sequence 3, Appl
31	29	34.9	15	US-10-264-303-12	Sequence 12, Appl
32	29	34.9	16	US-09-543-608A-40	Sequence 40, Appl
33	29	34.9	16	US-09-239-043D-2574	Sequence 2574, Ap
34	29	34.9	16	US-09-935-430-653	Sequence 653, App
35	29	34.9	17	US-08-166-266-7	Sequence 7, Appl
36	28	33.7	9	US-09-644-600-93	Sequence 93, Appl
37	28	33.7	9	US-09-654-600A-93	Sequence 93, Appl
38	28	33.7	14	US-08-482-228-20	Sequence 20, Appl
39	28	33.7	14	US-08-482-528-20	Sequence 20, Appl
40	28	33.7	19	US-08-480-229C-15	Sequence 15, Appl
41	28	33.7	19	US-08-659-235C-15	Sequence 15, Appl
42	28	33.7	20	US-09-962-756-751	Sequence 751, App
43	28	33.7	20	US-09-962-756-905	Sequence 905, App
44	27	32.5	8	US-08-988-842-17	Sequence 27, Appl
45	27	32.5	8	US-08-635-886C-147	Sequence 147, App
46	27	32.5	8	US-08-974-690C-147	Sequence 147, App
47	27	32.5	8	US-08-974-685-147	Sequence 147, App
48	27	32.5	11	US-10-038-972A-2	Sequence 2, Appl
49	27	32.5	12	US-08-705-660-25	Sequence 25, Appl
50	27	32.5	12	US-08-989-045-25	Sequence 25, Appl
51	27	32.5	12	US-08-475-955-66	Sequence 66, Appl
52	27	32.5	12	US-09-315-355A-25	Sequence 25, Appl
53	27	32.5	12	US-07-867-819D-86	Sequence 86, Appl
54	27	32.5	14	US-10-373-090A-12	Sequence 12, Appl
55	27	32.5	14	5252466-8	Patent No. 5252466
56	27	32.5	16	US-08-974-549A-78	Sequence 78, Appl
57	27	32.5	16	US-08-912-951-78	Sequence 78, Appl
58	27	32.5	16	US-09-402-181B-78	Sequence 78, Appl
59	27	32.5	16	US-09-721-456-78	Sequence 78, Appl
60	27	32.5	19	US-09-441-502B-66	Sequence 66, Appl
61	27	32.5	19	US-10-117-846-30	Sequence 30, Appl
62	27	32.5	19	US-10-117-846-31	Sequence 31, Appl
63	27	32.5	20	US-10-117-846-34	Sequence 34, Appl
64	27	32.5	20	US-09-962-756-833	Sequence 833, App
65	27	32.5	20	US-09-962-756-834	Sequence 834, App
66	26	31.3	6	US-08-287-717-14	Sequence 14, Appl
67	26	31.3	6	US-08-441-914-14	Sequence 14, Appl
68	26	31.3	6	US-09-623-548A-1092	Sequence 1092, Ap
69	26	31.3	6	US-09-657-276-1092	Sequence 6, Appl
70	26	31.3	8	US-10-038-972A-6	Sequence 47, Appl
71	26	31.3	9	US-09-239-043D-47	Sequence 803, Appl
72	26	31.3	9	US-09-239-043D-803	Sequence 1591, Ap
73	26	31.3	9	US-09-239-043D-1591	Sequence 1591, Ap
74	26	31.3	10	US-08-983-157B-26	Sequence 26, Appl
75	26	31.3	10	US-09-239-043D-1194	Sequence 1194, Ap
76	26	31.3	11	US-08-557-146-17	Sequence 156, App
77	26	31.3	11	US-09-154-344-17	Sequence 17, Appl
78	26	31.3	11	US-09-154-344-17	Sequence 17, Appl
79	26	31.3	11	US-09-239-043D-107	Sequence 107, App
80	26	31.3	11	US-09-239-043D-957	Sequence 957, App
81	26	31.3	11	US-09-239-043D-1676	Sequence 1676, Ap
82	26	31.3	11	US-10-038-972A-5	Sequence 5, Appl
83	26	31.3	14	US-08-679-805A-4	Sequence 4, Appl
84	26	31.3	14	US-08-842-799-4	Sequence 4, Appl
85	26	31.3	14	PCT-US96-11458-4	Sequence 6, Appl
86	26	31.3	15	US-09-295-186-6	Sequence 2124, Ap
87	26	31.3	15	US-09-239-043D-2124	Sequence 38, Appl
88	26	31.3	15	US-09-112-524D-38	Sequence 25, Appl
89	26	31.3	16	US-08-313-565-25	Sequence 10, Appl
90	26	31.3	16	US-08-679-405-10	Sequence 10, Appl
91	26	31.3	16	US-08-679-405-10	Sequence 10, Appl
92	26	31.3	16	US-08-842-799-10	Sequence 10, Appl
93	26	31.3	16	PCT-US96-11458-10	Sequence 10, Appl
94	26	31.3	17	US-08-940-577-1	Sequence 3, Appl
95	26	31.3	17	US-10-117-846-32	Sequence 1117, Ap
96	26	31.3	20	US-09-962-756-1117	Sequence 1761, Ap
97	26	31.3	20	US-09-962-756-1161	Sequence 593, App
98	26	31.3	21	US-09-962-756-593	Sequence 659, App
99	26	31.3	21	US-09-962-756-659	
100	26	31.3	21	US-09-962-756-659	

ALIGNMENTS

RESULT 1

US-09-292-225-10
; Sequence 10, Application US/09292225
; Patent No. 6455686
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: AU-2-C3
; CURRENT APPLICATION NUMBER: US/09/292,225
; CURRENT FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: 60/098,909
; EARLIER FILING DATE: 1998-09-02
; EARLIER APPLICATION NUMBER: 60/085,295
; EARLIER FILING DATE: 1998-05-13
; EARLIER APPLICATION NUMBER: 60/098,565
; EARLIER FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: 09/062,013
; EARLIER FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
; FEATURE:
; OTHER INFORMATION: At location 14, Xaa = any amino acid
US-09-292-225-10

Query Match

Best Local Similarity 97.6%; Score 81; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKLVMGVPPYGRXSIE 17
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Db 1 DKLVMGVPPYGRXSIE 17

RESULT 2

US-09-171-705-39
; Sequence 39, Application US/09171705
; Patent No. 6184204
; GENERAL INFORMATION:
; APPLICANT: BOOTS, ANNA M.H.
; APPLICANT: VERHEIDEN, GILBERTUS F.M.
; TITLE OF INVENTION: NOVEL PEPTIDES SUITABLE FOR USE IN ANTIGEN SPECIFIC
; TITLE OF INVENTION: IMMUNOSUPPRESSIVE THERAPY
; FILE REFERENCE: O/96198 US
; CURRENT APPLICATION NUMBER: US/09/171,705
; CURRENT FILING DATE: 1999-02-09
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DERIVED FROM
; OTHER INFORMATION: SEQUENCE OF HUMAN CARTILAGE (HC) -39 PROTEIN
US-09-171-705-39

Query Match

Best Local Similarity 56.6%; Score 47; DB 2; Length 16;
Best Local Similarity 66.7%; Pred. No. 0.037;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 KLMVGVPFYGRA 13

Db 4 KLMVGIPFGRS 15
|||||
|||

RESULT 3

US-09-657-757-39
; Sequence 39, Application US/09657757
; Patent No. 6881824
; GENERAL INFORMATION:
; APPLICANT: BOOTS, ANNA M.H.
; APPLICANT: VERHEIDEN, GILBERTUS F.M.
; TITLE OF INVENTION: NOVEL PEPTIDES SUITABLE FOR USE IN ANTIGEN SPECIFIC
; TITLE OF INVENTION: IMMUNOSUPPRESSIVE THERAPY
; FILE REFERENCE: O/96198 US
; CURRENT APPLICATION NUMBER: US/09/657,757
; CURRENT FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: US/09/171,705
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DERIVED FROM
; OTHER INFORMATION: SEQUENCE OF HUMAN CARTILAGE (HC) -39 PROTEIN
US-09-657-757-39

Query Match

Best Local Similarity 56.6%; Score 47; DB 2; Length 16;
Best Local Similarity 66.7%; Pred. No. 0.037;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 KLMVGVPFYGRA 13
|||||
Db 4 KLMVGIPFGRS 15

RESULT 4

US-09-171-705-40
; Sequence 40, Application US/09171705
; Patent No. 6184204
; GENERAL INFORMATION:
; APPLICANT: BOOTS, ANNA M.H.
; APPLICANT: VERHEIDEN, GILBERTUS F.M.
; TITLE OF INVENTION: NOVEL PEPTIDES SUITABLE FOR USE IN ANTIGEN SPECIFIC
; TITLE OF INVENTION: IMMUNOSUPPRESSIVE THERAPY
; FILE REFERENCE: O/96198 US
; CURRENT APPLICATION NUMBER: US/09/171,705
; CURRENT FILING DATE: 1999-02-09
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DERIVED FROM
; OTHER INFORMATION: SEQUENCE OF HUMAN CARTILAGE (HC) -39 PROTEIN
US-09-171-705-40

Query Match

Best Local Similarity 43.4%; Score 36; DB 2; Length 16;
Best Local Similarity 41.7%; Pred. No. 4.2;
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 5 MGVPPYGRXSIE 16
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Db 1 MGIPTFGRSFTL 12

RESULT 5

US-09-657-757-40
; Sequence 40, Application US/09657757

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; Patent No. 6881824
; GENERAL INFORMATION:
; APPLICANT: BOOTS, ANNA M.H.
; APPLICANT: VERHEIJDEN, GILBERTUS F.M.
; TITLE OF INVENTION: NOVEL PEPTIDES SUITABLE FOR USE IN ANTIGEN SPECIFIC
; TITLE OF INVENTION: IMMUNOSUPPRESSIVE THERAPY
; FILE REFERENCE: O/96198 US
; CURRENT APPLICATION NUMBER: US/09/657,757
; CURRENT FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: US/09/171,705
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DERIVED FROM
; OTHER INFORMATION: SEQUENCE OF HUMAN CARTILAGE (HC) -39 PROTEIN
US-09-657-757-40
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Query Match 42.4%; Score 36; DB 2; Length 16;
Best Local Similarity 41.7%; Pred. No. 4.2;
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
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QY 5 MGVPFYGRANSI 16
Db 1 MGIPTFGRSFTL 12
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RESULT 6
US-09-311-784A-273
; Sequence 273, Application US/09311784A
; Patent No. 6534482
; GENERAL INFORMATION:
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: EpiImmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; TITLE OF INVENTION: Immune Response and Methods of Using the Same
; FILE REFERENCE: 39963-2002.01
; CURRENT APPLICATION NUMBER: US/09/311,784A
; CURRENT FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 273
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HCV 1378 (peptide 29.0035)
US-09-311-784A-273
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Query Match 42.2%; Score 35; DB 2; Length 8;
Best Local Similarity 71.4%; Pred. No. 4.6e+05;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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QY 7 VPFYGRA 13
Db 1 IPFYGKA 7
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RESULT 7
US-08-635-886C-146
; Sequence 146, Application US/08635886C
; Patent No. 6555114
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```
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: DELEYS, Robert
; APPLICANT: MAERTENS, Geert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; TITLE OF INVENTION: VIRUS
; FILE REFERENCE: 2752-18
; CURRENT APPLICATION NUMBER: US/08/635,886C
; CURRENT FILING DATE: 1996-04-25
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 146
; LENGTH: 8
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-08-635-886C-146
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Query Match 42.2%; Score 35; DB 2; Length 8;
Best Local Similarity 71.4%; Pred. No. 4.6e+05;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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```
QY 7 VPFYGRA 13
Db 1 IPFYGKA 7
```

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RESULT 8
US-08-974-690C-146
; Sequence 146, Application US/08974690C
; Patent No. 6613333
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: DELEYS, Robert
; APPLICANT: MAERTENS, Geert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; TITLE OF INVENTION: VIRUS
; FILE REFERENCE: 2551-94
; CURRENT APPLICATION NUMBER: US/08/974,690C
; CURRENT FILING DATE: 1997-11-19
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 146
; LENGTH: 8
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-08-974-690C-146
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Query Match 42.2%; Score 35; DB 2; Length 8;
Best Local Similarity 71.4%; Pred. No. 4.6e+05;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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QY 7 VPFYGRA 13
Db 1 IPFYGKA 7
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RESULT 9
US-08-974-685-146
; Sequence 146, Application US/08974685
; Patent No. 6689368
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: DELEYS, ROBERT
; APPLICANT: MAERTENS, GEERT
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF
```

HEPATITIS C VIRUS STRUCTURAL PROTEINS, PROPHYLACTIC AND
THERAPEUTIC COMPOSITIONS CONTAINING THE SAME

NUMBER OF SEQUENCES: 181
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHVE P. C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,685
FILING DATE: 19-NO. 6689368-1997
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS R.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1487-11
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100

INFORMATION FOR SEQ ID NO: 146:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 146:
US-08-974-685-146

Query Match 42.2%; Score 35; DB 2; Length 8;
Best Local Similarity 71.4%; Pred. No. 4.6e+05;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 7 VPFYGRA 13
:||||:
Db 1 IPFYGKA 7

RESULT 10
US-09-709-947-1
Sequence 1, Application US/09709947
Patent No. 6936424
GENERAL INFORMATION:
APPLICANT: Mackinn, Brynmor
TITLE OF INVENTION: Materials and Methods for Detection and Treatment of
FILE REFERENCE: MTP-024
CURRENT APPLICATION NUMBER: US/09/709,947
CURRENT FILING DATE: 2000-11-10
PRIOR APPLICATION NUMBER: US 60/165,173
PRIOR FILING DATE: 1999-11-16
PRIOR APPLICATION NUMBER: US 60/172,170
PRIOR FILING DATE: 1999-12-17
PRIOR APPLICATION NUMBER: US 60/178,860
PRIOR FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/201,721
PRIOR FILING DATE: 2000-05-03
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 1
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:Tryptic peptide
US-09-709-947-1

Query Match 41.0%; Score 34; DB 2; Length 13;
Best Local Similarity 55.6%; Pred. No. 7.9;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 4 VMGVFPYGR 12
:||||:
Db 2 LQGFPPYK 10

RESULT 11
US-08-851-843A-171
Sequence 171, Application US/08851843A
Patent No. 6093809
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6093809e1 Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843A
FILING DATE: 06-MAY-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 171:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..15
OTHER INFORMATION: /note="motif D peptide from human
telomerase core protein 1 (TCp1)"
US-08-851-843A-171

Query Match 41.0%; Score 34; DB 2; Length 15;
Best Local Similarity 77.8%; Pred. No. 9.3;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 LVMGVPPYG 11
Db 4 LVKGVPYEG 12

RESULT 12
US-08-974-549A-291

Sequence 291, Application US/08974549A
Patent No. 6166178

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3634

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/US97/17618

FILING DATE: 01-OCT-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/US97/17885

FILING DATE: 01-OCT-1997

ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph Ted

REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 015389-002610US

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
-INFORMATION FOR SEQ ID NO: 291:

SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:

NAME/KEY: Peptide
LOCATION: 1..15

OTHER INFORMATION: /note="motif D peptide from human
US-08-974-549A-291 telomerase core protein 1 (fcp1)"

Query Match 41.0%; Score 34; DB 2; Length 15;
Best Local Similarity 77.8%; Pred. No. 9.3;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 LVMGVPPYG 11
Db 4 LVKGVPYEG 12

RESULT 13
US-08-854-050-171

Sequence 171, Application US/08854050
Patent No. 6261836

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6261836el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
CLASSIFICATION: 536
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 171:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..15
OTHER INFORMATION: /note= "motif D peptide from human
telomerase core protein 1 (Tcpi)"
US-08-854-050-171

Query Match 41.0%; Score 34; DB 2; Length 15;
Best Local Similarity 77.8%; Pred. No. 9.3;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 3 LMGVPEYG 11
|||
Db 4 LVRGVPEYG 12

RESULT 14
US-09-430-323-171
Sequence 171, Application US/09430323
Patent No. 6309867
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin H.
Andrews, William H.
TITLE OF INVENTION: No. 6309867el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/430,323
FILING DATE: 29-Oct-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 171:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..15
OTHER INFORMATION: /note= "motif D peptide from human
telomerase core protein 1 (Tcpi)"
US-09-430-323-171

Query Match 41.0%; Score 34; DB 2; Length 15;
Best Local Similarity 77.8%; Pred. No. 9.3;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 3 LMGVPEYG 11
|||
Db 4 LVRGVPEYG 12

RESULT 15
US-09-402-181B-291
Sequence 291, Application US/09402181B
Patent No. 6610839
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin H.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/402,181B
FILING DATE: 29-Sep-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997

APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Aueenhue, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 291:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..15
OTHER INFORMATION: /note= "motif D peptide from human telomerase core protein 1 (TCPI)"
SEQUENCE DESCRIPTION: SEQ ID NO: 291:
US-09-402-181B-291

Query Match 41.0%; Score 34; DB 2; Length 15;
Best Local Similarity 77.8%; Pred. No. 9.3;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 LVMGVPPYG 11
Db 4 LVKGVPYEG 12

RESULT 16
US-09-721-456-291
Sequence 291, Application US/09721456
Patent No. 6617110
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-No. 6617110-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 291:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..15
OTHER INFORMATION: /note= "motif D peptide from human telomerase core protein 1 (TCPI)"
SEQUENCE DESCRIPTION: SEQ ID NO: 291:
US-09-721-456-291

Query Match 41.0%; Score 34; DB 2; Length 15;
Best Local Similarity 77.8%; Pred. No. 9.3;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 LVMGVPPYG 11
Db 4 LVKGVPYEG 12

RESULT 17
US-09-766-253-171
Sequence 171, Application US/09766253
Patent No. 6808880
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. 6808880el Telomerase
NUMBER OF SEQUENCES: 171
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/766,253
FILING DATE: 19-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/846,017
FILING DATE: 1997-04-25
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002920US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 171:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..15
OTHER INFORMATION: /note= "motif D peptide from human telomerase core protein 1 (Tcpl)"
SEQUENCE DESCRIPTION: SEQ ID NO: 171:

US-09-766-253-171

Query Match 41.0%; Score 34; DB 2; Length 15;
Best Local Similarity 77.8%; Pred. No. 9.3;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 LVMGVPEYG 11
|||
Db 4 LVKGVPYEG 12

RESULT 18
US-10-054-295-171
Sequence 171, Application US/10054295
Patent No. 6921664
GENERAL INFORMATION:
APPLICANT: Cecch, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: NO. 6921664e1 Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/054,295
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/854,050
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 171:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..15
OTHER INFORMATION: /note= "motif D peptide from human telomerase core protein 1 (Tcpl)"
SEQUENCE DESCRIPTION: SEQ ID NO: 171:

US-10-054-295-171

Query Match 41.0%; Score 34; DB 2; Length 15;
Best Local Similarity 77.8%; Pred. No. 9.3;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 LVMGVPEYG 11
|||
Db 4 LVKGVPYEG 12

RESULT 19
US-09-438-486A-171
Sequence 171, Application US/09438486A
Patent No. 6927285
GENERAL INFORMATION:
APPLICANT: CECH, THOMAS R.
LINGNER, JOACHIM
NAKAMURA, TORU
CHAPMAN, KAREN B.
MORIN, GREGG B.
HARLEY, CALVIN
ANDREWS, WILLIAM H.
TITLE OF INVENTION: GENE FOR HUMAN TELOMERASE REVERSE TRANSCRIPTASE AND
FILE REFERENCE: 018/062
CURRENT APPLICATION NUMBER: US/09/438,486A
CURRENT FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 08/851,843
PRIOR FILING DATE: 1997-05-06
PRIOR APPLICATION NUMBER: 08/846,017
PRIOR FILING DATE: 1997-04-25
PRIOR APPLICATION NUMBER: 08/844,419
PRIOR FILING DATE: 1997-04-18
PRIOR APPLICATION NUMBER: 08/724,643
PRIOR FILING DATE: 1996-10-01
NUMBER OF SEQ ID NOS: 223
SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 171
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Recombinant
OTHER INFORMATION: amino acid sequence
US-09-438-486A-171

Query Match 41.0%; Score 34; DB 2; Length 15;

Best Local Similarity 77.8%; Pred. No. 9.3;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 LVMGVPRYG 11
Db 4 LVRGVPEYX 12

RESULT 20

US-09-171-705-38
; Sequence 38, Application US/09171705
; Patent No. 6184204
; GENERAL INFORMATION:
; APPLICANT: BOOTS, ANNA M.H.
; TITLE OF INVENTION: NOVEL PEPTIDES SUITABLE FOR USE IN ANTIGEN SPECIFIC
; FILE REFERENCE: O/96198 US
; CURRENT APPLICATION NUMBER: US/09/171,705
; CURRENT FILING DATE: 1999-02-09
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 38
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: DERIVED FROM
; OTHER INFORMATION: SEQUENCE OF HUMAN CARTILAGE (HC) -39 PROTEIN
US-09-171-705-38

Query Match 41.0%; Score 34; DB 2; Length 16;
Best Local Similarity 85.7%; Pred. No. 10;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 KLVWGVP 8
Db 10 KLVWGIP 16

RESULT 21
US-09-657-757-38
; Sequence 38, Application US/09657757
; Patent No. 6881824
; GENERAL INFORMATION:
; APPLICANT: BOOTS, ANNA M.H.
; TITLE OF INVENTION: NOVEL PEPTIDES SUITABLE FOR USE IN ANTIGEN SPECIFIC
; FILE REFERENCE: O/96198 US
; CURRENT APPLICATION NUMBER: US/09/657,757
; CURRENT FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: US/09/171,705
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 38
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DERIVED FROM
; OTHER INFORMATION: SEQUENCE OF HUMAN CARTILAGE (HC) -39 PROTEIN
US-09-657-757-38

Query Match 41.0%; Score 34; DB 2; Length 16;
Best Local Similarity 85.7%; Pred. No. 10;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 KLVWGVP 8
Db 10 KLVWGIP 16

RESULT 22
US-08-444-818-420
; Sequence 420, Application US/08444818
; Patent No. 6150087
; GENERAL INFORMATION:
; APPLICANT: Chien, David Y.
; APPLICANT: Ruteer, William J.
; TITLE OF INVENTION: NANBV Diagnostics and Vaccines
; NUMBER OF SEQUENCES: 777
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,818
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,590
; FILING DATE: 14-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Harbin, Alisa A.
; REGISTRATION NUMBER: 33,895
; REFERENCE/DOCKET NUMBER: 0110.002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508)359-3876
; TELEFAX: (508)359-3885
; INFORMATION FOR SEQ ID NO: 420:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-444-818-420

Query Match 37.3%; Score 31; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 4.6e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 7 VPRYGR 12
Db 3 IPFYGK 8

RESULT 23
US-10-038-972A-4
; Sequence 4, Application US/10038972A
; Patent No. 6962815
; GENERAL INFORMATION:
; APPLICANT: J. Bartlett
; TITLE OF INVENTION: AAV VECTORS AND METHODS
; FILE REFERENCE: 28335/3699605
; CURRENT APPLICATION NUMBER: US/10/038,972A
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: US 60/260,124
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

OTHER INFORMATION: Bovine Papilloma Virus Peptide
US-10-038-972A-4

Query Match 37.3%; Score 31; DB 2; Length 11;
Best Local Similarity 60.0%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 6 GVPYGRAXS 15
DB 2 GTPPYLKALS 11

RESULT 24
5460961-8
PATENT NO. 5460961
APPLICANT: DEBY, CAROL; PINCEMAIL, JOEL; BOLLIN, ALEX
TITLE OF INVENTION: HUMAN MYELOPEROXIDASE AND ITS
THERAPEUTIC APPLICATION
NUMBER OF SEQUENCES: 13
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/641,678
FILING DATE: 16-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 460,931
FILING DATE: 14-FEB-1990
SEQ ID NO: 8:
LENGTH: 12
5460961-8

Query Match 37.3%; Score 31; DB 6; Length 12;
Best Local Similarity 83.3%; Pred. No. 26;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 5 MGVPY 10
DB 1 MGVPY 6

RESULT 25
US-08-968-542C-22
SEQUENCE 22, Application US/08968542C
PATENT NO. 5981728
GENERAL INFORMATION:
APPLICANT: Myers, et al.
TITLE OF INVENTION: dulli Codes For A No. 5981728el Starch
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mcgregor & Adler, LLP
STREET: 8011 Candle Lane
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word 6.0.1 for Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/968,542C
FILING DATE: No. 5981728ember 12, 1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benjamin Aaron Adler, Ph.D., J.D.
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D6036
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 777-2321
TELEFAX: (713) 777-6908

INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acid residues
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: amino acid
HYPOTHETICAL: no
ANTI-SENSE: no
FRAGMENT TYPE: internal
US-08-968-542C-22

Query Match 36.1%; Score 30; DB 1; Length 10;
Best Local Similarity 62.5%; Pred. No. 33;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 DKLVGVP 8
DB 1 DKLVGVP 8

Search completed: January 26, 2006, 08:07:02
Job time : 17.1408 secs

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OM protein - protein search, using sw model

Run on: January 26, 2006, 08:04:12 ; Search time 55.25 Seconds
(without alignments)
128.563 Million cell updates/sec

Title: US-09-662-293-10
Perfect score: 83
Sequence: 1 DKLVWGVPFGYGRAXSIE 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 41829326 residues
Total number of hits satisfying chosen parameters: 389445

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published Applications AA Main:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	97.6	17	4	US-10-218-743-10 Sequence 10, App1
2	41	49.4	10	3	US-09-791-378-324 Sequence 324, App
3	41	49.4	10	3	US-09-826-280-321 Sequence 321, App
4	41	49.4	10	3	US-09-791-383-111 Sequence 111, App
5	41	49.4	10	3	US-09-791-389-111 Sequence 111, App
6	41	49.4	10	3	US-09-791-377-324 Sequence 324, App
7	41	49.4	10	3	US-10-264-309-277 Sequence 277, App
8	41	49.4	10	5	US-10-264-309-277 Sequence 277, App
9	39	47.0	10	4	US-10-264-309-278 Sequence 278, App
10	39	47.0	10	5	US-10-264-309-278 Sequence 278, App
11	35	42.2	8	3	US-09-017-743C-3 Sequence 3, App11
12	35	42.2	8	4	US-10-371-525-273 Sequence 273, App
13	35	42.2	8	4	US-10-371-069-273 Sequence 273, App
14	35	42.2	8	4	US-10-371-645-273 Sequence 273, App
15	35	42.2	8	4	US-10-371-260-273 Sequence 273, App
16	35	42.2	8	4	US-10-651-155-146 Sequence 146, App
17	35	42.2	21	5	US-10-886-084-11 Sequence 1, App11
18	34	41.0	15	3	US-09-843-676-171 Sequence 171, App
19	34	41.0	15	3	US-09-766-253-171 Sequence 171, App
20	34	41.0	15	3	US-09-438-486-171 Sequence 171, App
21	34	41.0	15	4	US-10-053-758-171 Sequence 171, App
22	34	41.0	15	4	US-10-054-295-171 Sequence 171, App
23	34	41.0	15	4	US-10-054-611-171 Sequence 171, App
24	34	41.0	15	4	US-10-282-960-70 Sequence 70, App1
25	34	41.0	15	4	US-10-325-810-291 Sequence 291, App
26	34	41.0	15	5	US-10-877-124-291 Sequence 291, App
27	34	41.0	15	5	US-10-877-022-291 Sequence 291, App

28	34	41.0	15	5	US-10-877-146-291 Sequence 291, App
29	33	39.8	12	4	US-10-328-916-47 Sequence 47, App1
30	32	38.6	15	5	US-10-958-216-843 Sequence 843, App
31	32	38.6	18	3	US-09-864-761-42568 Sequence 42568, A
32	31	37.3	11	4	US-10-038-972A-4 Sequence 4, App11
33	31	37.3	20	3	US-09-864-761-41147 Sequence 41147, A
34	30	36.1	10	4	US-10-634-262-22 Sequence 22, App1
35	30	36.1	15	5	US-10-715-810-45 Sequence 45, App1
36	30	36.1	19	4	US-10-117-846-33 Sequence 33, App1
37	29	34.9	19	4	US-10-417-280A-7 Sequence 26, App1
38	29	34.9	11	3	US-09-965-967-76 Sequence 3, App11
39	29	34.9	14	3	US-09-731-092-3 Sequence 3, App11
40	29	34.9	15	3	US-10-423-855-3 Sequence 2757, App
41	29	34.9	15	3	US-09-880-748-2757 Sequence 12, App1
42	29	34.9	15	4	US-10-264-303-12 Sequence 2757, App
43	29	34.9	15	4	US-10-293-418-2757 Sequence 653, App
44	29	34.9	16	3	US-09-935-430-653 Sequence 1483, App
45	29	34.9	16	3	US-09-932-165-1483 Sequence 711, App
46	29	34.9	16	3	US-09-935-384-711 Sequence 712, App
47	29	34.9	16	3	US-09-942-052-712 Sequence 1405, App
48	29	34.9	16	4	US-10-001-469-1405 Sequence 34, App1
49	29	34.9	16	4	US-10-116-118-34 Sequence 762, App
50	29	34.9	16	4	US-10-062-109A-762 Sequence 762, App
51	29	34.9	16	4	US-10-005-480A-762 Sequence 653, App
52	29	34.9	16	4	US-10-277-292-653 Sequence 27, App1
53	29	34.9	16	4	US-10-291-241-27 Sequence 27, App1
54	29	34.9	16	4	US-10-280-340-653 Sequence 653, App
55	29	34.9	16	4	US-10-147-368-41 Sequence 41, App1
56	29	34.9	16	4	US-10-099-460-21 Sequence 21, App1
57	29	34.9	16	4	US-10-024-662-2584 Sequence 2584, App
58	29	34.9	16	4	US-10-013-312-2993 Sequence 2993, App
59	29	34.9	16	4	US-10-087-190-28 Sequence 28, App1
60	29	34.9	16	4	US-10-120-885A-26 Sequence 26, App1
61	29	34.9	16	4	US-10-107-532-3 Sequence 3, App11
62	29	34.9	16	4	US-10-121-016-53 Sequence 53, App1
63	29	34.9	16	4	US-10-114-669-3 Sequence 3, App11
64	29	34.9	16	4	US-10-120-835-45 Sequence 45, App1
65	29	34.9	16	4	US-10-149-138-4225 Sequence 4225, App
66	29	34.9	16	4	US-10-114-432-10 Sequence 40, App1
67	29	34.9	16	4	US-10-306-631-31 Sequence 31, App1
68	29	34.9	16	4	US-10-455-822-99 Sequence 99, App1
69	29	34.9	16	4	US-10-435-751-39 Sequence 39, App1
70	29	34.9	16	4	US-10-149-135-2212 Sequence 2212, App
71	29	34.9	16	4	US-10-120-807A-46 Sequence 46, App1
72	29	34.9	16	4	US-10-418-972-39 Sequence 39, App1
73	29	34.9	16	4	US-10-422-571-66 Sequence 46, App1
74	29	34.9	16	4	US-10-313-972-50 Sequence 50, App1
75	29	34.9	16	4	US-10-415-014-712 Sequence 712, App
76	29	34.9	16	4	US-10-149-138-4225 Sequence 4225, App
77	29	34.9	16	4	US-10-407-484-99 Sequence 99, App1
78	29	34.9	16	4	US-10-149-137A-461 Sequence 461, App
79	29	34.9	16	4	US-10-463-782A-26 Sequence 26, App1
80	29	34.9	16	4	US-10-641-633-28 Sequence 28, App1
81	29	34.9	16	4	US-10-764-390-15 Sequence 15, App1
82	29	34.9	16	5	US-10-830-699-66 Sequence 66, App1
83	29	34.9	16	5	US-10-654-601-2574 Sequence 2574, App
84	29	34.9	16	5	US-10-861-662-66 Sequence 66, App1
85	29	34.9	16	5	US-10-919-654-40 Sequence 40, App1
86	29	34.9	16	5	US-10-837-269-42 Sequence 42, App1
87	29	34.9	16	5	US-10-994-106-65 Sequence 65, App1
88	29	34.9	16	5	US-10-776-773-26 Sequence 26, App1
89	29	34.9	16	5	US-10-990-137-653 Sequence 653, App
90	29	34.9	16	6	US-11-051-411-1489 Sequence 1489, App
91	29	34.9	16	6	US-11-073-349-45 Sequence 45, App1
92	29	34.9	17	3	US-09-935-476-3 Sequence 3, App11
93	29	34.9	20	4	US-10-424-599-151159 Sequence 151159, App
94	28	33.7	9	4	US-10-600-187-93 Sequence 93, App1
95	28	33.7	10	3	US-09-746-371C-28 Sequence 28, App1
96	28	33.7	11	4	US-10-727-737-47 Sequence 47, App1
97	28	33.7	11	4	US-10-727-737-51 Sequence 51, App1
98	28	33.7	14	5	US-10-813-338-1308 Sequence 1308, App
99	28	33.7	15	4	US-10-282-660-25 Sequence 25, App1
100	28	33.7	20	3	US-09-962-756-751 Sequence 751, App

ALIGNMENTS

RESULT 1

US-10-218-743-10
; Sequence 10, Application US/10218743
; Publication No. US2003009679A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/10/218,743
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/292,225
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: 60/098,909
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/085,295
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/098,565
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: 09/062,013
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 10
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
; FEATURE:
; OTHER INFORMATION: At location 14, Xaa = any amino acid
US-10-218-743-10

Query Match

Best Local Similarity 97.6%; Score 81; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.8e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 DKLWGVFPYGRXSIE 17
|||||
1 DKLWGVFPYGRXSIE 17

DB

RESULT 2
US-09-791-378-324
; Sequence 324, Application US/09791378
; Patent No. US20020142303A1
; GENERAL INFORMATION:
; APPLICANT: Parekh, Rajesh
; TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF
; FILE REFERENCE: 9195-061-999
; CURRENT APPLICATION NUMBER: US/09/791,378
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 09/750,395
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 677
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 324
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-378-324

Query Match

Best Local Similarity 49.4%; Score 41; DB 3; Length 10;
Best Local Similarity 70.0%; Pred. No. 2.1;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 LWMGVFPYGR 12

DB 1 LWMGIPTFGR 10
|||||

RESULT 3

US-09-826-290-321
; Sequence 321, Application US/09826290
; Patent No. US2002016468A1
; GENERAL INFORMATION:
; APPLICANT: Durham, L. Kathryn
; APPLICANT: Friedman, David L.
; APPLICANT: Herath, Herath Mudiyanselage Achula Chandrasiri
; APPLICANT: Kimmel, Lida H.
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Potter, David M.
; APPLICANT: Rohlf, Christian
; APPLICANT: Silber, B. Michael
; APPLICANT: Stiger, Thomas R.
; APPLICANT: Sunderland, P. Trey
; APPLICANT: Townsend, Robert Reid
; APPLICANT: White, Frost
; APPLICANT: Williams, Stephen A.
; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and
; TITLE OF INVENTION: Uses Thereof, Including Diagnosis and Treatment of
; FILE REFERENCE: 2572-1-001 N2
; CURRENT APPLICATION NUMBER: US/09/826,290
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 60/194,504
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: US 60/253,647
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 492
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 321
; LENGTH: 10
; TYPE: PRT
; ORGANISM: homo sapien
US-09-826-290-321

Query Match

Best Local Similarity 49.4%; Score 41; DB 3; Length 10;
Best Local Similarity 70.0%; Pred. No. 2.1;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 LWMGVFPYGR 12
|||||

DB 1 LWMGIPTFGR 10

RESULT 4
US-09-791-393-111
; Sequence 111, Application US/09791393
; Publication No. US20030032200A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Herath Mudiyanselage Achula Chandrasiri
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Rohlf, Christian
; TITLE OF INVENTION: Proteins, Genes and Their Use for
; TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
; FILE REFERENCE: 2543-1-001 N1
; CURRENT APPLICATION NUMBER: US/09/791,393
; CURRENT FILING DATE: 2002-01-02
; PRIOR APPLICATION NUMBER: GB 0004412.3
; EARLIER FILING DATE: 2000-02-24
; EARLIER APPLICATION NUMBER: GB 0030050.9
; EARLIER FILING DATE: 2000-12-08
; EARLIER APPLICATION NUMBER: US 60/254,830
; EARLIER FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 111
; LENGTH: 10

TYPE: PRT
ORGANISM: homo sapien
US-09-791-393-111

Query Match 49.4%; Score 41; DB 3; Length 10;
Best Local Similarity 70.0%; Pred. No. 2.1;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 LVMGVPPYGR 12
||||:|:|
Db 1 LVMGIPTFGR 10

RESULT 5
US-09-791-389-111
Sequence 111, Application US/09791389
Publication No. US20030032773A1
GENERAL INFORMATION:
APPLICANT: Herath, Herath Mudiyanseelage Achula Chandrasiri
APPLICANT: Parekh, Rajesh Bhikhu
APPLICANT: Rohlf, Christian
APPLICANT: Terrett, Jonathan Alexander
APPLICANT: Tyson, Kerry Louise
TITLE OF INVENTION: Proteins, Genes and Their Use for
TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
FILE REFERENCE: 2543-1-001 N2
CURRENT APPLICATION NUMBER: US/09/791,389
CURRENT FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: GB 0004412.3
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: GB 0030050.9
PRIOR FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: US 60/254,830
PRIOR FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 308
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 111
LENGTH: 10
TYPE: PRT
ORGANISM: homo sapien
US-09-791-389-111

Query Match 49.4%; Score 41; DB 3; Length 10;
Best Local Similarity 70.0%; Pred. No. 2.1;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 LVMGVPPYGR 12
||||:|:|
Db 1 LVMGIPTFGR 10

RESULT 6
US-09-791-377-324
Sequence 324, Application US/09791377
Publication No. US20040110938A1
GENERAL INFORMATION:
APPLICANT: Parekh, Rajesh
TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF
FILE REFERENCE: 9195-060-999
CURRENT APPLICATION NUMBER: US/09/791,377
CURRENT FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: 09/750,395
PRIOR FILING DATE: 2000-12-28
NUMBER OF SEQ ID NOS: 677
SOFTWARE: PatentIn version 3.0
SEQ ID NO 324
LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapiens
US-09-791-377-324

Query Match 49.4%; Score 41; DB 3; Length 10;
Best Local Similarity 70.0%; Pred. No. 2.1;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 LVMGVPPYGR 12
||||:|:|
Db 1 LVMGIPTFGR 10

RESULT 7
US-10-264-309-277
Sequence 277, Application US/10264309
Publication No. US20040022794A1
GENERAL INFORMATION:
APPLICANT: DURHAM, L. KATHRYN
APPLICANT: FRIEDMAN, DAVID L.
APPLICANT: HERATH, HERATH
APPLICANT: KIMMEL, LIDA H.
APPLICANT: PAREKH, RAJESH B.
APPLICANT: POTTER, DAVID M.
APPLICANT: ROHLFF, CHRISTIAN
APPLICANT: SILBER, B. MICHAEL
APPLICANT: SNYDER, PETER J.
APPLICANT: SOARES, HOLLY D.
APPLICANT: STIGER, THOMAS R.
APPLICANT: SUNDERLAND, P. TREY
APPLICANT: TOWNSEND, ROBERT R.
APPLICANT: WHITE, W. FROST
TITLE OF INVENTION: NUCLEIC ACID MOLECULES, POLYPEPTIDES AND USES THEREOF.
TITLE OF INVENTION: INCLUDING DIAGNOSIS AND TREATMENT OF ALZHEIMER'S DISEASE
FILE REFERENCE: POA-002.01
CURRENT APPLICATION NUMBER: US/10/264,309
CURRENT FILING DATE: 2002-10-03
PRIOR APPLICATION NUMBER: 60/326,708
PRIOR FILING DATE: 2001-10-03
NUMBER OF SEQ ID NOS: 491
SOFTWARE: PatentIn Version 2.1
SEQ ID NO 277
LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapiens
US-10-264-309-277

Query Match 49.4%; Score 41; DB 4; Length 10;
Best Local Similarity 70.0%; Pred. No. 2.1;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 LVMGVPPYGR 12
||||:|:|
Db 1 LVMGIPTFGR 10

RESULT 8
US-10-264-309-277
Sequence 277, Application US/10264309
Publication No. US20050163789A9
GENERAL INFORMATION:
APPLICANT: DURHAM, L. KATHRYN
APPLICANT: FRIEDMAN, DAVID L.
APPLICANT: HERATH, HERATH
APPLICANT: KIMMEL, LIDA H.
APPLICANT: PAREKH, RAJESH B.
APPLICANT: POTTER, DAVID M.
APPLICANT: ROHLFF, CHRISTIAN
APPLICANT: SILBER, B. MICHAEL
APPLICANT: SNYDER, PETER J.
APPLICANT: SOARES, HOLLY D.
APPLICANT: STIGER, THOMAS R.
APPLICANT: SUNDERLAND, P. TREY
APPLICANT: TOWNSEND, ROBERT R.
APPLICANT: WHITE, W. FROST
APPLICANT: WILLIAMS, STEPHEN A.

```

; TITLE OF INVENTION: NUCLEIC ACID MOLECULES, POLYPEPTIDES AND USES THEREFOR,
; TITLE OF INVENTION: INCLUDING DIAGNOSIS AND TREATMENT OF ALZHEIMER'S DISEASE
; FILE REFERENCE: POA-002.01
; CURRENT APPLICATION NUMBER: US/10/264,309
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: 60/326,708
; PRIOR FILING DATE: 2001-10-03
; NUMBER OF SEQ ID NOS: 491
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 277
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-309-277

Query Match          49.4%; Score 41; DB 5; Length 10;
Best Local Similarity 70.0%; Pred. No. 2.1;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      3  LVMGVPFYGR 12
Db      1  LVMGLPTFGR 10

RESULT 9
US-10-264-309-278
; Sequence 278, Application US/10264309
; Publication No. US20040022794A1
; GENERAL INFORMATION:
; APPLICANT: DURHAM, L. KATHRYN
; APPLICANT: FRIEDMAN, DAVID L.
; APPLICANT: HERATH, HERATH
; APPLICANT: KIMMEL, LIDA H.
; APPLICANT: PAREKH, RAJESH B.
; APPLICANT: POTTER, DAVID M.
; APPLICANT: ROHLF, CHRISTIAN
; APPLICANT: SILBER, B. MICHAEL
; APPLICANT: SNYDER, PETER J.
; APPLICANT: SOARES, HOLLY D.
; APPLICANT: STIGER, THOMAS R.
; APPLICANT: SUNDERLAND, P. TREV
; APPLICANT: TOWNSEND, ROBERT R.
; APPLICANT: WHITE, W. FROST
; APPLICANT: WILLIAMS, STEPHEN A.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES, POLYPEPTIDES AND USES THEREFOR,
; TITLE OF INVENTION: INCLUDING DIAGNOSIS AND TREATMENT OF ALZHEIMER'S DISEASE
; FILE REFERENCE: POA-002.01
; CURRENT APPLICATION NUMBER: US/10/264,309
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: 60/326,708
; PRIOR FILING DATE: 2001-10-03
; NUMBER OF SEQ ID NOS: 491
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 278
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-309-278

Query Match          47.0%; Score 39; DB 4; Length 10;
Best Local Similarity 70.0%; Pred. No. 4.8;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      3  LVMGVPFYGR 12
Db      1  LVMGLPTFGR 10

RESULT 10
US-10-264-309-278
; Sequence 278, Application US/10264309
; Publication No. US20050163789A9
; GENERAL INFORMATION:
; APPLICANT: DURHAM, L. KATHRYN
; APPLICANT: FRIEDMAN, DAVID L.
; APPLICANT: HERATH, HERATH
; APPLICANT: KIMMEL, LIDA H.
; APPLICANT: PAREKH, RAJESH B.
; APPLICANT: POTTER, DAVID M.
; APPLICANT: ROHLF, CHRISTIAN
; APPLICANT: SILBER, B. MICHAEL
; APPLICANT: SNYDER, PETER J.
; APPLICANT: SOARES, HOLLY D.
; APPLICANT: STIGER, THOMAS R.
; APPLICANT: SUNDERLAND, P. TREV
; APPLICANT: TOWNSEND, ROBERT R.
; APPLICANT: WHITE, W. FROST
; APPLICANT: WILLIAMS, STEPHEN A.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES, POLYPEPTIDES AND USES THEREFOR,
; TITLE OF INVENTION: INCLUDING DIAGNOSIS AND TREATMENT OF ALZHEIMER'S DISEASE
; FILE REFERENCE: POA-002.01
; CURRENT APPLICATION NUMBER: US/10/264,309
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: 60/326,708
; PRIOR FILING DATE: 2001-10-03
; NUMBER OF SEQ ID NOS: 491
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 278
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-309-278

Query Match          47.0%; Score 39; DB 5; Length 10;
Best Local Similarity 70.0%; Pred. No. 4.8;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      3  LVMGVPFYGR 12
Db      1  LVMGLPTFGR 10

RESULT 11
US-09-017-743C-3
; Sequence 3, Application US/09017743C
; Patent No. US2002017694A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; TITLE OF INVENTION: HLA Binding Peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 146
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/017,743C
; FILING DATE: 03-Feb-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/590,298
; FILING DATE: 23-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Parent, Annette S.
; REGISTRATION NUMBER: 42,058
; REFERENCE/DOCKET NUMBER: 018623-008050US
```

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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
TELEX: <unknown>
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-017-743C-3

Query Match      42.2% Score 35; DB 3; Length 8;
Best Local Similarity 71.4%; Pred. No. 1.7e+06;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      7 VPFYGRA 13
       :||||:|
Db      1 IPFYGKA 7

RESULT 12
US-10-371-525-273
Sequence 273, Application US/10371525
Publication No. US20030203869A1
GENERAL INFORMATION:
APPLICANT: Fikes, John D.
APPLICANT: Hermanson, Gary G.
APPLICANT: Sette, Alessandro
APPLICANT: Livingston, Brian
APPLICANT: Ishioka, Glenn Y.
APPLICANT: Chesnut, Robert W.
APPLICANT: Epimmune Inc.
TITLE OF INVENTION: Expression Vectors for Stimulating an
FILE REFERENCE: 39963-20022.01
CURRENT APPLICATION NUMBER: US/10/371,525
CURRENT FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: US 09/311,784
PRIOR FILING DATE: 1999-05-13
PRIOR APPLICATION NUMBER: US 60/085,751
PRIOR FILING DATE: 1998-05-15
NUMBER OF SEQ ID NOS: 463
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 273
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: HCV 1378 (peptide 29.0035)
US-10-371-525-273

Query Match      42.2% Score 35; DB 4; Length 8;
Best Local Similarity 71.4%; Pred. No. 1.7e+06;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      7 VPFYGRA 13
       :||||:|
Db      1 IPFYGKA 7

RESULT 13
US-10-371-069-273
Sequence 273, Application US/10371069
Publication No. US20030216342A1
GENERAL INFORMATION:
APPLICANT: EPIMMUNE INC.
APPLICANT: Fikes, John D.
APPLICANT: Hermanson, Gary G.
APPLICANT: Sette, Alessandro
APPLICANT: Ishioka, Glenn Y.
```

```
APPLICANT: Livingston, Brian
APPLICANT: Chesnut, Robert W.
APPLICANT: Epimmune Inc.
TITLE OF INVENTION: Expression Vectors for Stimulating an
FILE REFERENCE: 39963-20022.10
CURRENT APPLICATION NUMBER: US/10/371,069
CURRENT FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: US 09/078,904
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: US 60/085,751
PRIOR FILING DATE: 1998-05-15
NUMBER OF SEQ ID NOS: 463
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 273
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: HCV 1378 (peptide 29.0035)
US-10-371-069-273

Query Match      42.2% Score 35; DB 4; Length 8;
Best Local Similarity 71.4%; Pred. No. 1.7e+06;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      7 VPFYGRA 13
       :||||:|
Db      1 IPFYGKA 7

RESULT 14
US-10-371-645-273
Sequence 273, Application US/10371645
Publication No. US20030216343A1
GENERAL INFORMATION:
APPLICANT: EPIMMUNE INC.
APPLICANT: Fikes, John D.
APPLICANT: Hermanson, Gary G.
APPLICANT: Sette, Alessandro
APPLICANT: Ishioka, Glenn Y.
APPLICANT: Livingston, Brian
APPLICANT: Chesnut, Robert W.
APPLICANT: Epimmune Inc.
TITLE OF INVENTION: Expression Vectors for Stimulating an
FILE REFERENCE: 39963-20022.11
CURRENT APPLICATION NUMBER: US/10/371,645
CURRENT FILING DATE: 2003-06-20
PRIOR APPLICATION NUMBER: US 09/078,904
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: US 60/085,751
PRIOR FILING DATE: 1998-05-15
NUMBER OF SEQ ID NOS: 463
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 273
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: HCV 1378 (peptide 29.0035)
US-10-371-645-273

Query Match      42.2% Score 35; DB 4; Length 8;
Best Local Similarity 71.4%; Pred. No. 1.7e+06;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      7 VPFYGRA 13
       :||||:|
Db      1 IPFYGKA 7

RESULT 15
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US-10-371-260-273
 ; Sequence 273, Application US/10371260
 ; Publication No. US20030220285A1
 ; GENERAL INFORMATION:
 ; APPLICANT: EPIMUNE Inc.
 ; APPLICANT: Fikes, John D.
 ; APPLICANT: Hermanson, Gary G.
 ; APPLICANT: Sette, Alessandro
 ; APPLICANT: Ishioka, Glenn Y.
 ; APPLICANT: Livingston, Brian
 ; APPLICANT: Chesnut, Robert W.
 ; APPLICANT: Epimmune Inc.
 ; TITLE OF INVENTION: Expression Vectors for Stimulating an
 ; TITLE OF INVENTION: Immune Response and Methods of Using the Same
 ; FILE REFERENCE: 39963-20022.13 US/10/371,260
 ; CURRENT FILING DATE: 2003-02-21
 ; PRIOR APPLICATION NUMBER: US 09/078,904
 ; PRIOR FILING DATE: 1998-05-13
 ; PRIOR APPLICATION NUMBER: US 60/085,751
 ; PRIOR FILING DATE: 1998-05-15
 ; NUMBER OF SEQ ID NOS: 463
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 273
 ; LENGTH: 8
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: HCV 1378 (peptide 29.0035)
 US-10-371-260-273

Query Match 42.2%; Score 35; DB 4; Length 8;
 Best Local Similarity 71.4%; Pred. No. 1.7e+06;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 7 VPFYGRA 13
 :|||:|
 1 IPFYGKA 7

RESULT 16
 US-10-651-165-146
 ; Sequence 146, Application US/10651165
 ; Publication No. US20040047877A1
 ; GENERAL INFORMATION:
 ; APPLICANT: LEROUX-ROELS, Geert
 ; APPLICANT: DELBYS, Robert
 ; APPLICANT: MAERTENS, Geert
 ; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
 ; TITLE OF INVENTION: VIRUS
 ; FILE REFERENCE: 2551-94
 ; CURRENT APPLICATION NUMBER: US/10/651,165
 ; CURRENT FILING DATE: 2003-09-02
 ; PRIOR APPLICATION NUMBER: US/08/974,690C
 ; PRIOR FILING DATE: 1997-11-19
 ; PRIOR APPLICATION NUMBER: PCT/EP94/03555
 ; PRIOR FILING DATE: 1994-10-28
 ; PRIOR APPLICATION NUMBER: EP 93402718.6
 ; PRIOR FILING DATE: 1993-11-04
 ; NUMBER OF SEQ ID NOS: 286
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 146
 ; LENGTH: 8
 ; TYPE: PRT
 ; ORGANISM: hepatitis C virus
 US-10-651-165-146

Query Match 42.2%; Score 35; DB 4; Length 8;
 Best Local Similarity 71.4%; Pred. No. 1.7e+06;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 OY 7 VPFYGRA 13
 :|||:|

DB 1 IPFYGKA 7
 RESULT 17
 US-10-888-084-1
 ; Sequence 1, Application US/10888084
 ; Publication No. US20050095649A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Aebersold, Ruedi
 ; APPLICANT: Zhang, Ruedi
 ; TITLE OF INVENTION: Affinity Capture of Peptides by
 ; TITLE OF INVENTION: Microarray and Related Methods
 ; FILE REFERENCE: 66661-113
 ; CURRENT APPLICATION NUMBER: US/10/888,084
 ; CURRENT FILING DATE: 2004-07-09
 ; PRIOR APPLICATION NUMBER: 60/486,581
 ; PRIOR FILING DATE: 2003-07-10
 ; NUMBER OF SEQ ID NOS: 1
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 21
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Exemplary peptide
 US-10-888-084-1

Query Match 42.2%; Score 35; DB 5; Length 21;
 Best Local Similarity 46.2%; Pred. No. 55;
 Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 4 VMGVPFYGRAXSI 16
 :|||:|:|
 DB 1 VGVGVPGDARAL 13

RESULT 18
 US-09-843-676-171
 ; Sequence 171, Application US/09843676
 ; Patent No. US20020164786A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cech, Thomas R.
 ; APPLICANT: Lingner, Joachim
 ; APPLICANT: Nakamura, Toru
 ; APPLICANT: Chapman, Karen B.
 ; APPLICANT: Morin, Gregg B.
 ; APPLICANT: Harley, Calvin
 ; APPLICANT: Andrews, William H.
 ; TITLE OF INVENTION: No. US20020164786A1e1 Telomerase
 ; NUMBER OF SEQUENCES: 225
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, 8th Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: United States of America
 ; ZIP: 94111
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/843,676
 ; FILING DATE: 26-Apr-2001
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/854,050
 ; FILING DATE: 09-MAY-1997
 ; APPLICATION NUMBER: US 08/846,017
 ; FILING DATE: 25-APR-1997
 ; APPLICATION NUMBER: US 08/844,419
 ; FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 171:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..15
OTHER INFORMATION: /note= "motif D peptide from human
telomerase core protein 1 (TCPI)"
SEQUENCE DESCRIPTION: SEQ ID NO: 171:
US-09-643-676-171

Query Match 41.0%; Score 34; DB 3; Length 15;
Best Local Similarity 77.8%; Pred. No. 58;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 LVNGVPEYFG 11
|||
Db 4 LVKGVPEYFG 12

RESULT 19
US-09-766-253-171
Sequence 171, Application US/09766253
Publication No. US20020187471A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20020187471A1 Telomerase
NUMBER OF SEQUENCES: 171
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/766,253
FILING DATE: 19-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/846,017
FILING DATE: 1997-04-25
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002920US
TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 171:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..15
OTHER INFORMATION: /note= "motif D peptide from human
telomerase core protein 1 (TCPI)"
SEQUENCE DESCRIPTION: SEQ ID NO: 171:
US-09-766-253-171

Query Match 41.0%; Score 34; DB 3; Length 15;
Best Local Similarity 77.8%; Pred. No. 58;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 LVNGVPEYFG 11
|||
Db 4 LVKGVPEYFG 12

RESULT 20
US-09-438-486-171
Sequence 171, Application US/09438486
Publication No. US20030009019A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. US20030009019A1 Telomerase
NUMBER OF SEQUENCES: 223
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/438,486
FILING DATE: 12-NOV-1999
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002931US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 171:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..15
OTHER INFORMATION: /note="motif D peptide from human
telomerase core protein 1 (TCP1)"
US-09-438-486-171

Query Match 41.0%; Score 34; DB 3; Length 15;
Best Local Similarity 77.8%; Pred. No. 58;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 LVMGVPPYG 11
|||
Db 4 LVRGVPEYG 12

RESULT 21
US-10-053-758-171
Sequence 171, Application US/10053758
Publication No. US20030032075A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin H.
Andrews, William H.
TITLE OF INVENTION: No. US20030032075A1e1 Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/053,758
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 015389-0029310US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 171:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..15
OTHER INFORMATION: /note="motif D peptide from human
telomerase core protein 1 (TCP1)"
US-10-053-758-171

Query Match 41.0%; Score 34; DB 4; Length 15;
Best Local Similarity 77.8%; Pred. No. 58;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 LVMGVPPYG 11
|||
Db 4 LVRGVPEYG 12

RESULT 22
US-10-054-295-171
Sequence 171, Application US/10054295
Publication No. US20030044953A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin H.
Andrews, William H.
TITLE OF INVENTION: No. US20030044953A1e1 Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/054,295
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/854,050
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-0029310US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 171:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..15
OTHER INFORMATION: /note= "motif D peptide from human
telomerase core protein 1 (TCPI)"
SEQUENCE DESCRIPTION: SEQ ID NO: 171:
US-10-054-295-171

Query Match 41.0%; Score 34; DB 4; Length 15;
Best Local Similarity 77.8%; Pred. No. 58;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 LVMGVPPYG 11
DB 4 LVRGVPEYG 12

RESULT 23
US-10-054-611-171
Sequence 171, Application US/10054611
Publication No. US20030059787A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20030059787A1 Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/054,611
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/854,050
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 171:
SEQUENCE CHARACTERISTICS:

LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..15
OTHER INFORMATION: /note= "motif D peptide from human
telomerase core protein 1 (TCPI)"
SEQUENCE DESCRIPTION: SEQ ID NO: 171:
US-10-054-611-171

Query Match 41.0%; Score 34; DB 4; Length 15;
Best Local Similarity 77.8%; Pred. No. 58;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 LVMGVPPYG 11
DB 4 LVRGVPEYG 12

RESULT 24
US-10-282-960-70
Sequence 70, Application US/10282960
Publication No. US20030143228A1
GENERAL INFORMATION:
APPLICANT: Chen, Si-Yi
APPLICANT: ZhaoYang, You
APPLICANT: Schreiers, Roland
TITLE OF INVENTION: Human Telomerase Reverse Transcriptase as a Class-II Restricted
FILE REFERENCE: P02193US1
CURRENT APPLICATION NUMBER: US/10/282,960
CURRENT FILING DATE: 2002-10-29
PRIOR APPLICATION NUMBER: US 60/345,012
PRIOR FILING DATE: 2001-10-29
NUMBER OF SEQ ID NOS: 100
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 70
LENGTH: 15
TYPE: PRT
ORGANISM: Human
US-10-282-960-70

Query Match 41.0%; Score 34; DB 4; Length 15;
Best Local Similarity 77.8%; Pred. No. 58;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 LVMGVPPYG 11
DB 7 LVRGVPEYG 15

RESULT 25
US-10-325-810-291
Sequence 291, Application US/10325810
Publication No. US20030204069A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California

COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/325,810
FILING DATE: 20-Dec-2002
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/402,181
FILING DATE: 29-Sep-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-Oct-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-Apr-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-Apr-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-May-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-May-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-Oct-1997
ATTORNEY/AGENT INFORMATION:
NAME: Auehue, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 291:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..15
OTHER INFORMATION: /note="motif D peptide from human telomerase core protein 1 (TCPI)"
SEQUENCE DESCRIPTION: SEQ ID NO: 291:
US-10-325-810-291
Query Match 41.0%; Score 34; DB 4; Length 15;
Best Local Similarity 77.8%; Pred. No. 58;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 LMGVPEYQ 11
Db 4 LVRGVPEYQ 12

Search completed: January 26, 2006, 08:38:37
Job time : 56.25 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 26, 2006, 07:48:50 ; Search time 8.5 Seconds

(without alignments)
192.454 Million cell updates/sec

Title: US-09-662-293-10

Perfect score: 83
Sequence: 1 DKLVGVPFGRAKSIE 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 4071

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Listing first 100 summaries

Database :

1: PIR.80:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	33.7	7	2	B33932
2	26	31.3	16	2	A12729
3	25	30.1	20	2	B39089
4	24	28.9	14	2	PH1763
5	24	28.9	16	4	I79565
6	24	28.9	17	2	PH1820
7	24	28.9	20	2	I46652
8	23	27.7	12	2	PQ0730
9	23	27.7	19	2	PQ0730
10	22	26.5	9	2	PT0324
11	22	26.5	15	2	PW0004
12	22	26.5	15	2	S57584
13	22	26.5	16	2	PH1782
14	22	26.5	17	2	PH1801
15	22	26.5	17	2	SI6929
16	22	26.5	18	2	A32917
17	22	26.5	19	2	PH1304
18	22	26.5	21	2	S03504
19	22	26.5	21	2	A85712
20	22	26.5	10	2	B49581
21	21	25.3	11	2	A49581
22	21	25.3	11	2	B39853
23	21	25.3	13	2	P50325
24	21	25.3	13	2	B61620
25	21	25.3	14	2	G44957
26	21	25.3	15	2	PA0026
27	21	25.3	15	2	PH1610
28	21	25.3	15	2	UT0610
29	21	25.3	16	2	H41299

30	21	25.3	17	2	C24166
31	21	25.3	18	1	PD23PP
32	21	25.3	19	2	PC2326
33	21	25.3	19	2	A44356
34	21	25.3	19	2	PH1624
35	21	25.3	20	2	PH1338
36	21	25.3	21	2	C49042
37	20	24.1	11	2	A40693
38	20	24.1	13	2	S21152
39	20	24.1	14	2	PA0013
40	20	24.1	15	2	PT0085
41	20	24.1	15	2	A56970
42	20	24.1	15	2	S04586
43	20	24.1	16	2	PA1289
44	20	24.1	16	2	C49048
45	20	24.1	16	2	A41170
46	20	24.1	17	2	B36727
47	20	24.1	18	2	S09086
48	20	24.1	18	2	I52651
49	20	24.1	18	2	S51734
50	20	24.1	20	2	S50022
51	20	24.1	20	2	S46205
52	20	24.1	20	2	I64036
53	20	24.1	20	2	S53440
54	20	24.1	20	2	A58903
55	20	24.1	21	2	B12055
56	20	24.1	21	2	A27719
57	20	24.1	21	2	S09088
58	20	24.1	21	2	F64121
59	20	24.1	21	2	I52794
60	19	22.9	9	2	E28854
61	19	22.9	10	1	ECLQIM
62	19	22.9	10	1	ECLQ3M
63	19	22.9	10	2	S68033
64	19	22.9	10	2	B61033
65	19	22.9	10	2	A24867
66	19	22.9	11	1	ECLQ2M
67	19	22.9	11	2	A26120
68	19	22.9	11	2	S07203
69	19	22.9	11	2	S07201
70	19	22.9	11	2	A61033
71	19	22.9	12	2	C39109
72	19	22.9	12	2	S07436
73	19	22.9	13	2	A32486
74	19	22.9	13	2	D61491
75	19	22.9	14	2	A61361
76	19	22.9	14	2	JN0390
77	19	22.9	14	2	PA0015
78	19	22.9	14	2	B39111
79	19	22.9	14	2	S48685
80	19	22.9	15	1	LEFCP
81	19	22.9	15	2	PA0014
82	19	22.9	15	2	PN0173
83	19	22.9	15	2	PH0808
84	19	22.9	15	2	I40655
85	19	22.9	17	2	S26747
86	19	22.9	17	2	PH1789
87	19	22.9	17	2	B31769
88	19	22.9	17	2	PH0809
89	19	22.9	18	1	DRUPPD
90	19	22.9	18	2	J50647
91	19	22.9	18	2	PT0239
92	19	22.9	18	2	PH1794
93	19	22.9	18	2	A45590
94	19	22.9	19	2	S43960
95	19	22.9	19	2	A28814
96	19	22.9	19	2	PT0332
97	19	22.9	20	2	I49039
98	19	22.9	20	2	A24589
99	19	22.9	20	2	S58382
100	19	22.9	20	2	A85645

photosystem II ext
distal-retinal-pig
proteasome endopep
37k adherens junct
Ig H chain V-D-J r
Ig heavy chain V r
Ig heavy chain V r
transgelin - sheep
tryptophyltin-rela
photosystem II oxy
protein QA600027 -
GLYMA1 - soybean (NADH2 dehydrogenas
T-cell receptor al
T-cell receptor al
photosystem II 6.1
cytochrome c554 -
proteasome chain 5
brain-derived neur
T-cell receptor al
trypsin-like prote
comosain (EC 3.4.2
hypothetical prote
glutathione-bindin
metalloprotease
glyceraledehyde-3-P
trypsin (EC 3.4.21
proteasome chain 7
hypothetical prote
hypothetical BCR/A
fibrinopeptide B -
tachykinin I - mig
tachykinin III - m
cytochrome P450 1A
ranatichykinin B -
scyllorhizin I - s
scyllorhizin II - m
6-phosphofructokin
upetolein - frog (physisalaemin - frog
ranatichykinin A -
hypothetical 1.2K
tachykinin - Afri
beta protein - rat
seed protein wa-4
bradykinin-like pe
histamine-release
seed storage prote
Ig heavy chain V r
extension protein
phe operon leader
seed storage prote
T-cell receptor al
T-cell receptor al
IvBN leader pepti
Ig heavy chain J r
T-cell receptor al
T-cell receptor de
T-cell receptor al
pigment-dispersing
pheromotropin -
Ig heavy chain CDR
T-cell receptor al
beta-pigment-dispe
Ig mu chain V regi
Ig kappa chain V r
Ig heavy chain CRD
T-cell receptor be
photosystem II chl
hypothetical prote
Amino terminal of

ALIGNMENTS

RESULT 1

E33932
Ig mu chain D region (E7) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 16-Aug-1996
C:Accession: E33932
R:Baccala, R., Vo Quang, T., Gilbert, M., Ternynck, T., Avrameas, S.
Proc. Natl. Acad. Sci. U.S.A. 86, 4624-4628, 1989
A:Title: Two murine natural polyreactive autoantibodies are encoded by nonmutated germ-
A:Reference number: A33932; MUID:89282823; PMID:2499887
C:Accession: E33932
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-7 <BAC>
A:Cross-references: UNIPARC:UPI000017C6D9; GB:M27106
C:Keywords: immunoglobulin

Query Match 33.7%; Score 28; DB 2; Length 7;
Best Local Similarity 80.0%; Pred. No. 2.8e+05;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 PFYGR 12
| | | | |
| | | | |

Db 2 PFYGR 6

RESULT 2

A12729
glutamate dehydrogenase (EC 1.4.1.2) - bluefin tuna (tentative sequence) (fragment)
C:Species: Thunnus thynnus (bluefin tuna)
C:Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 05-Oct-2004
C:Accession: A12729
R:Veronase, F.M.; Bevilacqua, R.; Boccu, E.; Brown, D.M.
Biochim. Biophys. Acta 445, 1-13, 1976
A:Title: Glutamate dehydrogenase from tuna liver. Purification, characteristics and sequ
A:Reference number: A12729; MUID:7653947; PMID:182270
C:Accession: A12729
A:Molecule type: protein
A:Residues: 1-16 <VER>
A:Cross-references: UNIPROT:P20016; UNIPARC:UPI00001292E1
A:Experimental source: liver
C:Keywords: oxidoreductase

Query Match 31.3%; Score 26; DB 2; Length 16;
Best Local Similarity 35.7%; Pred. No. 3.3e+02;

Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 4 VMGVPFYGRAXSIE 17
| | | | |
| | | | |

Db 3 VVDVDFGAKAKGVK 16

RESULT 3

B39089
hydrogenase (EC 1.18.99.1) 34K chain - Thiocapsa roseopersicina (fragment)
C:Species: Thiocapsa roseopersicina
C:Date: 27-Nov-1991 #sequence_revision 27-Nov-1991 #text_change 23-Jun-1993
C:Accession: B39089
R:Kovacs, K.L.; Tiley, G.; Thanh, L.T.; Lakatos, S.; Kiss, Z.; Bagyinka, C.
J. Biol. Chem. 266, 947-951, 1991
A:Title: Structural rearrangements in active and inactive forms of hydrogenase from Thic
A:Reference number: A39089; MUID:91093297; PMID:1845998
C:Accession: B39089
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-20 <KOV>
A:Cross-references: UNIPARC:UPI000017AB7F
C:Keywords: oxidoreductase

Query Match 30.1%; Score 25; DB 2; Length 20;

Best Local Similarity 66.7%; Pred. No. 6.2e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 VMGVPF 9
| | | | |
| | | | |

Db 10 VIGLRF 15

RESULT 4

PH1763
T cell receptor alpha chain V region (clone 1V alpha 23-2) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C:Accession: PH1763
R:Porcellli, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.
J. Exp. Med. 178, 1-16, 1993
A:Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood
A:Reference number: PH1754; MUID:93301585; PMID:8391057
C:Accession: PH1763
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-14 <POR>
A:Cross-references: UNIPARC:UPI000017C36E

Query Match 28.9%; Score 24; DB 2; Length 14;
Best Local Similarity 66.7%; Pred. No. 6.4e+02;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DKLYMG 6
| | | | |
| | | | |

Db 9 DKLIFG 14

RESULT 5

I79565
hypothetical TGL3/TCRD (T-cell receptor delta chain) mutant fusion protein - human (frag
C:Species: Homo sapiens (man)
C:Date: 28-Jan-2000 #sequence_revision 28-Jan-2000 #text_change 09-Jul-2004
C:Accession: I79565
R:Zutter, M.; Hockett, R.D.; Roberts, C.W.; McGuire, E.A.; Bloomstone, J.; Morton, C.C.;
Proc. Natl. Acad. Sci. U.S.A. 87, 3161-3165, 1990
A:Title: The t(10;14)(q24;q11) of T-cell acute lymphoblastic leukemia juxtaposes the del
A:Reference number: I59162; MUID:90222189; PMID:2336274
C:Accession: I79565
A:Status: translation not shown; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-16 <ZUT>
A:Cross-references: UNIPROT:Q15632; UNIPARC:UPI000007279D; GB:M33602; NID:9339907; PIDN:
C:Comment: This sequence is the hypothetical translation of a chimeric translocation mut
C:Keywords: fusion protein
F:1-5/Region: TGL3 proto-oncogene derived
F:10-16/Region: T-cell receptor delta chain derived

Query Match 28.9%; Score 24; DB 4; Length 16;
Best Local Similarity 66.7%; Pred. No. 7.4e+02;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DKLYMG 6
| | | | |
| | | | |

Db 11 DKLIFG 16

RESULT 6

PH1820
T cell receptor alpha chain V region (clone 5PBL V alpha 24-3) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C:Accession: PH1820
R:Porcellli, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.
J. Exp. Med. 178, 1-16, 1993
A:Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood

A:Reference number: PH1754; MUID:93301585; PMID:8391057
A:Accession: PH1820
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-17 <P>
A:Cross-references: UNIPARC:UPI000017C388

Query Match 28.9%; Score 24; DB 2; Length 17;
Best Local Similarity 66.7%; Pred. No. 7.9e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 DKLVMG 6
|||:
Db 12 DKLIFG 17

RESULT 7

I46652
T-cell receptor delta-chain J-delta-1 segment - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 05-Nov-1999
C:Accession: I46652
R:Yang, Y.G.; Ohta, S.; Yamada, S.; Shimizu, M.; Takagaki, Y.
J. Immunol. 155, 1981-1993, 1995
A:Title: Diversity of T cell receptor delta-chain cDNA in the thymus of a one-month-old
A:Reference number: I46623; MUID:95363165; PMID:7636249
A:Accession: I46652
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-20 <Y>
A:Cross-references: UNIPARC:UPI000011B2B7; GB:D49560; NID:G1041172; PIDN:BA08504.1; PIR
C:Keywords: T-cell receptor

Query Match 28.9%; Score 24; DB 2; Length 20;
Best Local Similarity 66.7%; Pred. No. 9.3e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 DKLVMG 6
|||:
Db 6 DKLIFG 11

RESULT 8

P00730
unidentified 5.4/35K protein [imported] - rice (fragment)
C:Species: Oryza sativa (rice)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C:Accession: P00730
R:Komatsu, S.; Kajiwara, H.; Hirano, H.
Theor. Appl. Genet. 86, 935-942, 1993
A:Title: A rice protein library; a data-file of rice proteins separated by two-dimension
A:Reference number: P00696
A:Accession: P00730
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-12 <K>
A:Cross-references: UNIPROT:Q7M1U3; UNIPARC:UPI000017B124

Query Match 27.7%; Score 23; DB 2; Length 12;
Best Local Similarity 80.0%; Pred. No. 8.2e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 9 FYGRA 13
|||:
Db 7 FYGBA 11

RESULT 9

P00790
NADH dehydrogenase (EC 1.6.99.3) 14K chain - fava bean mitochondrion (fragment)
N:Alternate names: complex I 14K chain; NADH-ubiquinone reductase 14K chain
C:Species: mitochondrion Vicia faba (fava bean)
C:Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004

C:Accession: P00790
R:Letenne, S.; Boutry, M.
Plant Physiol. 102, 435-443, 1993
A:Title: Purification and preliminary characterization of mitochondrial complex I (NADH
A:Reference number: P00775; MUID:94151437; PMID:8108509
A:Accession: P00790
A:Molecule type: protein
A:Residues: 1-19 <L>
A:Cross-references: UNIPROT:Q7M2G7; UNIPARC:UPI0000175118
C:Comment: Complex I, mitochondrial NADH-ubiquinone reductase, is the first of the c
ranging from 5K to 75K.
C:Comment: This enzyme catalyzes electron transfer from endogenous NADH to ubiquinone b
C:Genetics:
A:Genome: mitochondrion
C:Superfamily: NADH dehydrogenase
C:Keywords: electron transfer; mitochondrion; oxidoreductase

Query Match 27.7%; Score 23; DB 2; Length 19;
Best Local Similarity 66.7%; Pred. No. 1.3e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 LVMGP 8
|||:
Db 13 LVSGIP 18

RESULT 10

PT0324
Ig heavy chain CRD3 region (clone J2-106C) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0324
R:Imada, M.; Maeseman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A:Reference number: PT0222; MUID:91108337; PMID:1899102
A:Accession: PT0324
A:Molecule type: DNA
A:Residues: 1-9 <Y>
A:Cross-references: UNIPARC:UPI000017C217
A:Experimental source: B lymphocyte
C:Keywords: heterotrimer; immunoglobulin

Query Match 26.5%; Score 22; DB 2; Length 9;
Best Local Similarity 57.1%; Pred. No. 2.6e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 7 VPFYGRA 13
|||:
Db 1 VPGYGS 7

RESULT 11

PM0004
chlorophyll a/b-binding protein 24.5K - green alga (Dunaliella tertiolecta) (fragment)
N:Alternate names: photosystem II light-harvesting chlorophyll 24.5K protein
C:Species: Dunaliella tertiolecta
C:Date: 04-Sep-1998 #sequence_revision 24-Nov-1999 #text_change 24-Nov-1999
C:Accession: PM0004
R:LaRoche, J.; Bennett, J.; Falkowski, P.G.
Gene 95, 165-171, 1990
A:Title: Characterization of a cDNA encoding for the 28.5-kDa LHCI apoprotein from the
A:Reference number: JMW040; MUID:91065528; PMID:2249775
A:Accession: PM0004
A:Molecule type: protein
A:Residues: 1-15 <L>
A:Cross-references: UNIPARC:UPI000017B174
C:Superfamily: chlorophyll a/b-binding protein
C:Keywords: chloroplast; grana; light-harvesting complex; membrane adhesion; membrane p

Query Match 26.5%; Score 22; DB 2; Length 15;
Best Local Similarity 80.0%; Pred. No. 1.6e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 7 VEPYG 11
|||
Db 1 VEPYG 5

RESULT 12

S57584
T cell receptor V-D-J junctional alpha chain region - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 19-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 05-Nov-1999
C/Accession: S57584
R/Burrows, S.R.; Silins, S.L.; Moss, D.J.; Khanna, R.; Misko, I.S.; Argac, V.P.
submitted to the EMBL Data Library, June 1995
A/Description: T cell receptor repertoire for a viral epitope in humans is diversified b
A/Reference number: S57494
A/Accession: S57584
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-15 <BUR>
A/Cross-references: UNIPARC:UPI0000116747; EMBL:Z49956; NID:g887466; PIDN:CAA90227.1; PI
C/Keywords: T-cell receptor

Query Match 26.5%; Score 22; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 DKLWVG 6
|||
Db 10 DKIRFG 15

RESULT 13

PH1782
T cell receptor alpha chain V region (clone 2DN V alpha 24-3) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C/Accession: PH1782
R/Portelli, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.
J. Exp. Med. 178, 1-16, 1993
A/Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood
A/Reference number: PH1754; MUID:93301585; PMID:8391057
A/Accession: PH1782
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-16 <POR>
A/Cross-references: UNIPARC:UPI000017C375

Query Match 26.5%; Score 22; DB 2; Length 16;
Best Local Similarity 50.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 DKLWVG 6
|||
Db 11 DKIRFG 16

RESULT 14

PH1801
T cell receptor alpha chain V region (clone 3PBL V alpha 24-7) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C/Accession: PH1801
R/Portelli, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.
J. Exp. Med. 178, 1-16, 1993
A/Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood
A/Reference number: PH1754; MUID:93301585; PMID:8391057
A/Accession: PH1801
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-17 <POR>

A/Cross-references: UNIPARC:UPI000017C383

Query Match 26.5%; Score 22; DB 2; Length 17;
Best Local Similarity 50.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 DKLWVG 6
|||
Db 12 DKIRFG 17

RESULT 15

S16929
Flavodoxin A - Azotobacter chroococcum (fragment)
N/Alternate names: AcFlaA
C/Species: Azotobacter chroococcum
C/Date: 19-Mar-1997 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C/Accession: S16929
R/Bagby, S.; Barker, P.D.; Hill, H.A.O.; Sanghera, G.S.; Dunbar, B.; Ashby, G.A.; Eady, J.
Biochem. J. 277, 313-319, 1991
A/Title: Direct electrochemistry of two genetically distinct flavodoxins isolated from A.
A/Reference number: S16929; MUID:91315397; PMID:1859358
A/Accession: S16929
A/Molecule type: protein
A/Residues: 1-17 <BAG>
A/Cross-references: UNIPROT:P23002; UNIPARC:UPI000012A8CA
A/Experimental source: strain MCD1155
C/Function:
C/Description: acts as an electron donor to the Mo-containing nitrogenase
C/Keywords: electron transfer; flavoprotein; FMN

Query Match 26.5%; Score 22; DB 2; Length 17;
Best Local Similarity 37.5%; Pred. No. 1.8e+03;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 9 FYGRAXSI 16
|||
Db 6 FYGSSGV 13

RESULT 16

A32917
protein phosphatase - rat (fragment)
C/Species: Rattus norvegicus (Norway rat)
C/Date: 08-Dec-1989 #sequence_revision 08-Dec-1989 #text_change 30-Sep-1993
C/Accession: A32917
R/Tamura, S.; Yasui, A.; Tsukit, S.
Biochem. Biophys. Res. Commun. 163, 131-136, 1989
A/Title: Expression of rat protein phosphatase 2C (1A) in Escherichia coli.
A/Reference number: A32917; MUID:89374212; PMID:2549985
A/Accession: A32917
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-18 <TAM>
A/Cross-references: UNIPARC:UPI000017C9A7

Query Match 26.5%; Score 22; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 DKLWVG 6
|||
Db 13 DQVIMG 18

RESULT 17

PH1304
Ig heavy chain DJ region (clone C439-111) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C/Accession: PH1304
R/Maserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992

A>Title: Predominance of fetal type DJH joining in young children with B precursor lymph
A:Reference number: PH1302; MUID:93094761; PMID:1460419

A:Accession: PH1304
A:Molecule type: DNA
A:Residues: 1-19 <WAS>
A:Cross-references: UNIPARC:UPI0000176934
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 26.5%; Score 22; DB 2; Length 19;
Best Local Similarity 60.0%; Pred. No. 2e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 6 GVPY 10
| | | |
| | | |
Db 2 GVPY 6

RESULT 18

S03504
T-cell receptor alpha chain J region (TT11) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 23-May-1997
C:Accession: S03504
R:Minoto, A.; Mjolsness, S.; Hood, L.
Nature 316, 832-836, 1985
A>Title: Genomic organization of the genes encoding mouse T-cell receptor alpha-chain.
A:Reference number: S03503; MUID:85296332; PMID:2993908
A:Accession: S03504
A:Molecule type: DNA
A:Residues: 1-21 <WIN>
A:Cross-references: UNIPARC:UPI0000176DB6; EMBL:X02858
C:Note: this sequence was determined from the gemmine gene
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: T-cell receptor

Query Match 26.5%; Score 22; DB 2; Length 21;
Best Local Similarity 42.9%; Pred. No. 2.2e+03;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 DKLVGV 7
| | | |
| | | |
Db 7 NKLIFGI 13

RESULT 19

A85712
Unknown protein encoded by prophage CP-9330 (imported) - Escherichia coli (strain O157:H
C:Species: Escherichia coli
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: A85712
R:Perma, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A>Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: A85712
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-21 <STO>
A:Cross-references: UNIPROT:Q8X4E1; UNIPARC:UPI00000D0DFB; GB:AE005174; NID:q12515036; F
C:Experimental source: strain O157:H7, substrain EDL933
A:Genetics:
A:Gene: Z2087

Query Match 26.5%; Score 22; DB 2; Length 21;
Best Local Similarity 33.3%; Pred. No. 2.2e+03;
Matches 4; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 5 MGVPFYGRAXSI 16
| | | | |
| | | | |
Db 1 MSIDFFERALPV 12

RESULT 20

B49581
Stalokinin II - yellow fever mosquito
C:Species: Aedes aegypti (yellow fever mosquito)
C>Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 16-Aug-2004
C:Accession: B49581
R:Champagne, D.E.; Ribeiro, J.M.
Proc. Natl. Acad. Sci. U.S.A. 91, 138-142, 1994
A>Title: Stalokinin I and II: vasodilatory tachykinins from the yellow fever mosquito A
A:Reference number: A49581; MUID:94105119; PMID:8278354
A:Accession: B49581
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <CHA>
A:Cross-references: UNIPROT:P42635; UNIPARC:UPI0000136FEC
A:Experimental source: Rockefeller, salivary gland
A:Note: sequence extracted from NCBI backbone (NCBIF:141842)

Query Match 25.3%; Score 21; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.5e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 6 GVPFYG 11
| | | | |
| | | | |
Db 3 GDKFYG 8

RESULT 21

A49581
Stalokinin I - yellow fever mosquito
C:Species: Aedes aegypti (yellow fever mosquito)
C>Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 05-Oct-2004
C:Accession: A49581
R:Champagne, D.E.; Ribeiro, J.M.
Proc. Natl. Acad. Sci. U.S.A. 91, 138-142, 1994
A>Title: Stalokinin I and II: vasodilatory tachykinins from the yellow fever mosquito A
A:Reference number: A49581; MUID:94105119; PMID:8278354
A:Accession: A49581
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <CHA>
A:Cross-references: UNIPROT:P42634; UNIPARC:UPI0000136FEB
A:Experimental source: Rockefeller, salivary gland
A:Note: sequence extracted from NCBI backbone (NCBIF:141841)

Query Match 25.3%; Score 21; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.5e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 6 GVPFYG 11
| | | | |
| | | | |
Db 3 GDKFYG 8

RESULT 22

B39853
LuxC protein - Photobacterium phosphoreum (fragment)
C:Species: Photobacterium phosphoreum
C>Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 09-Jul-2004
C:Accession: B39853
R:Perri, S.R.; Meighen, E.A.
J. Biol. Chem. 266, 12852-12857, 1991
A>Title: A lux-specific myristoyl transferase in luminescent bacteria related to eukary.
A:Reference number: A39853; MUID:91302295; PMID:2071574
A:Accession: B39853
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-11 <FER>
A:Cross-references: UNIPROT:P19841; UNIPARC:UPI000016FDC7; GB:M64224; NID:q150701; PIDN

Query Match 25.3%; Score 21; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 1.7e+03;

Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DKLVGVVP 8
 ||::||
 Db 4 DKPLVFPV 11

RESULT 23

PS0325
 tetrahydroberberine oxidase (EC 1.3.3.8) - rice (strain Nihonbare) (fragment)

C/Species: Oryza sativa (rice)

C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 11-Apr-1995

C/Accession: PS0325

R/Tungita, A. JIPID, April 1993

submitted to JIPID, April 1993

A/Reference number: PS0206

A/Accession: PS0325

A/Molecule type: protein

A/Residues: 1-13 <TSU>

A/Cross-references: UNIPARC:UPI000017B121

A/Experimental source: callus

C/Keywords: oxidoreductase

Query Match 25.3%; Score 21; DB 2; Length 13;
 Best Local Similarity 50.0%; Pred. No. 2e+03;
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 KLVNGVPPYG 11
 ||::||
 Db 4 KLVGVGLXYG 13

RESULT 24

B61620

locustamyotropin IV - migratory locust

C/Species: Locusta migratoria (migratory locust)

C/Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 09-Jul-2004

C/Accession: B61620

R/SchoofB, L.; Holman, G.M.; Hayes, T.K.; Nachman, R.J.; Kochansky, J.P.; De Loof, A.

Insect Biochem. Mol. Biol. 22, 447-452, 1992

A/Title: Isolation, identification and synthesis of locustamyotropin III and IV, two add

A/Reference number: B61620

A/Accession: B61620

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-13 <SCH>

A/Cross-references: UNIPROT:P41490; UNIPARC:UPI000012E792

C/Keywords: amidated carboxyl end; neuropeptide

F.13/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 25.3%; Score 21; DB 2; Length 13;
 Best Local Similarity 57.1%; Pred. No. 2e+03;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 GVPFYGR 12
 ||::||
 Db 6 GVPFSFR 12

RESULT 25

G44957

photosystem II oxygen-evolving complex protein 2 - common tobacco (cv. Samsum NN) (fragm

C/Species: Nicotiana tabacum (common tobacco)

C/Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 18-Jun-1993

C/Accession: G44957

R/Takeda, S.; Sato, F.; Ida, K.; Yamada, Y.

Plant Cell Physiol. 31, 215-221, 1990

A/Title: Characterization of polypeptides that accumulate in cultured Nicotiana tabacum

A/Reference number: A44957

A/Accession: G44957

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-14 <PAK>

A/Cross-references: UNIPARC:UPI000017B0AD

Query Match 25.3%; Score 21; DB 2; Length 14;

Best Local Similarity 42.9%; Pred. No. 2.2e+03; Indels 0; Gaps 0;

Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 10 YGRAKSI 16
 ||::||
 Db 2 YGEANV 8

Search completed: January 26, 2006, 08:05:03
 Job time : 9.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 26, 2006, 08:05:12 : Search time 3.22414 Seconds
(without alignments)
57.099 Million cell updates/sec

Title: US-09-662-293-10

Perfect score: 83

Sequence: 1 DKLVGVPFGRAXSIE 17

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 75621 seqs, 10829074 residues 37628

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 21

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA New:
1: /cgn2_6/ptodata/1/pubppaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubppaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubppaa/PTCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubppaa/US09_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubppaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubppaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep:*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
1	37.3	11	7	US-11-145-035-4	Sequence 4, Appli
2	34.9	15	7	US-11-054-515-2757	Sequence 2757, Ap
3	34.9	16	6	US-10-859-643-762	Sequence 762, App
4	34.9	16	7	US-11-097-864-762	Sequence 762, App
5	34.9	16	7	US-11-097-912-762	Sequence 762, App
6	34.9	16	7	US-11-045-024-14490	Sequence 14490, A
7	33.7	11	6	US-10-665-658-53	Sequence 53, Appl
8	33.7	11	6	US-10-665-658-57	Sequence 57, Appl
9	32.5	11	6	US-10-665-658-54	Sequence 54, Appl
10	32.5	11	7	US-11-145-035-2	Sequence 2, Appli
11	31.3	8	7	US-11-145-035-6	Sequence 6, Appli
12	31.3	10	6	US-10-929-988-156	Sequence 156, App
13	31.3	11	7	US-11-145-035-5	Sequence 5, Appli
14	30.7	19	7	US-11-139-435-4	Sequence 4, Appli
15	30.1	11	6	US-10-665-658-51	Sequence 51, Appl
16	30.1	11	6	US-10-665-658-56	Sequence 56, Appl
17	30.1	12	6	US-10-665-658-58	Sequence 58, Appl
18	30.1	12	6	US-10-665-658-12	Sequence 12, Appl
19	30.1	16	7	US-11-054-515-2893	Sequence 2893, Ap
20	28.9	6	6	US-10-431-638-9	Sequence 9, Appli
21	28.9	8	6	US-10-431-638-10	Sequence 10, Appl
22	28.9	9	6	US-10-859-643-597	Sequence 597, App
23	28.9	9	6	US-10-859-643-685	Sequence 685, App
24	28.9	9	7	US-11-097-864-597	Sequence 597, App
25	28.9	9	7	US-11-097-864-685	Sequence 685, App

26	28.9	9	7	US-11-097-912-597	Sequence 597, App
27	28.9	9	7	US-11-097-912-685	Sequence 685, App
28	28.9	9	7	US-11-136-079-145	Sequence 145, App
29	28.9	10	7	US-11-041-893-56	Sequence 56, Appl
30	28.9	14	6	US-10-431-638-2	Sequence 2, Appli
31	28.9	14	6	US-10-431-638-38	Sequence 38, Appl
32	28.9	14	6	US-10-431-638-46	Sequence 46, Appl
33	28.9	17	6	US-10-945-853-4	Sequence 4, Appli
34	28.9	18	6	US-10-518-441-15	Sequence 15, Appl
35	28.9	18	6	US-10-431-638-19	Sequence 39, Appl
36	28.9	18	6	US-10-431-638-42	Sequence 42, Appl
37	28.9	18	6	US-10-431-638-43	Sequence 43, Appl
38	28.9	18	7	US-11-054-515-2752	Sequence 2752, App
39	28.9	19	7	US-11-033-1321	Sequence 1321, Ap
40	28.9	19	6	US-10-982-891-72	Sequence 72, Appl
41	28.9	20	6	US-10-939-990-174	Sequence 174, App
42	28.9	20	7	US-11-053-100-18	Sequence 18, Appl
43	28.9	12	6	US-10-982-891-55	Sequence 55, Appl
44	23.5	8	7	US-11-066-967-82	Sequence 82, Appl
45	27.7	9	6	US-10-073-301A-5	Sequence 5, Appli
46	27.7	9	7	US-11-203-137-5	Sequence 5, Appli
47	27.7	11	7	US-11-116-144-76	Sequence 76, Appl
48	27.7	12	7	US-11-193-512-42	Sequence 42, Appl
49	27.7	12	7	US-11-089-266-9	Sequence 9, Appli
50	27.7	14	7	US-11-054-515-2755	Sequence 2755, Ap
51	27.7	16	7	US-11-054-515-2796	Sequence 2796, Ap
52	27.7	16	7	US-11-054-515-3047	Sequence 3047, Ap
53	27.7	16	7	US-11-071-259-16	Sequence 16, Appl
54	27.7	17	7	US-11-097-812-91	Sequence 91, Appl
55	27.7	17	7	US-11-097-812-93	Sequence 93, Appl
56	27.7	17	7	US-11-097-812-94	Sequence 94, Appl
57	27.7	17	7	US-11-097-812-163	Sequence 163, App
58	27.7	17	7	US-11-097-812-166	Sequence 166, App
59	27.7	18	6	US-10-939-890-143	Sequence 143, App
60	27.7	18	7	US-11-054-515-2802	Sequence 2802, Ap
61	27.7	20	6	US-10-939-890-173	Sequence 173, App
62	27.7	20	6	US-10-901-576-14	Sequence 14, Appl
63	27.7	20	7	US-11-071-259-15	Sequence 15, Appl
64	27.7	20	7	US-10-491-096-44	Sequence 44, Appl
65	26.5	10	6	US-10-491-096-89	Sequence 89, Appl
66	26.5	10	6	US-10-491-096-185	Sequence 185, Appl
67	26.5	10	7	US-11-009-873A-209	Sequence 209, App
68	26.5	10	7	US-11-009-873A-209	Sequence 209, App
69	26.5	12	6	US-10-982-891-53	Sequence 53, Appl
70	26.5	12	6	US-10-982-891-53	Sequence 53, Appl
71	26.5	12	7	US-11-033-165-47	Sequence 47, Appl
72	26.5	15	7	US-11-054-515-2292	Sequence 2292, Ap
73	26.5	16	7	US-11-054-515-2760	Sequence 2760, Ap
74	26.5	17	7	US-11-054-515-2135	Sequence 2135, Ap
75	26.5	17	7	US-11-054-515-2156	Sequence 2156, Ap
76	26.5	18	7	US-11-054-515-3060	Sequence 3060, Ap
77	26.5	18	7	US-11-041-893-113	Sequence 113, App
78	26.5	18	7	US-11-156-163-11	Sequence 11, Appl
79	26.5	19	6	US-10-503-575-168	Sequence 168, App
80	26.5	19	7	US-11-054-515-2996	Sequence 2996, Ap
81	26.5	20	6	US-10-901-576-20	Sequence 20, Appl
82	26.5	20	7	US-11-094-142-32	Sequence 32, Appl
83	26.5	20	7	US-11-113-324-56	Sequence 56, Appl
84	26.5	21	7	US-11-113-324-56	Sequence 56, Appl
85	26.5	9	7	US-11-033-039-559	Sequence 559, App
86	26.5	9	7	US-11-033-039-616	Sequence 616, App
87	26.5	9	7	US-11-033-039-746	Sequence 746, App
88	26.5	9	7	US-11-033-039-766	Sequence 766, App
89	26.5	10	7	US-11-125-837-12	Sequence 12, Appl
90	26.5	10	7	US-11-045-024-750	Sequence 750, App
91	26.5	10	7	US-11-097-812-58	Sequence 58, Appl
92	26.5	11	7	US-11-033-165-52	Sequence 52, Appl
93	26.5	11	7	US-11-045-024-898	Sequence 898, App
94	26.5	12	7	US-11-058-135-35	Sequence 35, Appl
95	26.5	13	7	US-11-105-708-16	Sequence 16, Appl
96	26.5	14	6	US-10-929-988-448	Sequence 448, App
97	26.5	14	7	US-11-033-039-759	Sequence 759, App
98	26.5	15	6	US-10-939-890-467	Sequence 467, App

99 21 25.3 15 7 US-11-054-515-2213
100 21 25.3 15 7 US-11-054-515-2223

ALIGNMENTS

Sequence 2213, Ap
Sequence 2223, Ap

RESULT 1

US-11-145-035-4
; Sequence 4, Application US/11145035
; Publication No. US20050287122A1
; GENERAL INFORMATION:
; APPLICANT: Bartlett et al.
; TITLE OF INVENTION: AAV VECTORS AND METHODS
; FILE REFERENCE: 28335/41335
; CURRENT APPLICATION NUMBER: US/11/145,035
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: US 10/038,972
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: US 60/260,124
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: Patent version 3.3
; SEQ ID NO 4
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-145-035-4

Query Match 37.3%; Score 31; DB 7; Length 11;
Best Local Similarity 60.0%; Pred. No. 4.5;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 GVPPYGRAXS 15
Db 2 GTPFYLRKALS 11

RESULT 2

US-11-054-515-2757
; Sequence 2757, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2757

; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2757

Query Match 34.9%; Score 29; DB 7; Length 15;
Best Local Similarity 62.5%; Pred. No. 15;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 LVMGVPPY 10
Db 5 LVTGVPPY 12

RESULT 3

US-10-859-643-762
; Sequence 762, Application US/10859643
; Publication No. US20060002993A1
; GENERAL INFORMATION:
; APPLICANT: Challita-Bid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Farie, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Weyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; FILE REFERENCE: 511582006203
; CURRENT APPLICATION NUMBER: US/10/859,643
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 762
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-859-643-762

Query Match 34.9%; Score 29; DB 6; Length 16;
Best Local Similarity 46.2%; Pred. No. 16;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 DKLVMGVPPYGRA 13
Db 4 DSIIGVATYGA 16

RESULT 4

US-11-097-864-762
; Sequence 762, Application US/11097864
; Publication No. US20050265924A1
; GENERAL INFORMATION:
; APPLICANT: Challita-Bid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Farie, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Weyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2F10B
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 511582006205
; CURRENT APPLICATION NUMBER: US/11/097,864
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 762

REGISTRATION NUMBER: 59/44/
REFERENCE/DOCKET NUMBER: P1014R1CID1C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-4462
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 53:

SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: Amino Acid
TOPOLOGY: <Unknown>
SEQUENCE DESCRIPTION: SEQ ID NO: 53:
US-10-665-658-53

Query Match 33.7% Score 28; DB 6; Length 11;
Best Local Similarity 62.5%; Pred. No. 16;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GVPPYGRA 13
|: ||| |
Db 1 GIYFYGAA 8

RESULT 8
US-10-665-658-57
Sequence 57, Application US/10665658
Publication No. US20050276801A1
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
Presta, Leonard G.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/665,658
FILING DATE: 19-Sep-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 27-NOV-1996
APPLICATION NUMBER: 08/974899
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: 09/420745
FILING DATE: 20-OCT-1999
APPLICATION NUMBER: 09/975798
FILING DATE: 28-FEB-2001
ATTORNEY/AGENT INFORMATION:
NAME: Tan, Lee K.
REGISTRATION NUMBER: 39,447
REFERENCE/DOCKET NUMBER: P1014R1CID1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-4462
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: Amino Acid
TOPOLOGY: <Unknown>
SEQUENCE DESCRIPTION: SEQ ID NO: 57:
US-10-665-658-57

Query Match 33.7% Score 28; DB 6; Length 11;
Best Local Similarity 62.5%; Pred. No. 16;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GVPPYGRA 13
|: ||| |
Db 1 GIYFYGTA 8

RESULT 9
US-10-665-658-54
Sequence 54, Application US/10665658
Publication No. US20050276801A1
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
Presta, Leonard G.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/665,658
FILING DATE: 19-Sep-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 27-NOV-1996
APPLICATION NUMBER: 08/974899
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: 09/420745
FILING DATE: 20-OCT-1999
APPLICATION NUMBER: 09/975798
FILING DATE: 28-FEB-2001
ATTORNEY/AGENT INFORMATION:
NAME: Tan, Lee K.
REGISTRATION NUMBER: 39,447
REFERENCE/DOCKET NUMBER: P1014R1CID1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-4462
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: Amino Acid
TOPOLOGY: <Unknown>
SEQUENCE DESCRIPTION: SEQ ID NO: 54:
US-10-665-658-54

Query Match 32.5% Score 27; DB 6; Length 11;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 6 GVPPYG 11
|: ||| |
Db 1 GIYFYG 6

RESULT 10
US-11-145-035-2
Sequence 2, Application US/11145035
Publication No. US20050287122A1
GENERAL INFORMATION:
APPLICANT: Bartlett et al.
TITLE OF INVENTION: AAV VECTORS AND METHODS
FILE REFERENCE: 28335/4135
CURRENT APPLICATION NUMBER: US/11/145,035
CURRENT FILING DATE: 2005-06-03
PRIOR APPLICATION NUMBER: US 10/038,972
PRIOR FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: US 60/260,124
PRIOR FILING DATE: 2001-01-05

```
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Bovine Papilloma Virus Peptide
US-11-145-035-2
```

```
Query Match          32.5%; Score 27; DB 7; Length 11;
Best Local Similarity 50.0%; Pred. No. 24;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy      6 GVPPYGRAXS 15
      | | | | |
Db      2 GTPPYLKGLS 11
```

RESULT 11

```
US-11-145-035-6
; Sequence 6, Application US/11145035
; Publication No. US20050287122A1
; GENERAL INFORMATION:
; APPLICANT: Bartlett et al.
; TITLE OF INVENTION: AAV VECTORS AND METHODS
; FILE REFERENCE: 28335/41335
; CURRENT APPLICATION NUMBER: US/11/145,035
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: US 10/038,972
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: US 60/260,124
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Bovine Papilloma Virus Peptide
US-11-145-035-6
```

```
Query Match          31.3%; Score 26; DB 7; Length 8;
Best Local Similarity 80.0%; Pred. No. 5; 8e+04;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      6 GVPPY 10
      | | | |
Db      2 GTPPY 6
```

RESULT 12

```
US-10-929-988-156
; Sequence 156, Application US/109299988
; Publication No. US2005027588A1
; GENERAL INFORMATION:
; APPLICANT: Cwirala, Steven E.
; APPLICANT: BALU, PALANI
; APPLICANT: DUFFIN, DAVID J.
; APPLICANT: PIPLANI, SUNITA
; APPLICANT: MERRILL, BARBARA MCEOMEN
; APPLICANT: SCHATZ, PETER JOSEPH
; TITLE OF INVENTION: COMPOUNDS HAVING AFFINITY FOR THE GRANULOCYTE-COLONY
; TITLE OF INVENTION: STIMULATING FACTOR RECEPTOR (G-CSFR) AND ASSOCIATED
; FILE REFERENCE: 0300-0014
; CURRENT APPLICATION NUMBER: US/10/929,988
; CURRENT FILING DATE: 2004-08-30
; PRIOR APPLICATION NUMBER: US/09/620,091
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 491
; SOFTWARE: PatentIn Ver. 2.1
```

```
; SEQ ID NO 156
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-929-988-156
```

```
Query Match          31.3%; Score 26; DB 6; Length 10;
Best Local Similarity 40.0%; Pred. No. 32;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      1 DKLYMGVPPY 10
      | | | | |
Db      1 DEMVYTVPPY 10
```

RESULT 13

```
US-11-145-035-5
; Sequence 5, Application US/11145035
; Publication No. US20050287122A1
; GENERAL INFORMATION:
; APPLICANT: Bartlett et al.
; TITLE OF INVENTION: AAV VECTORS AND METHODS
; FILE REFERENCE: 28335/41335
; CURRENT APPLICATION NUMBER: US/11/145,035
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: US 10/038,972
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: US 60/260,124
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Bovine Papilloma Virus Peptide
US-11-145-035-5
```

```
Query Match          31.3%; Score 26; DB 7; Length 11;
Best Local Similarity 80.0%; Pred. No. 36;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      6 GVPPY 10
      | | | |
Db      2 GTPPY 6
```

RESULT 14

```
US-11-139-435-4
; Sequence 4, Application US/11139435
; Publication No. US20050287664A1
; GENERAL INFORMATION:
; APPLICANT: Fann, Ming-Ji
; TITLE OF INVENTION: Cellular Proliferation Control Factors
; FILE REFERENCE: 17741-002001
; CURRENT APPLICATION NUMBER: US/11/139,435
; CURRENT FILING DATE: 2005-05-27
; PRIOR APPLICATION NUMBER: US 60/575,611
; PRIOR FILING DATE: 2004-05-27
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: conditioned medium (CM)
US-11-139-435-4
```



```

;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/665,658
; FILING DATE: 19-Sep-2003
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/031971
; FILING DATE: 27-NOV-1996
; APPLICATION NUMBER: 08/974899
; FILING DATE: 20-NOV-1997
; APPLICATION NUMBER: 09/420745
; FILING DATE: 20-OCT-1999
; APPLICATION NUMBER: 09/975798
; FILING DATE: 28-FEB-2001
; ATTORNEY/AGENT INFORMATION:
; NAME: Tan, Lee K.
; REGISTRATION NUMBER: 39,447
; REFERENCE/DOCKET NUMBER: P1014R1C1D1C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-4462
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: Amino Acid
; TOPOLOGY: <unknown>
; SEQUENCE DESCRIPTION: SEQ ID NO: 58:
US-10-665-658-58

;
; Query Match 30.1%; Score 25; DB 6; Length 11;
; Best Local Similarity 66.7%; Pred. No. 54;
; Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 6 GVPPYG 11
Db 1 GIVPYG 6

RESULT 18
US-10-665-658-12
; Sequence 12, Application US/10665658
; Publication No. US20050276801A1
; GENERAL INFORMATION:
; APPLICANT: Jarden, Paula M.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/665,658
; FILING DATE: 19-Sep-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/031971
; FILING DATE: 27-NOV-1996
; APPLICATION NUMBER: 08/974899
; FILING DATE: 20-NOV-1997
; APPLICATION NUMBER: 09/420745
; FILING DATE: 20-OCT-1999
; APPLICATION NUMBER: 09/975798
; FILING DATE: 28-FEB-2001
; ATTORNEY/AGENT INFORMATION:
; NAME: Tan, Lee K.
```

```

;
; REGISTRATION NUMBER: 39,447
; REFERENCE/DOCKET NUMBER: P1014R1C1D1C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-4462
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-665-658-12

;
; Query Match 30.1%; Score 25; DB 6; Length 12;
; Best Local Similarity 66.7%; Pred. No. 60;
; Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 6 GVPPYG 11
Db 1 GIVPYG 6

RESULT 19
US-11-054-515-2893
; Sequence 2893, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Bly5
; FILE REFERENCE: P5523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2893
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2893

;
; Query Match 30.1%; Score 25; DB 7; Length 16;
; Best Local Similarity 44.4%; Pred. No. 83;
; Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 LVNGVPPYG 11
Db 5 ILNGVYYG 13

RESULT 20
US-10-431-638-9
; Sequence 9, Application US/10431638
; Publication No. US20060003939A1
```

```

; GENERAL INFORMATION:
; APPLICANT: The Rockefeller Institute
; APPLICANT: Steller, Hermann
; TITLE OF INVENTION: PEPTIDES AND METHODS FOR CELL DEATH REGULATION
; FILE REFERENCE: P-5004-US
; CURRENT APPLICATION NUMBER: US/10/431.638
; CURRENT FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 9
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-431-638-9
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```

Query Match      28.9%; Score 24; DB 6; Length 7;
Best Local Similarity 100.0%; Pred. No. 5.8e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy      7 VPFY 10
      |||
Db      2 VPFY 5
```

```

RESULT 21
; Sequence 10, Application US/10431638
; Publication No. US20060003939A1
; GENERAL INFORMATION:
; APPLICANT: The Rockefeller Institute
; APPLICANT: Steller, Hermann
; TITLE OF INVENTION: PEPTIDES AND METHODS FOR CELL DEATH REGULATION
; FILE REFERENCE: P-5004-US
; CURRENT APPLICATION NUMBER: US/10/431.638
; CURRENT FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 10
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-431-638-10
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Query Match      28.9%; Score 24; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.8e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      7 VPFY 10
      |||
Db      2 VPFY 5
```

```

RESULT 22
US-10-859-643-597
; Sequence 597, Application US/10859643
; Publication No. US20060002993A1
; GENERAL INFORMATION:
; APPLICANT: Chailita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Farris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; FILE REFERENCE: 511582006203
; CURRENT APPLICATION NUMBER: US/10/859,643
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
```

```

; SEQ ID NO 597
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-859-643-597
```

```

Query Match      28.9%; Score 24; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.8e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      7 VPFY 10
      |||
Db      1 VPFY 4
```

```

RESULT 23
US-10-859-643-685
; Sequence 685, Application US/10859643
; Publication No. US20060002993A1
; GENERAL INFORMATION:
; APPLICANT: Chailita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Farris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; FILE REFERENCE: 511582006203
; CURRENT APPLICATION NUMBER: US/10/859,643
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 685
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-859-643-685
```

```

Query Match      28.9%; Score 24; DB 6; Length 9;
Best Local Similarity 44.4%; Pred. No. 5.8e+04;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      2 KLVNGVPFFY 10
      ::::
Db      1 ELTGTLDYF 9
```

```

RESULT 24
US-11-097-864-597
; Sequence 597, Application US/11097864
; Publication No. US20050265924A1
; GENERAL INFORMATION:
; APPLICANT: Chailita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Farris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2F10B
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 511582006205
; CURRENT APPLICATION NUMBER: US/11/097,864
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
```

SEQ ID NO 597
LENGTH: 9
TYPE: PRT
ORGANISM: Homo Sapien
US-11-097-864-597

Query Match 28.9%; Score 24; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.8e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VPFY 10
|||
Db 1 VPFY 4

RESULT 25
US-11-097-864-685
Sequence 685, Application US/11097864
Publication No. US20050265924A1
GENERAL INFORMATION:
APPLICANT: Chailica-Eid, Pia M.
APPLICANT: Raitano, Arthur B.
APPLICANT: Paris, Mary
APPLICANT: Hubert, Rene S.
APPLICANT: Morrison, Karen Jane Meyrick
APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2F10B
TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 511582006205
CURRENT APPLICATION NUMBER: US/11/097,864
CURRENT FILING DATE: 2005-04-01
PRIOR APPLICATION NUMBER: US 10/062,109
PRIOR FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: US 10/005,480
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 765
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 685
LENGTH: 9
TYPE: PRT
ORGANISM: Homo Sapien
US-11-097-864-685

Query Match 28.9%; Score 24; DB 7; Length 9;
Best Local Similarity 44.4%; Pred. No. 5.8e+04;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 KLWGVVPFY 10
|||
Db 1 ELTGGLDPY 9

Search completed: January 26, 2006, 08:39:07
Job time : 4.22414 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 26, 2006, 07:47:56 ; Search time 50.5603 Seconds
(without alignments)
237.221 Million cell updates/sec

Title: US-09-662-293-10
Perfect score: 83
Sequence: 1 DKLVGMGVFYGRAXSIE 17

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 15779

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Uniprot 05.80.*
1: uniprot_sprot.*
2: uniprot_tr embl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	33.7	16	2	099898_HUMAN
2	27	32.5	21	2	04YWI1_PLABE
3	26	31.3	12	2	Q7AU55_GGAMM
4	26	31.3	16	1	DHE2_THROT
5	25	30.1	16	2	Q9S8A0_PINKO
6	24	28.9	14	1	TY13_BOWVA
7	24	28.9	16	2	015632_HUMAN
8	24	28.9	16	2	Q9AUA1_SBRAS
9	24	28.9	20	2	Q9S8H8_BRANA
10	24	28.9	21	2	Q4XLR5_PLACH
11	23	27.7	8	2	06LID23_MOUSE
12	23	27.7	12	2	Q7MUI3_ORYSA
13	23	27.7	13	2	Q7S2J9_NEUCR
14	23	27.7	14	2	Q8AXQ7_XENLA
15	23	27.7	15	2	Q9BXQ0_HUMAN
16	23	27.7	18	2	Q7TSR9_MOUSE
17	23	27.7	19	2	Q7M2G7_VICFA
18	23	27.7	19	2	06LIDN4_RHOCA
19	23	27.7	19	2	08K3K5_MOUSE
20	23	27.7	20	1	OM4VA_VIBAL
21	23	27.7	20	1	TLI9_SPTOL
22	23	27.7	20	2	Q9TWN3_THESA
23	23	27.7	20	2	P81896_SOLTU
24	23	27.7	21	1	TL19_ARATH
25	23	27.7	21	2	Q7RZT1_NEUCR
26	23	27.7	21	2	Q9RFZ1_MYCNS
27	23	27.7	21	2	Q5C9K1_MYCMY
28	23	27.7	21	2	Q80817_GDELA
29	22	26.5	9	2	05IA44_PABAE
30	22	26.5	10	2	06JL97_NEIGO
31	22	26.5	12	2	050019_MYCLE

32	22	26.5	13	1	CRBL_ICASP
33	22	26.5	13	1	SOVO_SEPOP
34	22	26.5	16	2	Q4X7B4_PLACH
35	22	26.5	16	2	Q8H9Z9_VIRU
36	22	26.5	16	2	Q9QVU1_9MURI
37	22	26.5	17	1	FLAW_AZOCH
38	22	26.5	17	2	Q7S3B2_NEUCR
39	22	26.5	17	2	Q7RBC2_PLAVO
40	22	26.5	17	2	Q7RTN3_PLATO
41	22	26.5	18	2	Q8NFB4_HUMAN
42	22	26.5	18	2	Q9R7B8_BORBU
43	22	26.5	18	2	Q9R7B9_BORBU
44	22	26.5	19	2	Q6XMK6_MACNG
45	22	26.5	19	2	Q9TR77_RABIT
46	22	26.5	20	1	FLAW_AZOVI
47	22	26.5	21	2	Q6W8P8_HUMAN
48	22	26.5	21	2	Q4YXH0_PLABE
49	22	26.5	21	2	Q9TRK1_CANPA
50	22	26.5	21	2	Q8X4E1_ECO57
51	22	26.5	21	2	Q57019_ARATH
52	21.5	25.9	18	2	Q09258_SYNFB
53	21	25.3	10	1	TKS1_AEDAE
54	21	25.3	10	1	TKS2_AEDAE
55	21	25.3	10	1	Q85V66_EUCGR
56	21	25.3	10	2	Q9UAR8_AEDAE
57	21	25.3	12	1	GRAR_RANRU
58	21	25.3	13	1	FLWT_LWFT
59	21	25.3	13	1	LMT4_LOCFI
60	21	25.3	13	1	PSBP_PINPS
61	21	25.3	13	1	TEMA_RANTE
62	21	25.3	15	2	Q7M2Q2_SHEEP
63	21	25.3	15	2	Q9RGQ3_MYCCA
64	21	25.3	15	2	Q9TH04_GRUMM
65	21	25.3	16	2	Q8LIY8_9CYVN
66	21	25.3	17	2	Q7RDV1_PLAVO
67	21	25.3	18	1	PDH_PANBO
68	21	25.3	19	2	Q6XMK0_MACGL
69	21	25.3	19	2	Q9RFZ7_MYCCA
70	21	25.3	20	1	FERA_PABDE
71	21	25.3	20	1	PSAL_SYNVU
72	21	25.3	20	2	Q9UWH0_9EURY
73	21	25.3	20	2	Q8NED5_HUMAN
74	21	25.3	20	2	Q96AH6_HUMAN
75	21	25.3	20	2	Q8MUP7_MACNU
76	21	25.3	21	2	Q52SL0_PIG
77	21	25.3	21	2	Q5C9K4_MYCMY
78	20.5	24.7	16	2	Q04246_9PARA
79	20.5	24.7	16	2	Q88250_9PARA
80	20.5	24.7	16	2	Q88250_9PARA
81	20.5	24.7	16	2	Q99154_9PARA
82	20.5	24.7	21	2	Q84204_9PARA
83	20.5	24.1	10	1	ANGT1_BOTVA
84	20	24.1	11	1	TKU2_DREUN
85	20	24.1	11	2	Q7M2V7_SHEEP
86	20	24.1	12	1	H2AX_ONCMY
87	20	24.1	13	2	Q7LZ51_PHYBI
88	20	24.1	14	1	TKN1_SCHGR
89	20	24.1	14	2	Q9UH91_HUMAN
90	20	24.1	14	2	P82219_BOMMO
91	20	24.1	15	2	Q9UWG1_9EURY
92	20	24.1	15	2	Q7M1W4_9EURY
93	20	24.1	15	2	Q7M2B5_9ORYN
94	20	24.1	15	2	Q35188_TOBAC
95	20	24.1	15	2	Q9RQ22_SALYT
96	20	24.1	15	2	Q9PRZ9_MITCN
97	20	24.1	16	1	TRYP_FELCA
98	20	24.1	16	2	Q4W372_9LECA
99	20	24.1	16	2	Q4W373_9LECA
100	20	24.1	16	2	Q7M1U4_CHLRE

ALIGNMENTS

P17237	icaria.sp.
P83567	sepia.offic
Q4X7B4	plasmodium
Q8H9Z9	bacterioph
Q9QVU1	mus.sp..s
P33002	acrobacter
Q7S3B2	neurospora
Q7RBC2	plasmodium
Q7RTN3	plasmodium
Q8NFB4	homo.sapien
Q9R7B8	borrelia.bu
Q9R7B9	borrelia.bu
Q6XMK6	macaca.nigr
Q9TR77	oryzocelagus
P52964	azotobacter
Q6W8P8	homo.sapien
Q4YXH0	plasmodium
Q9TRK1	canis.famil
Q8X4E1	escherichia
Q57019	arabidopsis
Q09258	synecococc
P42634	aedes.aegypt
P42635	aedes.aegypt
Q85V66	eucalyptus
Q9UAR8	aedes.aegypt
P40754	rana.rugosa
P82064	ilmodynast
P41490	locusta.mig
P81668	pinus.pinus
P56197	rana.tempor
Q7M2Q2	ovis.arles
Q9RGQ3	mycoplasma
Q9TH04	grus.americ
Q8LIY8	oscillator
Q7RDV1	plasmodium
P01209	pandanus.bo
Q6XMK0	macaca.sille
Q9RFZ7	mycoplasma
P84468	paracoccus
P25937	synecococc
Q9UWH0	thermococc
Q8NED5	homo.sapien
Q96AH6	homo.sapien
Q8MUP7	macaca.mula
Q52SL0	sus.scrofa
Q5C9K4	mycoplasma
Q04246	sendai.viru
Q88250	sendai.viru
Q88250	sendai.viru
Q99154	sendai.viru
Q84204	sendai.viru
Q10581	bothrops.ja
P40752	urechis.unl
Q7M2V7	ovis.arles
P83377	oncohychnu
Q7LZ51	phyllomedus
P82470	schistocerc
Q9UH91	homo.sapien
P82219	bombyx.mori
Q9UWG1	pyrococcus
Q7M1W4	arabidopsis
Q7M2B5	glycine.max
Q35188	nicotiana.t
Q9RQ22	salmonella
Q9PRZ9	micropogon
P81071	felis.silve
Q4W372	dolichoune
Q4W373	dolichoune
Q7M1U4	chlamydomon

```

RESULT 1
O98988_HUMAN
ID O98988_HUMAN PRELIMINARY; PRT; 16 AA.
AC O98988;
DT 01-MAY-1997 (TRENBLREL. 03, Created)
DT 01-MAY-1997 (TRENBLREL. 03, Last sequence update)
DT 01-MAR-2001 (TRENBLREL. 16, Last annotation update)
DE Mutant Soc isoform 1 (Fragment).
GN Name=hSOS1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OC NCBI_TaxID=9606;
OX [1]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Brain;
RX MEDLINE=96239588; PubMed=8649768;
RA Rojas J.M., Coque J.J., Lorentz M.V., Esteban L.M., Santos E.;
RA de la Cruz X., Lorentz M.V., Esteban L.M., Santos E.;
RT "A 15 amino acid stretch close to the Grb2-binding domain defines two
RT differentially expressed hSOS1 isoforms with markedly different Grb2
RT binding affinity and biological activity."
RL Oncogene 12:2291-2300(1996).
DR EMBL; S82270; AAB47139.2; -; mRNA.
FT NON_TER
FT NON_TER
SQ SEQUENCE 16 AA; 1701 MW; 0D019B3983244198 CRC64;

Query Match 33.7%; Score 28; DB 2; Length 16;
Best Local Similarity 44.4%; Pred. No. 1.3e+03;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Oy 8 PFYGRAXSI 16
Db 5 PFHSRSASV 13

RESULT 2
O4YWI1_PLABE
ID O4YWI1_PLABE PRELIMINARY; PRT; 21 AA.
AC O4YWI1;
DT 13-SEP-2005 (TRENBLREL. 31, Created)
DT 13-SEP-2005 (TRENBLREL. 31, Last sequence update)
DT 13-SEP-2005 (TRENBLREL. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=PB105279.00.0;
OS Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5681;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RP Hall N., Karras M., Raine J.D., Carlson J.M., Kooij T.W.A.,
RA Jermann M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rubenford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Bartell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses."
RL Science 307:82-86(2005).
CC -i- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; CAI01002172; CAH97795.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON_TER
FT NON_TER
SQ SEQUENCE 21 AA; 2553 MW; BDEE331C6A63146B CRC64;

Query Match 32.5%; Score 27; DB 2; Length 21;
Best Local Similarity 37.5%; Pred. No. 2.5e+03;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

```

```

Oy 3 LVMGVPEY 10
Db 13 IITGFPPF 20

RESULT 3
O7AUS5_9GAMM
ID O7AUS5_9GAMM PRELIMINARY; PRT; 12 AA.
AC O7AUS5;
DT 05-JUL-2004 (TRENBLREL. 27, Created)
DT 05-JUL-2004 (TRENBLREL. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLREL. 27, Last annotation update)
DE Putative transposase (Fragment).
GN Name=tnp1006;
OS Acinetobacter sp. BM3.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OX NCBI_TaxID=106395;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=BM3;
RX PubMed=15073307; DOI=10.1099/mic.0.26844-0;
RA Kholodil G., Mindlin S., Gorienko Z., Petrova M., Hobman J.,
RA Nikiforov V.;
RT "Translocation of transposition-deficient [Tn(d)PKH2-like]
RT transposons in the natural environment: mechanistic insights from the
RT study of adjacent DNA sequences."
RL Microbiology 150:979-992(2004).
RN [2]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=BM3;
RA Kholodil G.Y.;
RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ486856; CAD31077.1; -; Genomic_DNA.
FT NON_TER
FT NON_TER
SQ SEQUENCE 12 AA; 1457 MW; E5832A70F8F40871 CRC64;

Query Match 31.3%; Score 26; DB 2; Length 12;
Best Local Similarity 80.0%; Pred. No. 2.1e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 8 PFYGR 12
Db 3 PFHGR 7

RESULT 4
DHE2_THUTH
ID DHE2_THUTH STANDARD; PRT; 16 AA.
AC P20016;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-MAY-2005 (Rel. 47, Last annotation update)
DE NAD-specific glutamate dehydrogenase (EC 1.4.1.2) (NAD-GDH)
DE (Fragment).
OS Thunnus thynnus (Bluefin tuna).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
OC Scombridae; Thunnus.
OX NCBI_TaxID=8237;
RN [1]
RN PROTEIN SEQUENCE.
RP TISSUE=Liver;
RX MEDLINE=76253947; PubMed=182270; DOI=10.1016/0005-2744(76)90156-X;
RA Veronese F.M., Bevilacqua R., Bocca E., Brown D.M.;
RT "Purification, characteristics and sequence of a peptide containing an
RT essential lysine residue."
RL Biochim. Biophys. Acta 445:1-13(1976).
CC -i- CATALYTIC ACTIVITY: L-glutamate + H(2)O + NAD(+) = 2-oxoglutarate

```

```

CC      + NH(3) + NADH.
CC      -1- SIMILARITY: Belongs to the Glu/Leu/Phe/Val dehydrogenases family.
CC      -----
CC      This Swiss-Prot entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use as long as its content is in no way modified and this statement is not
CC      removed.
CC      -----
CC      PIR: A12729, A12729.
CC      InterPro: IPR006095; GLFV_dehydrog.
CC      InterPro: IPR006097; GLFV_dehydrog_N.
CC      Pfam: PF02812; ELFV_dehydrog_N; 1.
CC      DR PROSITE: PS00074; GLFV_DEHYDROGENASE; PARTIAL.
CC      Direct protein sequencing; NAD; Oxidoreductase.
CC      ACT_SITE 12 12
CC      FT NON_TER 1 1
CC      FT NON_TER 16 16
CC      SQ SEQUENCE 16 AA; 1518 MW; FF299AATC5F1062F CRC64;

Query Match 31.3%; Score 26; DB 1; Length 16;
Best Local Similarity 35.7%; Pred. No. 2.8e+03;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Oy 4 VMGVPFYGRAXSIE 17
Db 3 VVDVFPFGAKAGVK 16

RESULT 5
O958A0_PINMO PRELIMINARY; PRT; 16 AA.
AC O958A0;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2000 (Tremblrel. 14, Last annotation update)
DE Ribulose BIPHOSPHATE carboxylase small subunit (Fragment).
OS Pinus monticola (Western white pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinus; Strobus.
OX NCBI_TaxID=3345;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=96213005; PubMed=8665095;
RA Ekramoddoullah A.K., Taylor D.W.;
RT "Seasonal variation of western white pine (Pinus monticola D. Don)
RT foliage proteins."
RL Plant Cell Physiol. 37:189-199(1996).
SQ SEQUENCE 16 AA; 1803 MW; 27D4934C881717DE CRC64;

Query Match 30.1%; Score 25; DB 2; Length 16;
Best Local Similarity 50.0%; Pred. No. 4.3e+03;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 8 PFYGRAXSIE 17
Db 5 PFYGNAAKFE 14

RESULT 6
TY13_BOMVA STANDARD; PRT; 14 AA.
AC P84215;
DT 01-FEB-2005 (Rel. 46, Created)
DT 01-FEB-2005 (Rel. 46, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Tyrocinophyllin-13.
OS Bombina variegata (Yellow-bellied toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Archaeobatrachia; Bombinatoridae; Bombina.
OX NCBI_TaxID=8348;
RN [1]
RP PROTEIN SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, TISSUE SPECIFICITY,

```

```

RP AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RX PubMed=15134346; DOI=10.1515/BC.2004.027;
RA Marechal L., Flact P.R., Orr D.F., McClean S., Shaw C.,
RA Abdel-Wahab Y.H.;
RT "Skin secretion of the toad Bombina variegata contains multiple
RT insulin-releasing peptides including bombesin and entirely novel
RT insulinotropic structures."
RL Biol. Chem. 385:315-321(2004).
CC -1- FUNCTION: Possesses insulin-releasing activity.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the skin glands.
CC -1- MASS SPECTROMETRY: MW=1650.5; METHOD=Electrospray; RANGE=1-14;
CC NOTE=Ref.1.
CC -----
CC      This Swiss-Prot entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use as long as its content is in no way modified and this statement is not
CC      removed.
CC      -----
CC      DR GO: GO:0005576; C:extracellular region; IDA.
CC      DR GO: GO:0005179; F:hormone activity; TAS.
CC      DR GO: GO:0006952; P:defense response; TAS.
CC      DR GO: GO:0050796; P:regulation of insulin secretion; IDA.
CC      KM Amphibian defense peptide; Direct protein sequencing.
CC      SQ SEQUENCE 14 AA; 1651 MW; 23C4809C33A0DC77 CRC64;

Query Match 28.9%; Score 24; DB 1; Length 14;
Best Local Similarity 80.0%; Pred. No. 5.6e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 6 GVPPY 10
Db 1 GKPPY 5

RESULT 7
Q15632_HUMAN PRELIMINARY; PRT; 16 AA.
ID Q15632_HUMAN
AC Q15632;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE TCl3 oncogene (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=90222189; PubMed=2326274;
RA Zutter M., Hockett R.D., Roberts C.W., McGuire E.A., Bloomstone J.,
RA Morton C.C., Deaven L.L., Crist W.M., Carroll A.J., Kormeyer S.J.;
RT "The t(10;14)(q24;q11) of T-cell acute lymphoblastic leukemia
RT juxtaposes the delta T-cell receptor with TCl3, a conserved and
RT activated locus at 10q24."
RL Proc. Natl. Acad. Sci. U.S.A. 87:3161-3165(1990).
DR EMBL: M33602; AAA6450.1; -; Genomic_DNA.
DR PIR: I79565; I79565.
CC FT NON_TER 1 1
CC FT NON_TER 16 16
CC SQ SEQUENCE 16 AA; 1812 MW; EBCF0A05EAE77D24 CRC64;

Query Match 28.9%; Score 24; DB 2; Length 16;
Best Local Similarity 66.7%; Pred. No. 6.4e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 DKLVWG 6
Db 11 DKLVFG 16

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RESULT 8
Q9ADU1_9BRAS PRELIMINARY; PRT; 16 AA.
ID Q9ADU1_9BRAS PRELIMINARY; PRT; 16 AA.
AC Q9ADU1;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Chalcone synthase (Fragment).
OS Arabis pauciflora.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabis.
OX NCBI_TaxID=81980;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=2141848; PubMed=11557794;
RA Koch M.A., Weisshaar B., Kroymann J., Haubold B., Mitchell-Olds T.;
RT "Comparative genomics and regulatory evolution: conservation and
function of the Chs and Atp1a3 promoters.";
RL Mol. Biol. Evol. 18:1882-1891(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Koch M., Kroymann J., Haubold B., Weisshaar B., Mitchell-Olds T.;
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF248998; AAK31933.1; -; Genomic_DNA.
FT NON_TER
SQ SEQUENCE 16 AA; 1763 MW; 7D744974539F6176 CRC64;

Query Match 28.9%; Score 24; DB 2; Length 16;
Best Local Similarity 66.7%; Pred. No. 6.4e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 LVNGVP 8
Db 1 MVMGTP 6

RESULT 9
Q9S8H8_BRANA PRELIMINARY; PRT; 20 AA.
ID Q9S8H8_BRANA PRELIMINARY; PRT; 20 AA.
AC Q9S8H8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Myosinase-binding protein 50 (Fragment).
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3708;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=95218603; PubMed=7766044; DOI=10.1007/BF00202596;
RA Falk A., Taipaleensuu J., Ek B., Lenman M., Raek L.;
RA Planta 195:387-395(1995).
DR InterPro: IPR001229; Jaccalin_lectin.
DR Pfam: PF01419; Jaccalin; 1.
SQ SEQUENCE 20 AA; 2101 MW; A12000918972901A CRC64;

Query Match 28.9%; Score 24; DB 2; Length 20;
Best Local Similarity 57.1%; Pred. No. 8e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 7 VPFYGRA 13
Db 2 IGFHGRA 8

RESULT 10
Q4XLT5_PLACH PRELIMINARY; PRT; 21 AA.
ID Q4XLT5_PLACH PRELIMINARY; PRT; 21 AA.
AC Q4XLT5;
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DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=PC109111.00.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5825;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berrihan M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churche C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Jansz C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -! CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
CC EMBL; CAU01004799; CAH82127.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON_TER
SQ SEQUENCE 21 AA; 2641 MW; 98FCAF5AC6E06614 CRC64;

Query Match 28.9%; Score 24; DB 2; Length 21;
Best Local Similarity 33.3%; Pred. No. 8.4e+03;
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 2 KLVNGVPFY 10
Db 3 KMTATITFY 11

RESULT 11
Q6LD23_MOUSE PRELIMINARY; PRT; 8 AA.
ID Q6LD23_MOUSE PRELIMINARY; PRT; 8 AA.
AC Q6LD23;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Interferon alpha/beta receptor (Fragment).
GN Name=Ifnar1; Synonyms=IFNAR;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95047447; PubMed=7958966; DOI=10.1016/0378-1119(94)90710-2;
RA Lucifalla G., Uze G.;
RT "Structure of the murine interferon alpha/beta receptor-encoding gene:
high-frequency rearrangements in the interferon-resistant Li210 cell
line.";
RL Gene 148:343-346(1994).
DR EMBL; U06237; AAA65003.1; -; Genomic_DNA.
DR MGI; MGI:107658; Ifnar1.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
KW Receptor.
FT NON_TER
FT NON_TER
SQ SEQUENCE 8 AA; 999 MW; CSBBS9D76059D76A CRC64;

Query Match 27.7%; Score 23; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 2.2e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 7 VPFY 10
Db 1
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Db 4 IPFY 7

RESULT 12

Q7MU3 ORYSA PRELIMINARY; PRT; 12 AA.

AC 07MU3

DT 01-MAR-2004 (TREMBlrel. 26, Created)

DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)

DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)

DE Unidentified 5.4/35K protein (Fragment).

OS Oryza sativa (Rice).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; OC Euphorbiaceae; Oryzae; Oryza.

NCBI_TaxID=4530;

OX NCBI

NP [1]

PROTEIN SEQUENCE.

RA Komatsu S., Kajiwara H., Hirano H.;

RT "A rice protein library; a data-file of rice proteins separated by RT two-dimensional electrophoresis."

RL Theor. Appl. Genet. 86:935-942(1993).

DR PIR; PQ0730; PQ0730.

DR Gramene; Q7MU3; -

FT NON_TER 1 1

FT SEQUENCE 12 AA; 1316 MW; SED102D36E59C9C3 CRC64;

Query Match 27.7%; Score 23; DB 2; Length 12;

Best Local Similarity 80.0%; Pred. No. 7.1e+03;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 FYGRA 13

Db 7 FYGRA 11

RESULT 13

Q7S2J9 NEUCR PRELIMINARY; PRT; 13 AA.

AC Q7S2J9

DT 01-MAR-2004 (TREMBlrel. 26, Created)

DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)

DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)

DE Predicted protein.

GN Name=NCU04977.1;

OS Neurospora crassa.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.

NCBI_TaxID=5141;

OX NCBI

NP [1]

NUCLEOTIDE SEQUENCE.

RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D., RA Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B., RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M., RA Qui D., Iankiev P., Pedersen D., Nelson M., Washburne M., RA Seltrenikoff C.P., Knesey J.A., Braun E.L., Zelter A., Schulte D., RA Koche G.O., Jedd G., Mewes W., Straben C., Marcotte E., Greenberg D., RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S., RA Kamal M., Kamysseles M., Mauceli E., Bielke C., Rudd S., Frisman D., RA Kyrkocofva S., Karmussen C., Metznerberg R.L., Perkins D.D., Kroken S., RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmari S.A., RA Desouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R., RA Varden O., Piamann M., Sellar S., Dunlap J., Radford A., Aramayo R., RA Natvig P.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M., RA Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B., RA "The Genome Sequence of the Filamentous Fungus Neurospora crassa.", RL Nature 0:0-0(2003).

CC -1- CANTUION: The sequence shown here is derived from an EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is preliminary data.

EMBL; AABX01000422; EAA29651.1; -; Genomic_DNA.

SQ SEQUENCE 13 AA; 1703 MW; 099245360492586B CRC64;

Query Match 27.7%; Score 23; DB 2; Length 13;

Best Local Similarity 42.9%; Pred. No. 7.7e+03;

Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 MGVPFYG 11

Db 1 MAIDYVG 7

RESULT 14

Q8AXO7 XENLA PRELIMINARY; PRT; 14 AA.

AC Q8AXO7

DT 01-MAR-2003 (TREMBlrel. 23, Created)

DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)

DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

DE Mannose-binding lectin-associated serine protease (Fragment).

GN Name=MASP;

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae; OC Xenopodinae; Xenopus; Xenopus.

NCBI_TaxID=8355;

OX NCBI

NP [1]

NUCLEOTIDE SEQUENCE.

RA MEDLINE=22593355; PubMed=12707349;

RA Endo Y., Nonaka M., Suga H., Kakimura Y., Matsueita A., Takahashi M., RA Matsushita M., Fujita T.;

RT "Origin of mannose-binding lectin complement pathway traced back to RT and MASP-3 involved in the lectin complement pathway traced back to RT the invertebrate, amphioxus."

RL J. Immunol. 170:4701-4707(2003).

DR EMBL; AB078909; BAC41345.1; -; Genomic_DNA.

DR GO; GO:0008223; F:peptidase activity; IEA.

DR GO; GO:0005529; F:sugar binding; IEA.

KM Lectin; Protease.

FT NON_TER 1 1

FT SEQUENCE 14 AA; 1533 MW; 99DD285F40C2B15 CRC64;

Query Match 27.7%; Score 23; DB 2; Length 14;

Best Local Similarity 50.0%; Pred. No. 8.3e+03;

Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 GVPEFYGA 13

Db 2 GVPEFSRS 9

RESULT 15

Q9BXO0 HUMAN PRELIMINARY; PRT; 15 AA.

AC Q9BXO0

DT 01-JUN-2001 (TREMBlrel. 17, Created)

DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)

DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)

DE Tissue transglutaminase (EC 2.3.2.13) (Fragment).

GN Name=TG2;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; OC Homo.

NCBI_TaxID=9606;

OX NCBI

NP [1]

NUCLEOTIDE SEQUENCE.

RA TISSUE=Brain;

RA Clifton B.A., Santa Cruz K.S., Davies P.J.A., Pestoff B.W.;

RT "Intron-exon swapping of transglutaminase mRNA and neuronal tau RT aggregation in Alzheimer's disease.";

RL J. Biol. Chem. 0:0-0(2001).

EMBL; AF311286; AAK15272.1; -; mRNA.

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DR GO: GO:0005622; C:intracellular; NAS.
DR GO: GO:0005524; F:ATP binding; TAS.
DR GO: GO:0005525; F:GTP binding; TAS.
DR GO: GO:0003924; F:GTPase activity; TAS.
DR GO: GO:0003810; F:protein-glutamine gamma-glutamyltransferase; . . . ; TAS.
DR GO: GO:0006916; F:anti-apoptosis; TAS.
DR GO: GO:0019933; P:cAMP-mediated signaling; TAS.
DR GO: GO:0019221; P:cytokine and chemokine mediated signaling P. . . ; NAS.
DR GO: GO:0007186; P:G-protein coupled receptor protein signalin. . . ; IMP.
DR GO: GO:0018276; P:isopeptide cross-linking via N6-glycyl-L-ly. . . ; IDA.
DR GO: GO:0012501; P:programmed cell death; TAS.
KM Acyltransferase; Transferase.
FT NON_TER 1
SQ SEQUENCE 15 AA; 1641 MW; C340982AFBFB851 CRC64;

Query Match 27.7%; Score 23; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 9e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 PFYGRA 13
DB 3 PFSGKA 8

RESULT 16
Q7TSR9 MOUSE PRELIMINARY; PRT; 18 AA.
AC Q7TSR9;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Candidate plasticity gene 15 (Fragment).
GN Name=Cpg15;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
NX NCBI_TaxID=10090;
RX [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6;
RA Fujino T., Lee W.-C.A., Nedivi E.;
RT "Regulation of cpg15 by Signaling Pathways that Mediate Synaptic
RT Plasticity.";
RL Mol. Cell. Neurosci. 24:538-554(2003).
DR EMBL; AY150584; AAN64528.1; -; Genomic_DNA.
FT NON_TER 18
SQ SEQUENCE 18 AA; 2002 MW; ACC71930108873CC CRC64;

Query Match 27.7%; Score 23; DB 2; Length 18;
Best Local Similarity 41.7%; Pred. No. 1.1e+04;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 5 MGVPFYGRAXSI 16
DB 1 MGLKMGKRYISL 12

RESULT 17
Q7M2G7 VICFA PRELIMINARY; PRT; 19 AA.
AC Q7M2G7;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE NADH2 dehydrogenase (EC 1.6.99.3) 14K chain (Fragment).
OS Vicia faba (Broad bean).
OG Mitochondrion.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eustosida 1; Fabales; Fabaceae; Papilionoideae; Viciae; Vicia.
OX NCBI_TaxID=3906;
RN [1]

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RP PROTEIN SEQUENCE.
RX MEDLINE=94151437; PubMed=8108509; DOI=10.1104/jp.102.2.435;
RA Letenne S., Boutry M.;
RT "Purification and preliminary characterization of mitochondrial
RT complex I (NADH:ubiquinone reductase) from broad bean (Vicia faba
RT L.) .";
RL Plant Physiol. 102:435-443(1993).
DR PIR; P00790; P00790.
DR GO: GO:0003954; F:NADH dehydrogenase activity; IEA.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 19 AA; 1913 MW; 4113C369A5F11704 CRC64;

Query Match 27.7%; Score 23; DB 2; Length 19;
Best Local Similarity 66.7%; Pred. No. 1.1e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 LVWGVP 8
DB 13 LVSGIP 18

RESULT 18
Q6LDN4 RHQCA PRELIMINARY; PRT; 19 AA.
ID Q6LDN4 RHQCA PRELIMINARY;
AC Q6LDN4;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE R. capsulata nifHDK operon. (Fragment).
OS Rhodospirillum rubrum (Rhodospirillum rubrum).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
OC Rhodobacteraceae; Rhodobacter.
OX NCBI_TaxID=1061;
RX [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=88313675; PubMed=3410321; DOI=10.1016/0378-1119(88)90463-5;
RA Pollack D., Bauer C.E., Scolnik P.A.;
RT "Transcription of the Rhodospirillum rubrum nifHDK operon is
RT modulated by the nitrogen source: Construction of plasmid expression
RT vectors based on the nifHDK promoter.";
RL Gene 65:269-275(1988).
DR EMBL; M29400; AAA26142.1; -; Genomic_DNA.
FT NON_TER 19
SQ SEQUENCE 19 AA; 2012 MW; 61392A571F316AB7 CRC64;

Query Match 27.7%; Score 23; DB 2; Length 19;
Best Local Similarity 50.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 VPFYGR 12
DB 7 IAFYRK 12

RESULT 19
Q8KXK5 MOUSE PRELIMINARY; PRT; 19 AA.
ID Q8KXK5 MOUSE PRELIMINARY;
AC Q8KXK5;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Arginase I (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
NX NCBI_TaxID=10090;
RX [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=129/SvJ;
RC PubMed=15922518; DOI=10.1016/j.gene.2005.04.004;
RX Gray M.J., Poljakovic M., Kepka-Lenhart D., Morris S.M. Jr.;

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RT "Induction of arginase I transcription by IL-4 requires a composite DNA response element for STAT6 and C/EBPbeta."

RL Gene 353:98-106(2005).

DR EMBL; AY074884; AAL79623.1; -; Genomic_DNA.

FT NON TER 19

SQ SEQUENCE 19 AA; 2005 MW; B4D0E34BB3508F90 CRC64;

Query Match 27.7%; Score 23; DB 2; Length 19;

Best Local Similarity 50.0%; Pred. No. 1.1e+04;

Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 VMGVVF 9

DB 10 IICAPF 15

RESULT 20

OM4VA VIBAL STANDARD; PRT; 20 AA.

AC P81149;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE Outer membrane protein 40Va (Omp40Va) (Fragment).

OS *Vibrio alginolyticus*.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; *Vibrio*.

OC NCBI_TaxId=663;

RN [1]

RP PROTEIN SEQUENCE.

RC STRAIN=NCIMB 1903T;

RA Ochi M., Hirabayashi J., Suzuki S.;

RT "Characterization of major outer membrane proteins of *Vibrio alginolyticus* and the stability against proteases."

RL Microbes Environ. 0:0-0(2002).

CC -1- SUBUNIT: Homotrimer (By similarity).

CC -1- SUBCELLULAR LOCATION: Outer membrane.

CC -1- SIMILARITY: Belongs to the Gram-negative porin family.

CC -----

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CC -----

CC Direct protein sequencing; Ion transport; Membrane; Outer membrane;

KM Porin; Transmembrane; Transport.

FT NON TER 20

SQ SEQUENCE 20 AA; 2229 MW; 4FA95CB24FEC3CDE CRC64;

Query Match 27.7%; Score 23; DB 1; Length 20;

Best Local Similarity 66.7%; Pred. No. 1.2e+04;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 VPFYGR 12

DB 11 VDFYGO 16

RESULT 21

TL19 SPIOL STANDARD; PRT; 20 AA.

AC P82799;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Thylakoid lumenal 18.4 kDa protein (P18.4) (Fragment).

OS *Spinacia oleracea* (Spinach).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; OC Caryophyllales; Amaranthaceae; Spinacia.

OC NCBI_TaxId=3562;

RN [1]

RP PROTEIN SEQUENCE.

RA Kieselbach T., Petersson U., Bystedt M., Schroeder W.P.;

RL Submitted (JUL-2000) to Swiss-Prot.

CC -1- SUBCELLULAR LOCATION: Chloroplast; within the thylakoid lumen.

CC -----

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CC -----

CC Chloroplast; Direct protein sequencing; Thylakoid.

KM NON TER 20

SQ SEQUENCE 20 AA; 2131 MW; 460408C32420991B CRC64;

Query Match 27.7%; Score 23; DB 1; Length 20;

Best Local Similarity 57.1%; Pred. No. 1.2e+04;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FYGRAXS 15

DB 11 YYGTMAAS 17

RESULT 22

O9TMN3 THESE PRELIMINARY; PRT; 20 AA.

AC O9TMN3;

DT 01-MAY-2000 (TRENBLUREL. 13, Created)

DT 01-MAY-2000 (TRENBLUREL. 13, Last sequence update)

DT 01-JUN-2000 (TRENBLUREL. 14, Last annotation update)

DE 45 kDa immunodominant polypeptide (Fragment).

OS *Theileria sergenti*.

OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileridae; OC Theileria.

OC NCBI_TaxId=5877;

RN [1]

RP PROTEIN SEQUENCE.

RA Baek B.K., Kim B.S., Rhim B.M., Lee H.I., Park Y.H., Kakoma I.;

RT "Immunogenicity and protective efficacy of solubilized merozoite-enriched *Theileria sergenti* immunogens. III. Characterization of immunodominant peptides."

RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.

SQ SEQUENCE 20 AA; 2270 MW; 97F9C630713B8284 CRC64;

Query Match 27.7%; Score 23; DB 2; Length 20;

Best Local Similarity 55.6%; Pred. No. 1.2e+04;

Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DKLVGVVF 9

DB 12 DKVVARDPF 20

RESULT 23

P81896 SOLTU PRELIMINARY; PRT; 20 AA.

AC P81896;

DT 01-JUN-2000 (TRENBLUREL. 14, Created)

DT 01-JUN-2000 (TRENBLUREL. 14, Last sequence update)

DT 01-JUN-2000 (TRENBLUREL. 24, Last annotation update)

DE Dihydroisoprenyl succinyltransferase component of 2-oxoglutarate dehydrogenase complex (EC 2.3.1.61) (E2) (OGDC-E2) (Fragment).

OS *Solanum tuberosum* (Potato).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; OC Lamiales; Solanales; Solanaceae; *Solanum*.

OC NCBI_TaxId=4113;

RN [1]

RP PROTEIN SEQUENCE.

RC STRAIN=cv. ROMANO; TISSUE=TUBER;

RX MEDLINE=99441232; PubMed=10510296; DOI=10.1042/0264-6021:3430327; Miller A.H., Hill S.A., Leaver C.J.;

RT "Plant mitochondrial 2-oxoglutarate dehydrogenase complex:
RT purification and characterization in potato."; Biochem. J. 343:1327-1334(1999).
RL
CC -1- FUNCTION: THE 2-OXOGLOUTARATE DEHYDROGENASE COMPLEX CATALYZES THE
CC OVERALL CONVERSION OF 2-OXOGLOUTARATE TO SUCCINYL-COA & CO(2). IT
CC CONTAINS MULTIPLE COPIES OF 3 ENZYMAIC COMPONENTS: 2-OXOGLOUTARATE
CC DEHYDROGENASE (E1), DIHYDROLIPOAMIDE SUCCINYLTRANSFERASE (E2) AND
CC LIPOAMIDE DEHYDROGENASE (E3).
CC -1- CATALYTIC ACTIVITY: SUCCINYL-COA + DIHYDROLIPOAMIDE = COA + S-
CC SUCCINYLDIHYDROLIPOAMIDE.
CC -1- COFACTOR: THE E2 COMPONENT CONTAINS ONE COVALENTLY-BOUND LIPOYL
CC COFACTOR.
CC -1- SUBUNIT: FORMS A 24-POLYPEPTIDE STRUCTURAL CORE WITH OCTAHEDRAL
CC SYMMETRY (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL.
CC -1- CAUTION: X IN THE SEQUENCE MIGHT BE CYS RESIDUE.
CC -1- SIMILARITY: TO OTHER SPECIES E2 COMPONENT.
DR GO; GO:0005739; C:mitochondrion; IEA.
DR GO; GO:0008415; F:acylttransferase activity; IEA.
DR GO; GO:0004149; F:diacylttransferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006096; P:glycolysis; IEA.
KW Acyltransferase; Glycolysis; Lipoyl; Mitochondrion; Transferase.
FT NON TER 20
SQ SEQUENCE 20 AA; 2050 MW; 9256BE292E26A344 CRC64;

Query Match 27.7%; Score 23; DB 2; Length 20;
Best Local Similarity 44.4%; Pred. No. 1.2e+04;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 7 VFYGRAXS 15
||| : |
DB 12 VPMGESIS 20

RESULT 24
TL19_ARATH STANDARD; PRT; 21 AA.
AC P82658;
DT 16-OCT-2001 (Rel. 40; Created)
DT 16-OCT-2001 (Rel. 40; Last sequence update)
DT 05-JUL-2004 (Rel. 44; Last annotation update)
DE Thylakoid lumenal 19 kDa protein (P19) (Fragment).
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP PROTEIN SEQUENCE.
RC STRAIN=cv. Columbia;
RA Kieselbach T., Bystedt M., Schroeder W.P.;
RL Submitted (JUL-2000) to Swiss-Prot.
CC -1- SUBCELLULAR LOCATION: Chloroplast; within the thylakoid lumen.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC Chloroplast; Direct protein sequencing; Thylakoid.
KW NON TER 21
FT SEQUENCE 21 AA; 2199 MW; EAA1345E72C00054 CRC64;

Query Match 27.7%; Score 23; DB 1; Length 21;
Best Local Similarity 57.1%; Pred. No. 1.3e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 9 FYGRAXS 15
: ||| |
DB 9 YFGTAAAS 15

RESULT 25
Q7RZ21_NEUCR PRELIMINARY; PRT; 21 AA.
ID Q7RZ21_NEUCR
AC Q7RZ21;
DT 01-MAR-2004 (TRENBLREL. 26; Created)
DT 01-MAR-2004 (TRENBLREL. 26; Last sequence update)
DT 01-MAR-2004 (TRENBLREL. 26; Last annotation update)
DE Predicted protein.
GN Name=NCU10082.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
RA Selitrenikoff C.P., Kinsey J.A., Braun E.L., Zeller A., Schulte U.,
RA Koche G.O., Jedd G., Nemes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barlett R., Gnerre S.,
RA Kamal M., Kamysseilis M., Mauceli E., Bietke C., Rudd S., Frisman D.,
RA Krystofova S., Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmani S.A.,
RA Desouza C.C., Glase L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Eboile D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.,
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa."
RL Nature 0:0-0(2003).
CC -1- CAUTION: The sequence shown here is derived from an
CC preliminary data.
CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
DR EMBL; AABX0100651; EAA28603.1; -; Genomic DNA.
SQ SEQUENCE 21 AA; 2379 MW; E1CE7FEAD658B6D5 CRC64;

Query Match 27.7%; Score 23; DB 2; Length 21;
Best Local Similarity 50.0%; Pred. No. 1.3e+04;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 5 MGVPFYGR 12
||| : ||
DB 1 MGTVPFGR 8

Search completed: January 26, 2006, 08:04:00
Job time : 53.5603 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 26, 2006, 07:47:09 ; Search time 64.5345 Seconds

(without alignments)
129.360 Million cell updates/sec

Title: US-09-662-293-11

Perfect score: 109
Sequence: 1 DHPPTNHHKYLVCESVNG 19Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 897420

Minimum DB seq length: 0
Maximum DB seq length: 21Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database :

A_GeneSeq_21:*

1: geneeqp1980s:*
2: geneeqp1980s:*
3: geneeqp2000s:*
4: geneeqp2001s:*
5: geneeqp2002s:*
6: geneeqp2003as:*
7: geneeqp2003bs:*
8: geneeqp2004s:*
9: geneeqp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	109	100.0	19	3	AA552520 House dus
2	109	100.0	19	5	AAU96324 Der HMW-m
3	109	100.0	20	3	AA552512 House dus
4	109	100.0	20	5	AAU96316 Der HMW-m
5	37.5	34.4	20	4	AAU18898 Peptide #
6	37.5	34.4	20	4	AB838020 Peptide #
7	37.5	34.4	20	4	AAU18898 Peptide #
8	37.5	34.4	20	4	AAU18898 Peptide #
9	37.5	34.4	20	4	AAU18898 Peptide #
10	37.5	34.4	20	4	AAU18898 Peptide #
11	37.5	34.4	20	4	AAU18898 Peptide #
12	37.5	34.4	20	4	AAU18898 Peptide #
13	37.5	34.4	20	4	AAU18898 Peptide #
14	37.5	34.4	20	4	AAU18898 Peptide #
15	37.5	34.4	20	4	AAU18898 Peptide #
16	37.5	34.4	20	4	AAU18898 Peptide #
17	37.5	34.4	20	4	AAU18898 Peptide #
18	37.5	34.4	20	4	AAU18898 Peptide #
19	37.5	34.4	20	4	AAU18898 Peptide #
20	37.5	34.4	20	4	AAU18898 Peptide #
21	37.5	34.4	20	4	AAU18898 Peptide #
22	37.5	34.4	20	4	AAU18898 Peptide #
23	37.5	34.4	20	4	AAU18898 Peptide #
24	37.5	34.4	20	4	AAU18898 Peptide #
25	37.5	34.4	20	4	AAU18898 Peptide #
26	37.5	34.4	20	4	AAU18898 Peptide #
27	37.5	34.4	20	4	AAU18898 Peptide #
28	37.5	34.4	20	4	AAU18898 Peptide #
29	37.5	34.4	20	4	AAU18898 Peptide #
30	37.5	34.4	20	4	AAU18898 Peptide #
31	37.5	34.4	20	4	AAU18898 Peptide #
32	37.5	34.4	20	4	AAU18898 Peptide #
33	37.5	34.4	20	4	AAU18898 Peptide #
34	37.5	34.4	20	4	AAU18898 Peptide #
35	37.5	34.4	20	4	AAU18898 Peptide #
36	37.5	34.4	20	4	AAU18898 Peptide #
37	37.5	34.4	20	4	AAU18898 Peptide #
38	37.5	34.4	20	4	AAU18898 Peptide #
39	37.5	34.4	20	4	AAU18898 Peptide #
40	37.5	34.4	20	4	AAU18898 Peptide #
41	37.5	34.4	20	4	AAU18898 Peptide #
42	37.5	34.4	20	4	AAU18898 Peptide #
43	37.5	34.4	20	4	AAU18898 Peptide #
44	37.5	34.4	20	4	AAU18898 Peptide #
45	37.5	34.4	20	4	AAU18898 Peptide #
46	37.5	34.4	20	4	AAU18898 Peptide #
47	37.5	34.4	20	4	AAU18898 Peptide #
48	37.5	34.4	20	4	AAU18898 Peptide #
49	37.5	34.4	20	4	AAU18898 Peptide #
50	37.5	34.4	20	4	AAU18898 Peptide #
51	37.5	34.4	20	4	AAU18898 Peptide #
52	37.5	34.4	20	4	AAU18898 Peptide #
53	37.5	34.4	20	4	AAU18898 Peptide #
54	37.5	34.4	20	4	AAU18898 Peptide #
55	37.5	34.4	20	4	AAU18898 Peptide #
56	37.5	34.4	20	4	AAU18898 Peptide #
57	37.5	34.4	20	4	AAU18898 Peptide #
58	37.5	34.4	20	4	AAU18898 Peptide #
59	37.5	34.4	20	4	AAU18898 Peptide #
60	37.5	34.4	20	4	AAU18898 Peptide #
61	37.5	34.4	20	4	AAU18898 Peptide #
62	37.5	34.4	20	4	AAU18898 Peptide #
63	37.5	34.4	20	4	AAU18898 Peptide #
64	37.5	34.4	20	4	AAU18898 Peptide #
65	37.5	34.4	20	4	AAU18898 Peptide #
66	37.5	34.4	20	4	AAU18898 Peptide #
67	37.5	34.4	20	4	AAU18898 Peptide #
68	37.5	34.4	20	4	AAU18898 Peptide #
69	37.5	34.4	20	4	AAU18898 Peptide #
70	37.5	34.4	20	4	AAU18898 Peptide #
71	37.5	34.4	20	4	AAU18898 Peptide #
72	37.5	34.4	20	4	AAU18898 Peptide #
73	37.5	34.4	20	4	AAU18898 Peptide #
74	37.5	34.4	20	4	AAU18898 Peptide #
75	37.5	34.4	20	4	AAU18898 Peptide #
76	37.5	34.4	20	4	AAU18898 Peptide #
77	37.5	34.4	20	4	AAU18898 Peptide #
78	37.5	34.4	20	4	AAU18898 Peptide #
79	37.5	34.4	20	4	AAU18898 Peptide #
80	37.5	34.4	20	4	AAU18898 Peptide #
81	37.5	34.4	20	4	AAU18898 Peptide #
82	37.5	34.4	20	4	AAU18898 Peptide #
83	37.5	34.4	20	4	AAU18898 Peptide #
84	37.5	34.4	20	4	AAU18898 Peptide #
85	37.5	34.4	20	4	AAU18898 Peptide #
86	37.5	34.4	20	4	AAU18898 Peptide #
87	37.5	34.4	20	4	AAU18898 Peptide #
88	37.5	34.4	20	4	AAU18898 Peptide #
89	37.5	34.4	20	4	AAU18898 Peptide #
90	37.5	34.4	20	4	AAU18898 Peptide #
91	37.5	34.4	20	4	AAU18898 Peptide #
92	37.5	34.4	20	4	AAU18898 Peptide #
93	37.5	34.4	20	4	AAU18898 Peptide #
94	37.5	34.4	20	4	AAU18898 Peptide #
95	37.5	34.4	20	4	AAU18898 Peptide #
96	37.5	34.4	20	4	AAU18898 Peptide #
97	37.5	34.4	20	4	AAU18898 Peptide #


```
XX Mite allergen protein; map; high molecular weight; HMW-map; allergy;  
KW house dust mite; IgE; immunoglobulin E; allergen; mapB; mapC;  
KM hypersensitivity reaction; therapy; treatment; diagnosis; human; feline;  
RW canine; veterinary; antibody; vaccine; immunisation.  
XX  
OS Dermatophagoides farinae.  
XN WO9954349-A2.  
XX  
PD 28-OCT-1999.  
XX  
PF 16-APR-1999;    99WO-US008524.  
XX  
PR 17-APR-1998;    98US-00062013.  
PR 13-MAY-1998;    98US-0085295P.  
PR 02-SEP-1998;     98US-0098909P.  
XX  
PA (HESK-) HESKA CORP.  
XX  
PI McCall CA, Hunter SW, Weber ER;  
XX  
XX MPI; 2000-052700/04.  
DR  
PT Novel high molecular weight Dermatophagoides nucleic acid polypeptides  
PT used to modify an animals' hypersensitivity to mite allergens.  
XX  
PS Claim 3; Page 69; 154pp; English.  
XX  
CC Sequences AAU52510-Y52522 represent proteolytic fragments of  
CC Dermatophagoides farinae high molecular weight mite allergen protein (HMW  
CC -map) composition. The HMW-map composition was isolated from a D. Farinae  
CC homeogenate by gel filtration, with each fraction being analysed for the  
CC presence of proteins that bound to IgE present in mite-allergic dog  
CC antisera. The HMW-map composition comprises mapA (a 109 kD protein) and  
CC mapB (98 kD). Mite allergenic proteins and peptides, and nucleic acids  
CC encoding them, may be used in therapeutic compositions to modify an  
CC animal's hypersensitivity reaction to mite allergens. Animals that may be  
CC treated include mammals and birds, especially felines, canines, equines,  
CC humans, other pets, and work or domestic animals. The proteins or  
CC fragments may also be used to diagnose allergies via a skin test. The  
CC proteins and peptides can also be used to raise antibodies, which have a  
CC variety of potential uses. For example, they can be used as vaccines to  
CC passively immunise animals against dust mite hypersensitivity, as  
CC positive controls in test kits and as tools to recover desired dust mite  
CC allergens from a mixture of proteins  
XX  
SQ Sequence 20 AA:  
  
Query Match          100.0%; Score 109; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 4,2e+11;  
Matches   19; Conservative      0; Mismatches   0; Indels       0; Gaps        0;  
  
OY           1 DIHPHTNIHKYLVCSEVNG 19  
            |||||  
Db           1 DIHPFTNIHKLYLCESVNG 19  
            |  
  
RESULT 4  
AAU96316  
ID AU096316 standard; peptide; 20 AA.  
XX  
XX AAU96316;  
XX  
DT 15-JUL-2002 (first entry)  
XX  
DE Der HMW-map polypeptide #3.  
XX  
KW Der HMW-map; American house dust mite; antiallergic; mite; IgE;  
KW mite allergenic protein; immunoglobulin E; hypersensitivity;  
KW immunocomplex formation.  
XX  
XX Dermatophagoides farinae.
```

```

FN XX WO200222807-A2.
PN XX
XX XX 21-MAR-2002.
FD XX
XX XX
PF PF 14-SEP-2001; 2001WO-US028730.
XX XX
PR PR 14-SEP-2000; 2000US-00662293.
XX XX
PA PA (HESK-) HESKA CORP.
XX XX
PI PI Mccall CA, Hunter SW, Weber ER;
XX XX WPI; 2002-351888/38.
DR DR
XX XX
PT PT New mite allergenic protein isolated from Dermatophagoides, designated
PT PT Der HMW-map protein, useful as a vaccine for treating mite allergy.
XX XX
PS PS Claim 12; Page 70; 161pp; English.
XX XX
CC CC The invention relates to an isolated mite allergenic protein of
CC CC Dermatophagoides, designated Der HMW-map protein, and its related nucleic
CC CC acid. The Der HMW-map protein is useful for eliciting an immune response
CC CC against Der HMW-map protein. The protein or a reagent comprising a non-
CC CC proteinaceous epitope is useful for identifying an animal (e.g., dog,
CC CC cat) susceptible to or having an allergic response to a mite. A
CC CC therapeutic composition is useful for desensitizing a host animal to an
CC CC allergic response to a mite. The DNA and protein can be used in the
CC CC detection of anti-Der HMW-map antibodies in animal fluids, and inhibition
CC CC of immunoglobulin (IgE) or Der HMW-map protein activity associated with a
CC CC disease. Antibodies that bind to Der HMW-map are useful for inhibiting
CC CC binding of proteins to IgE, to prevent immunocomplex formation, thus
CC CC reducing hypersensitivity responses to mite allergens, and as vaccines
CC CC against mite allergen hypersensitivity. Sequences AAU96314-AAU96342
CC CC represent Der HMW-map polypeptides of the invention
XX XX
SQ SQ Sequence 20 AA;
XX XX
Query Match 100.0%; Score 109; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.2e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DIPHPTNIHKYLVCESVNG 19
Db 1 DIPHPTNIHKYLVCESVNG 19
| | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | |
RESULT 5 *
ID ID AAM18898 standard; protein; 20 AA.
AA AAM18898;
XX XX
DT DT 12-OCT-2001 (first entry)
DE DE Peptide #5332 encoded by probe for measuring cervical gene expression.
XX XX
KW KW Probe; human; microarray; gene expression; cervical epithelial cell;
OS OS cervical cancer.
XX XX
XX XX Homo sapiens.
XX XX
XX XX WO200157278-A2.
XX XX
XX XX PD 09-AUG-2001.
XX XX
XX XX 30-JAN-2001; 2001WO-US000670.
XX XX
XX XX 04-FEB-2000; 2000US-0180312P.
XX XX 26-MAY-2000; 2000US-0207456P.
XX XX 30-JUN-2000; 2000US-00608408.
XX XX 03-AUG-2000; 2000US-00632356.
XX XX 21-SEP-2000; 2000US-0234687P.
XX XX

```


Matches 6; Conservative 5; Mismatches 2; Indels 1; Gaps 1;
 QY 2 IPHPTNHHKYLVC 15
 :|||:|:|:|:
 Db 8 LPHP-HSHTHLLCQ 20

RESULT 8
 ABB23254
 ID ABB23254 standard; protein: 20 AA.

AC ABB23254;

DT 23-JAN-2002 (first entry)

DE Protein #5253 encoded by probe for measuring heart cell gene expression.

KW Human; gene expression; heart; microarray; vascular system;

KM cardiovascular disease; hypertension; cardiac arrhythmia;

OS Homo sapiens.

PN WO200157274-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US000666.

PR 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488899/53.

XX Single exon nucleic acid probes for analyzing gene expression in human

PT heart.

XX Claim 15; SEQ ID NO 25024; 530bp; English.

XX The present invention relates to single exon nucleic acid probes for

CC measuring human gene expression in a sample derived from human heart (see

CC ABA21535-ABA1305). The present sequence is a protein encoded by one such

CC probe. The probes may be used for predicting, measuring and displaying

CC gene expression in samples derived from the human heart via microarrays.

CC By measuring gene expression, the probes are useful for predicting,

CC diagnosing, grading, staging, monitoring and prognosing diseases of the

CC human heart and vascular system e.g. cardiovascular disease,

CC hypertension, cardiac arrhythmias and congenital heart disease. Note: The

CC sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at fcp.wipo.int/pub/published_pct_sequences

XX Sequence 20 AA;

SO

Query Match 34.4%; Score 37.5; DB 4; Length 20;

Best Local Similarity 42.9%; Pred. No. 58;

Matches 6; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

QY 2 IPHPTNHHKYLVC 15

:|||:|:|:|:

Db 8 LPHP-HSHTHLLCQ 20

RESULT 9

AAM71153
 ID AAM71153 standard; protein: 20 AA.

AC AAM71153;

DT 06-NOV-2001 (first entry)

DE Human bone marrow expressed probe encoded protein SEQ ID NO: 31459.

KW Human; bone marrow expressed exon; gene expression analysis; probe;

KM microarray; cancer; leukaemia; lymphoma; myeloma.

OS Homo sapiens.

PN WO200157276-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US000668.

PR 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488900/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing

PT gene expression in human bone marrow.

XX Example 4; SEQ ID NO 31459; 658bp + Sequence listing; English.

XX The present invention provides a number of single exon nucleic acid

CC probes which are derived from genomic sequences expressed in the human

CC bone marrow. They can be used to measure gene expression in bone marrow

CC samples, which may enable the improved diagnosis and treatment of cancers

CC such as lymphoma, leukaemia and myeloma. The present sequence is a

CC protein encoded by one of the probes of the invention

XX Sequence 20 AA;

SO

Query Match 34.4%; Score 37.5; DB 4; Length 20;

Best Local Similarity 42.9%; Pred. No. 58;

Matches 6; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

QY 2 IPHPTNHHKYLVC 15

:|||:|:|:|:

Db 8 LPHP-HSHTHLLCQ 20

RESULT 10

AAM58647

ID AAM58647 standard; protein: 20 AA.

AC AAM58647;

DT 05-NOV-2001 (first entry)

DE Human brain expressed single exon probe encoded protein SEQ ID NO: 30752.

KW Human; brain expressed exon; gene expression analysis; probe; microarray;

KM Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.

OS Homo sapiens.

PN WO200157275-A2.

XX 09-AUG-2001.
PD
PF 30-JAN-2001; 2001WO-US0000667.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-483446/52.
XX
PT Single exon nucleic acid probes for analyzing gene expression in human
XX brains.
XX
PS Example 4; SEQ ID NO 30752; 650bp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is a protein encoded by one of
CC the probes of the invention
XX
SQ Sequence 20 AA;

	Query Match	34.4%	Score 37.5	DB 4	Length 20
Best	Local Similarity	42.9%	Pred No. 58		
Matches	6; Conservative	5; Mismatches	2; Indels	1; Gaps	1
OY	2 IPHPTNIHKYLCVCE	15			
	: : : : : :				
Db	8 LPHH-HSHTHLLCQ	20			

```

RESULT 11
ABG52865
ID   ABG52865 standard; peptide, 20 AA.
XX
XX
AC   ABG52865;
XX
DT   25-FEB-2003 (first entry)
XX
DE   Human liver peptide, SEQ ID NO 31513.
XX
KW   Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
KM   hypercholesterolaemia; coronary heart disease.
XX
OS   Homo sapiens.
XX
PN   WO200157273-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US000664.
XX
PR   04-FEB-2000; 2000US-0180312P.
PR   26-MAY-2000; 2000US-0207456P.
PR   30-JUN-2000; 2000US-00608408.
PR   03-AUG-2000; 2000US-00632366.
PR   21-SEP-2000; 2000US-0234687P.
PR   27-SEP-2000; 2000US-0236359P.
PR   04-OCT-2000; 2000GB-00024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.

```

xx Penn SG, Hanzel DK, Chen W, Rank DR;
xx WPI; 2001-488898/53.
xx
xx Human genome-derived single exon nucleic acid probes useful for analyzing
xx PT gene expression in human adult liver.
xx
xx Claim 27; SEQ ID NO 31513; 658bp; English.
xx
xx The invention relates to a single exon nucleic acid probe (SENP) (I) for
xx measuring human gene expression in a sample derived from human adult
xx liver, comprising one of 13109 defined nucleotide sequences given in the
xx specification (or complements/ fragments). The probe hybridizes at high
xx stringency to a nucleic acid molecule expressed in the human adult liver.
xx (I) may be used for predicting, measuring and displaying gene expression
xx in samples derived from human adult liver. The genes identified may be
xx involved in genetic liver diseases such as cirrhosis,
xx hyperlipoproteinemia, hyperlipidemia and hypercholesterolaemia which is
xx associated with coronary heart disease. ABG47348-ABG5930 represent human
xx liver single exon encoded peptides of the invention. Note: The sequence
xx information for this patent does not appear in the printed specification
xx but was obtained in electronic format directly from WIPO at
xx ftp.wipo.int/pub/published_pct_sequences
xx
xx Sequence 20 AA;

	Query Match	Similarity	Score	DB	Length	
	Best Local	Similarity	42.9%		Pred. No. 58;	
	Matches	6; Conservative	5;	Mismatches	2;	Indels 1; Gaps 1
QY	2	IPHPPTINKYLVC	15			
DB	8	LPHP-HSHNTLLCQ	20			

```
RESULT 12
ABG40950
ID   ABG40950  standard; peptide; 20 AA.
XX
XX   ABG40950;
AC
XX
DT   19-AUG-2002 (first entry)
```

DE	Human peptide encoded by genome-derived single exon probe SEQ ID 30615
XX	
KM	Human; single exon probe; asthma; lung cancer; COPD; ILD;
KM	chronic obstructive pulmonary disease; interstitial lung disease;
KM	familial idiopathic pulmonary fibrosis; neurofibromatosis;
KM	tuberosus sclerosis; Gaucher's disease; Niemann-pick disease;
KM	Hernanx-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
KM	pulmonary histiocytosis; lymphangioleiomyomatosis; Kargener syndrome;
KM	pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
KM	primary ciliary dyskinesia; pulmonary hypertension;
XX	hyaline membrane disease.
XX	
OS	Homo sapiens.
XX	
PN	WO200186003-A2.
XX	
PD	
XX	15-NOV-2001.
XX	
PF	30-JAN-2001; 2001WO-US000665.
XX	
XX	04-FEB-2000; 2000US-0180312P.
PR	26-MAY-2000; 2000US-0207456P.
PR	30-JUN-2000; 2000US-00680408.
PR	03-AUG-2000; 2000US-00632366.
PR	21-SEP-2000; 2000US-0234687P.
PR	27-SEP-2000; 2000US-0236359P.
PR	04-OCT-2000; 2000GB-00024263.
PA	
(MOLE-) MOLECULAR DYNAMICS INC.	

XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI WPI; 2002-114183/15.
XX Spatially-addressable set of single exon nucleic acid probes, used to
PT measure gene expression in human lung samples.
XX
PS Claim 27; SEQ ID NO 30615; 634bp; English.
XX
CC The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human lung comprising single exon nucleic acid probes having one of
CC 12614 nucleic acid sequences mentioned in the specification, or their
CC complements or the 12387 open reading frames derived from the 12614
CC probes. Also included are a microarray comprising the novel set of probes
CC; the novel set of probes which hybridize at high stringency to a nucleic
CC acid expressed in the human lung; measuring gene expression in a sample
CC derived from human lung, comprising (a) contacting the array with a
CC collection of detectably labeled nucleic acids derived from human lung
CC mRNA, and (b) measuring the label detectably bound to each probe of the
CC array; identifying exons in a eukaryotic genome, comprising (a)
CC algorithmically predicting at least one exon from genomic sequences of
CC the eukaryote; and (b) detecting specific hybridization of detectably
CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
CC having a fragment identical to the predicted exon, the probe is included
CC in the above mentioned microarray; assigning exons to a single gene,
CC comprising (a) identifying exons from genomic sequence by the method
CC above and (b) measuring the expression of each of the exons in several
CC tissues and/or cell types using hybridization to a single exon
CC microarrays having a probe with the exon, where a common pattern of
CC expression of the exons in the tissues and/or cell types indicates that
CC the exons should be assigned to a single gene; a peptide comprising one
CC of 12011 sequences, mentioned in the specification, or encoded by the
CC probes/open reading frames (ORF). The probes are used for gene expression
CC analysis, and for identifying exons in a gene, particularly using human
CC lung derived mRNA and for the study of lung diseases such as asthma, lung
CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
CC Kargener syndrome, fibrocystic pulmonary dysplasia, primary ciliary
CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The
CC present sequence is a peptide/protein encoded by a single exon probe of
CC the invention. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 AA;
Query Match 34.4%; Score 37.5; DB 5; Length 20;
Best Local Similarity 42.9%; Pred. No. 58;
Matches 6; Conservative 5; Mismatches 2; Indels 1; Gaps 1;
QY 2 IHPPTNIHKVLVCE 15
:||||:|:|:|:
Db 8 LPHF-HSHTHLLCQ 20
RESULT 13
ADCC27861
ID ADCC27861 standard; peptide; 7 AA.
XX
AC ADCC27861;
XX
DT 18-DEC-2003 (first entry)
XX
DE Synthetic stain targeting peptide Seq ID54.
XX
KM target stain; phenol oxidizing enzyme; redox reaction;
KM detergent industry; paper and pulp industry; textile industry;
KM food industry; laccase enzyme; textile; carotenoid stain; fabric;

KW skin cosmetic; food; fruit ripening agent; oxidase protein;
KM stain targeting peptide.
XX
OS Synthetic.
XX
XX WO2003023067-A1.
PN
XX
XX 20-MAR-2003.
PD
XX
XX 03-SEP-2002; 2002WO-US027993.
PF
XX
XX 12-SEP-2001; 2001US-00954385.
PR
XX
PA (GENV) GENENCOR INT INC.
PI Aehle W, Baldwin TL, Janssen GG, Murray CJ, Van Gastel FJC;
PI Wang H, Winęczy DS;
XX WPI; 2003-532545/50.
DR
XX
XX Novel binding peptide useful for enhancing the binding of a laccase
PT enzyme to a target stain, to target a stain on a textile, and in skin
PT cosmetics.
XX
PS Claim 1; SEQ ID NO 54; 50pp; English.
XX
CC This invention relates to novel peptides which bind to a target stain.
CC The invention comprises phenol oxidizing enzyme-binding peptide complexes
CC wherein the binding peptide is attached to the C-terminus of the phenol
CC oxidizing enzyme or is inserted or substituted into the phenol oxidizing
CC enzyme. Phenol oxidizing enzymes function by catalysis of redox reactions
CC and are used for a wide range of applications (detergent industry, paper
CC and pulp industry, textile industry and food industry). The invention is
CC useful for enhancing the binding of a laccase enzyme to a target stain on
CC a textile, where the peptide binds to the stain and not the textile. This
CC may be useful for bleaching a carotenoid stain on a fabric or surface.
CC The invention is useful in skin cosmetics and in food as fruit ripening
CC agents. The present sequence is that of a stain targeting peptide of the
CC invention.
XX
SQ Sequence 7 AA;
Query Match 32.1%; Score 35; DB 7; Length 7;
Best Local Similarity 83.3%; Pred. No. 2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 3 PHPTNI 8
:||||:
Db 1 PHPTNL 6
RESULT 14
ADY56230
ID ADY56230 standard; peptide; 7 AA.
XX
AC ADY56230;
XX
DT 02-JUN-2005 (first entry)
XX
DE Carotenoid-binding phage display cyclic 7-mer peptide, SEQ ID NO:54.
XX
KM Enzyme engineering; surfactant; textile; phage display; cyclic.
XX
OS Synthetic.
XX
XX US2005058996-A1.
FN
XX
PD 17-MAR-2005;
XX
XX 03-SEP-2002; 2002US-00235043.
PF
XX
PR 03-SEP-2002; 2002US-00235043.
XX

PA (WOLF/) WOLFGANG A.
PA (BALD/) BALDWIN T M.
PA (VGA/) VAN CASTEL F J C.
PA (JANS/) JANSSEN G G.
PA (MURR/) MURRAY C J.
PA (WANG/) WANG H.
PA (WINE/) WINETZKY D S.
PI Wolfgang A, Baldwin TM, Van Castel FJC, Janssen GG, Murray CJ;
PI Wang H, Winetzky DS;
XX WPI: 2005-222220/23.
XX
XX
XX New peptides that bind to carotenoid compounds, useful as detergents for
PT targeting or removing stains on textiles or fabrics, in personal care or
PT food industry applications, or in various diagnostic applications.
PS
PS Claim 1; SEQ ID NO 54; 107pp; English.
XX
XX The invention relates to 432 cyclic or linear carotenoid-binding phage
CC display peptides (ADY56178-ADY56609), to carotenoid-binding peptides
CC which comprise a repeatable motif selected from PPP, SSP, SSK, SPT, PDP,
CC SLH, SLL, TTS, NTS, APS, TYP or a motif shown in ADY56623-ADY56651; and
CC to a complex comprising a phenol-oxidizing enzyme (especially a
CC Stachybotrys laccase such as ADY56177 or variants thereof) covalently
CC attached to one of the 432 carotenoid-binding peptides. The invention
CC also relates to polynucleotides encoding a carotenoid-binding peptide,
CC and expression vectors and host cells comprising a polynucleotide
CC encoding a phenol-oxidizing enzyme/carotenoid-binding peptide complex.
CC The carotenoid-binding peptides are useful in complexes with a phenol-
CC oxidizing enzyme for enhancing the selectivity of the enzyme to a target
CC carotenoid stain on a textile or other surface, where the enzyme can then
CC act to bleach the stain. Such enzyme/peptide complexes can be used in
CC detergent or cleaning compositions for targeting or removing food stains
CC (e.g., tomato or paprika) on fabrics, and can also be used in the textile
CC industry in the treatment, processing, finishing, polishing or production
CC of fibers. The enzyme/peptide complexes are additionally useful in
CC personal care applications (e.g., in skin cosmetics as skin tanners), in
CC food industry applications (e.g., as fruit ripening agents) or in
CC diagnostic uses, such as in pharmaceutical applications e.g., to localize
CC the presence of carotenoids in tissues. The present sequence represents a
CC specifically claimed carotenoid-binding cyclic peptide isolated from a
CC phage display library.
SQ
SQ Sequence 7 AA:
Query Match 32.1%; Score 35; DB 9; Length 7;
Best Local Similarity 83.3%; Pred. No. 2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 3 PHPTNI 8
DB 1 PHPTNL 6
RESULT 15
AEC06055
ID AEC06055 standard; peptide; 10 AA.
XX
XX AEC06055;
AC
XX
XX 20-OCT-2005 (first entry)
DT
XX
XX
DE H3 or D3-acetylated tumor-associated peptide.
XX
XX cytosolic; vaccine; gene therapy; pharmaceutical; immunotherapy; tumor;
KW cancer; neoplasm.
XX
XX Unidentified.
OS
XX WO2005076009-A2.
PN
XX
PD 18-AUG-2005.

XX
XX 28-JAN-2005; 2005WO-EP000873.
PF
XX
XX 28-JAN-2004; 2004DE-10005273.
PR
XX 06-MAR-2004; 2004DE-10011503.
PR
XX (IMMA-) IMMATICS BIOTECHNOLOGIES GMBH.
PA
XX
XX Lemmel C, Rammensee H;
PI
XX WPI: 2005-618379/63.
DR
XX
XX
XX Identifying and quantifying tumor-associated peptides by chemically
PT identically modifying peptides to generate different physical
PT characteristics, useful for treating tumorous and/or adenomatous
PT diseases.
XX
XX
XX Disclosure; Page 12; 43pp; English.
PS
XX
XX The invention describes a method of identifying and quantifying tumor-
CC associated peptides comprising chemically identically modifying peptides
CC from samples in order to generate different physical characteristics in
CC the peptides from the different samples. The peptides are useful for
CC producing a medicament for the treatment of tumorous diseases and/or
CC adenomatous diseases, such as renal, lung, colon, stomach, pancreatic,
CC breast, prostate, ovarian and/or skin cancer. The peptide is used
CC together with an adjuvant. A peptide bound to an antigen-presenting cell
CC is used. The peptides are also useful for the labeling of leukocytes, in
CC particular of T-lymphocytes, for evaluating the progress of therapy in a
CC tumorous disease, and for producing an antibody. The nucleic acid and/or
CC vector and/or cell are useful in producing a medicament for the treatment
CC of tumorous and/or adenomatous diseases. This is the amino acid sequence
CC of a tumor-associated peptide that binds human MHC class I.
SQ
SQ Sequence 10 AA:
Query Match 32.1%; Score 35; DB 9; Length 10;
Best Local Similarity 50.0%; Pred. No. 70;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 DIPHTNIHK 10
DB 1 DAHPHTNVOR 10
RESULT 16
AEC06029
ID AEC06029 standard; peptide; 10 AA.
XX
XX AEC06029;
AC
XX
XX 20-OCT-2005 (first entry)
DT
XX
XX Tumor-associated peptide SEQ ID NO 12.
DE
XX
XX cytosolic; vaccine; gene therapy; pharmaceutical; immunotherapy; tumor;
KW cancer; neoplasm.
XX
XX Homo sapiens.
OS
XX WO2005076009-A2.
PN
XX
XX 18-AUG-2005.
PD
XX
XX 28-JAN-2005; 2005WO-EP000873.
PF
XX
XX 28-JAN-2004; 2004DE-10005273.
PR
XX 06-MAR-2004; 2004DE-10011503.
PR
XX (IMMA-) IMMATICS BIOTECHNOLOGIES GMBH.
PA
XX
XX Lemmel C, Rammensee H;
PI
XX

DR WPI; 2005-618379/63.

XX Identifying and quantifying tumor-associated peptides by chemically

PT Identically modifying peptides to generate different physical

PT characteristics, useful for treating tumorous and/or adenomatous

PT diseases.

XX

PS Claim 19; SEQ ID NO 12; 43pp; English.

XX

CC The invention describes a method of identifying and quantifying tumor-

CC associated peptides comprising chemically identifying modifying peptides

CC from samples in order to generate different physical characteristics in

CC the peptides from the different samples. The peptides are useful for

CC producing a medicament for the treatment of tumorous diseases and/or

CC adenomatous diseases, such as renal, lung, colon, stomach, pancreatic,

CC breast, prostate, ovarian and/or skin cancer. The peptide is used

CC together with an adjuvant. A peptide bound to an antigen-presenting cell

CC is used. The peptides are also useful for the labeling of leukocytes, in

CC particular of T-lymphocytes, for evaluating the progress of therapy in a

CC tumorous disease, and for producing an antibody. The nucleic acid and/or

CC vector and/or cell are useful in producing a medicament for the treatment

CC of tumorous and/or adenomatous diseases. This is the amino acid sequence

CC of a tumor-associated peptide that binds human MHC class I.

CC

XX

SQ Sequence 10 AA;

Query Match 32.1%; Score 35; DB 9; Length 10;

Best Local Similarity 50.0%; Pred. No. 70;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 DHPPTNIHK 10

1 DHPPTNIHK 10

DB 1 DAHPPTNIHK 10

RESULT 17

AAW30771

ID AAW30771 standard; peptide: 15 AA.

XX

AC AAW30771;

XX

DT 27-FEB-1998 (first entry)

XX

DE Prostate Specific Antigen (PSA) derived peptide ABT3.

XX

KW Prostate specific antigen; PSA; immunogenic; human glandular kallikrein;

KW hK2; antigen; antibody; detection; diagnosis; prostate cancer.

XX

OS Synthetic.

OS Homo sapiens.

XX

PN WO9729199-A2.

XX

PD 14-AUG-1997.

XX

PF 06-FEB-1997; 97WO-US001911.

XX

PR 06-FEB-1996; 96US-00595945.

XX

PA (ABBO) ABBOTT LAB.

XX

PI Dowell B., Bridon D., Qiu X., Lilja H., Pitonen T., Vihinen M;

PI Pectersson IK;

XX

DR WPI; 1997-415352/38.

XX

PT Prostate Specific Antigen peptide(s) - useful for diagnosis of prostate

PT cancer.

XX

PS Claim 2; Page 10; 42pp; English.

XX

CC AAW30769-84 are synthetic peptides derived from the prostate specific

CC antigen (PSA) sequence. These peptides are identical to a highly

CC immunogenic region of PSA, and also comprise one or more amino acids

CC identical or non-identical to the amino acid sequence of human glandular

CC kallikrein (hK2). The peptides are used as antigens for the production of

CC antibodies which are used to detect PSA in a test sample (claimed). This

CC is useful for diagnosis of prostate cancer. The peptides enable the

CC production of antisera necessary to determine the amount of total PSA,

CC free PSA and PSA-ACR complex present in a sample and thus improve the

CC ability of the clinician to distinguish, e.g., between BPH (benign

CC prostatic hyperplasia) and prostatic cancer in a patient

CC

XX

SQ Sequence 15 AA;

Query Match 32.1%; Score 35; DB 2; Length 15;

Best Local Similarity 36.4%; Pred. No. 1.1e+02;

Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 4 HPTNIHKYIWC 14

4 HPTNIHKYIWC 14

DB 5 HPQKVTYFMC 15

5 HPQKVTYFMC 15

RESULT 18

AAW58054

ID AAW58054 standard; peptide: 15 AA.

XX

AC AAW58054;

XX

DT 11-AUG-1998 (first entry)

XX

DE Human prostate specific antigen peptide SEQ ID NO:72.

XX

KW Human; prostate specific antigen; PSA; epitope; monoclonal antibody;

KW detection; cancer; serine protease.

XX

OS Synthetic.

OS Homo sapiens.

XX

PN WO9810292-A1.

XX

PD 12-MAR-1998.

XX

PF 25-AUG-1997; 97WO-US014909.

XX

PR 06-SEP-1996; 96US-0025404P.

XX

PA (CENZ) CENTOCOR INC.

XX

PI Hevner GA;

XX

DR WPI; 1998-193789/17.

XX

PT Monoclonal antibodies specific for prostate specific antigen - useful,

PT e.g. in screening for prostate or breast cancer and especially to

PT distinguish between benign prostatic hyperplasia and prostate cancer.

XX

PS Example; Page 59; 84pp; English.

XX

CC The present sequence represents a prostate specific antigen (PSA)

CC peptide. Monoclonal antibodies specific for PSA and hybridomas producing

CC them have been developed. The antibodies: (a) bind to free PSA; (b) are

CC monoclonal antibody 365 binding to amino acids 82-87 of free PSA (LKRFL)

CC or fragment, and (c) are monoclonal antibodies 10, 11, 16 or 22.2 and

CC 15.2, 156 or 225 binding to amino acids 139-144 (EHLFLP) and 55-60

CC (SLFHP) respectively of free and bound PSA, or fragments. The antibodies

CC are useful to detect PSA. For detecting free PSA only, an immunoassay

CC comprising a solid support with attached labelled monoclonal antibody

CC specific for free PSA (especially (b)) and a PSA standard can be used. To

CC detect both free and bound PSA, a second solid support with attached

CC (differently labelled) monoclonal antibody binding free and bound PSA

CC (especially selected from (c)) can be used either with, or in place of,

CC the first solid support. The antibodies are useful in cancer screening,

CC especially prostate and breast cancer. By obtaining total and free PSA

CC values, their ratio can be used to separate prostatic cancer (PCA) from

CC benign prostatic hyperplasia (BHP) patients. Measurement of PSA is also
 CC useful after radical prostatectomy, to predict disease persistence. The
 CC antibodies allow evaluation of PSA free/total ratio, enabling separation
 CC of BPH and PCA patients with PSA values 4-10 ng/ml not previously
 CC possible by total PSA testing, avoiding biopsies
 CC
 SQ Sequence 15 AA;

Query Match 32.1%; Score 35; DB 2; Length 15;
 Best Local Similarity 36.4%; Pred. No. 1.1e+02;
 Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 4 HPTIHXYLC 14
 || : ||:
 Db 5 HPQVTKFMLC 15

RESULT 19
 AAMS8055
 ID AAMS8055 standard; peptide; 15 AA.
 XX
 AC AAMS8055;

XX 11-AUG-1998 (first entry)

XX Human prostate specific antigen peptide SEQ ID NO:73.

XX Human; prostate specific antigen; PSA; epitope; monoclonal antibody;
 KM detection; cancer; serine protease.

XX Synthetic.

OS Homo sapiens.

XX MO9810292-A1.

XX 12-MAR-1998.

XX 25-AUG-1997; 97WO-US014909.

XX 06-SEP-1996; 96US-0025404P.

XX (CENZ) CENTOCOR INC.

XX Heavner GA;

XX WPI; 1998-193789/17.

XX Monoclonal antibodies specific for prostate specific antigen - useful,
 PT e.g. in screening for prostate or breast cancer and especially to
 PT distinguish between benign prostatic hyperplasia and prostate cancer.

XX Example; Page 60; 84pp; English.

XX The present sequence represents a prostate specific antigen (PSA)
 CC peptide. Monoclonal antibodies specific for PSA and hybridomas producing
 CC them have been developed. The antibodies: (a) bind to free PSA; (b) are
 CC monoclonal antibody 365 binding to amino acids 82-87 of free PSA (LKNEFL)
 CC or fragment, and (c) are monoclonal antibodies 10, 11, 16 or 22.2 and
 CC 15.2, 156 or 225 binding to amino acids 139-144 (BBLFPLP) and 35-60
 CC (SLFHPF) respectively of free and bound PSA, or fragments. The antibodies
 CC are useful to detect PSA. For detecting free PSA only, an immunoassay
 CC comprising a solid support with attached labelled monoclonal antibody
 CC specific for free PSA (especially (b)) and a PSA standard can be used. To
 CC detect both free and bound PSA, a second solid support with attached
 CC (differently labelled) monoclonal antibody binding free and bound PSA
 CC (especially selected from (c)) can be used either with, or in place of,
 CC the first solid support. The antibodies are useful in cancer screening,
 CC especially prostate and breast cancer. By obtaining total and free PSA
 CC values, their ratio can be used to separate prostatic cancer (PCA) from
 CC benign prostatic hyperplasia (BHP) patients. Measurement of PSA is also
 CC useful after radical prostatectomy, to predict disease persistence. The
 CC antibodies allow evaluation of PSA free/total ratio, enabling separation
 CC of BPH and PCA patients with PSA values 4-10 ng/ml not previously

CC possible by total PSA testing, avoiding biopsies
 XX
 SQ Sequence 15 AA;

Query Match 32.1%; Score 35; DB 2; Length 15;
 Best Local Similarity 36.4%; Pred. No. 1.1e+02;
 Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 4 HPTIHXYLC 14
 || : ||:
 Db 2 HPQVTKFMLC 12

RESULT 20
 ADM37502
 ID ADM37502 standard; peptide; 15 AA.
 XX
 AC ADM37502;

XX 10-MAR-2005 (first entry)

XX HLA binding epitope #8252.

XX Virucide; cytostatic; gene therapy; vaccine; epitope; cytotoxic T cell;
 KM MHC class I; CTL; HTL; A2-restricted cytotoxic lymphocyte; HLA;
 KM viral disease; cancer.

XX Unidentified.

XX MO2003040165-A2.

XX 15-MAY-2003.

XX 18-OCT-2001; 2001WO-US051650.

XX 19-OCT-2000; 2000US-0242350P.

XX 20-APR-2001; 2001US-0285624P.

XX (EPIM-) EPIMMUNE INC.

XX Sette A, Sidney J, Southwood S;

XX WPI; 2003-441519/41.

XX New composition comprising at least one peptide having allele-specific
 PT binding motifs for HLA, useful for preventing, treating or diagnosing
 PT viral diseases and cancer.

XX Claim 1; Page 52-379; 382pp; English.

XX The invention relates to a composition comprising at least one peptide
 CC having an isolated, prepared epitope selected from any of the sequences
 CC from 30 lists given in the specification. Also disclosed is a method for
 CC inducing a cytotoxic T cell response against a pre-selected antigen in a
 CC patient expressing a specific MHC class I allele by contacting cytotoxic
 CC T cells from the patient with the composition cited above. The
 CC composition comprises an epitope that is joined by an amino acid linker.
 CC The epitope is admixed or joined to a CTL or HTL epitope. The epitope is
 CC bound to an HLA molecule on the antigen-presenting cell, where when an A2
 CC -restricted cytotoxic lymphocyte (CTL) is present, a receptor of the CTL
 CC binds to a complex of the HLA molecule and the epitope. Specifically
 CC claimed are peptides having allele-specific binding motifs for HLA. The
 CC compositions and methods are useful for preventing, treating or
 CC diagnosing viral diseases and cancer. The peptide epitopes are useful as
 CC diagnostic agents for evaluating immune responses, for making antibodies
 CC and for evaluating efficacy of a vaccine. Sequences given in ADM29251-
 CC ADM37745 represent epitopes of the invention as given in Tables 2-31.

XX Sequence 15 AA;

Query Match 32.1%; Score 35; DB 7; Length 15;
 Best Local Similarity 36.4%; Pred. No. 1.1e+02;
 Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 4 HPTNHHKYLVC 14
 DB 5 HPQKVTKEFMLC 15

RESULT 21

ADM35209
 ID ADM35209 standard; peptide; 15 AA.

AC ADM35209;

DT 10-MAR-2005 (first entry)

DE HLA binding epitope #5959.

XX Virucide; cytostatic; gene therapy; vaccine; epitope; cytotoxic T cell;
 KM MHC class I; CTL; HTL; A2-restricted cytotoxic lymphocyte; HLA;
 KW viral disease; cancer.

XX Unidentified.

PN WO2003040165-A2.

PD 15-MAY-2003.

PF 18-OCT-2001; 2001WO-US051650.

PR 19-OCT-2000; 2000US-0242350P.

PR 20-APR-2001; 2001US-0285624P.

XX (EPIM-) EPIMMUNE INC.

PI Sette A, Sidney J, Southwood S;

XX WPI; 2003-441519/41.

PT New composition comprising at least one peptide having allele-specific
 binding motifs for HLA, useful for preventing, treating or diagnosing
 PT viral diseases and cancer.

PS Claim 1; Page 52-379; 382pp; English.

CC The invention relates to a composition comprising at least one peptide
 CC having an isolated, prepared epitope selected from any of the sequences
 CC from 30 lists given in the specification. Also disclosed is a method for
 CC inducing a cytotoxic T cell response against a pre-selected antigen in a
 CC patient expressing a specific MHC class I allele by contacting cytotoxic
 CC T cells from the patient with the composition cited above. The
 CC composition comprises an epitope that is joined by an amino acid linker.
 CC The epitope is admixed or joined to a CTL or HTL epitope. The epitope is
 CC bound to an HLA molecule on the antigen-presenting cell, where when an A2
 CC -restricted cytotoxic lymphocyte (CTL) is present, a receptor of the CTL
 CC binds to a complex of the HLA molecule and the epitope. Specifically
 CC claimed are peptides having allele-specific binding motifs for HLA. The
 CC compositions and methods are useful for preventing, treating or
 CC diagnosing viral diseases and cancer. The peptide epitopes are useful as
 CC diagnostic agents for evaluating immune responses, for making antibodies
 CC and for evaluating efficacy of a vaccine. Sequences given in ADM29251-
 CC ADM37745 represent epitopes of the invention as given in Tables 2-31.

SQ Sequence 15 AA;

Query Match 32.1%; Score 35; DB 7; Length 15;

Best Local Similarity 36.4%; Pred. No. 1.1e+02;
 Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 4 HPTNHHKYLVC 14

DB 5 HPQKVTKEFMLC 15

RESULT 22

ADM33268
 ID ADM33268 standard; peptide; 15 AA.

XX ADM33268;

DT 10-MAR-2005 (first entry)

DE HLA binding epitope #4018.

XX Virucide; cytostatic; gene therapy; vaccine; epitope; cytotoxic T cell;
 KM MHC class I; CTL; HTL; A2-restricted cytotoxic lymphocyte; HLA;
 KW viral disease; cancer.

XX Unidentified.

PN WO2003040165-A2.

PD 15-MAY-2003.

PF 18-OCT-2001; 2001WO-US051650.

PR 19-OCT-2000; 2000US-0242350P.

PR 20-APR-2001; 2001US-0285624P.

XX (EPIM-) EPIMMUNE INC.

PI Sette A, Sidney J, Southwood S;

XX WPI; 2003-441519/41.

PT New composition comprising at least one peptide having allele-specific
 binding motifs for HLA, useful for preventing, treating or diagnosing
 PT viral diseases and cancer.

PS Claim 1; Page 52-379; 382pp; English.

CC The invention relates to a composition comprising at least one peptide
 CC having an isolated, prepared epitope selected from any of the sequences
 CC from 30 lists given in the specification. Also disclosed is a method for
 CC inducing a cytotoxic T cell response against a pre-selected antigen in a
 CC patient expressing a specific MHC class I allele by contacting cytotoxic
 CC T cells from the patient with the composition cited above. The
 CC composition comprises an epitope that is joined by an amino acid linker.
 CC The epitope is admixed or joined to a CTL or HTL epitope. The epitope is
 CC bound to an HLA molecule on the antigen-presenting cell, where when an A2
 CC -restricted cytotoxic lymphocyte (CTL) is present, a receptor of the CTL
 CC binds to a complex of the HLA molecule and the epitope. Specifically
 CC claimed are peptides having allele-specific binding motifs for HLA. The
 CC compositions and methods are useful for preventing, treating or
 CC diagnosing viral diseases and cancer. The peptide epitopes are useful as
 CC diagnostic agents for evaluating immune responses, for making antibodies
 CC and for evaluating efficacy of a vaccine. Sequences given in ADM29251-
 CC ADM37745 represent epitopes of the invention as given in Tables 2-31.

SQ Sequence 15 AA;

Query Match 32.1%; Score 35; DB 7; Length 15;

Best Local Similarity 36.4%; Pred. No. 1.1e+02;
 Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 4 HPTNHHKYLVC 14

DB 5 HPQKVTKEFMLC 15

RESULT 23

ADM33976
 ID ADM33976 standard; peptide; 15 AA.

XX ADM33976;

DT 10-MAR-2005 (first entry)

DE HLA binding epitope #4726.
 XX
 KM Virucide; cytosaratic; gene therapy; vaccine; epitope; cytotoxic T cell;
 KM MHC class I; CTL; HTL; A2-restricted cytotoxic lymphocyte; HLA;
 KM viral disease; cancer.
 XX
 OS Unidentified.
 XX
 PN WO2003040165-A2.
 XX
 PD 15-MAY-2003.
 XX
 PF 18-OCT-2001; 2001WO-US051650.
 XX
 PR 19-OCT-2000; 2000US-0242350P.
 PR 20-APR-2001; 2001US-0285624P.
 PA (EPIM-) EPIMMUNE INC.
 XX
 PI Sette A, Sidney J, Southwood S;
 XX
 DR WPI; 2003-441519/41.
 XX
 PT New composition comprising at least one peptide having allele-specific
 PT binding motifs for HLA, useful for preventing, treating or diagnosing
 PT viral diseases and cancer.
 XX
 PS Claim 1; Page 52-379; 382pp; English.
 XX
 CC The invention relates to a composition comprising at least one peptide
 CC having an isolated, prepared epitope selected from any of the sequences
 CC from 30 lists given in the specification. Also disclosed is a method for
 CC inducing a cytotoxic T cell response against a pre-selected antigen in a
 CC patient expressing a specific MHC class I allele by contacting cytotoxic
 CC T cells from the patient with the composition cited above. The
 CC composition comprises an epitope that is joined by an amino acid linker.
 CC The epitope is admixed or joined to a CTL or HTL epitope. The epitope is
 CC bound to an HLA molecule on the antigen-presenting cell, where when an A2
 CC -restricted cytotoxic lymphocyte (CTL) is present a receptor of the CTL
 CC binds to a complex of the HLA molecule and the epitope. Specifically
 CC claimed are peptides having allele-specific binding motifs for HLA. The
 CC compositions and methods are useful for preventing, treating or
 CC diagnosing viral diseases and cancer. The peptide epitopes are useful as
 CC diagnostic agents for evaluating immune responses, for making antibodies
 CC and for evaluating efficacy of a vaccine. Sequences given in ADW29251-
 CC ADW37745 represent epitopes of the invention as given in Tables 2-31.
 CC
 XX
 SQ Sequence 15 AA;
 XX
 QY
 DB 4 HPTNIHKYLC 14
 5 HPQKVKFMLC 15
 32.1%; Score 35; DB 7; Length 15;
 Best Local Similarity 36.4%; Pred. No. 1.1e+02;
 Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

KM prostate cancer; AIDS; renal carcinoma; cervical carcinoma; lymphoma;
 KM chondylosa acuminatum.
 XX
 OS Unidentified.
 XX
 PN WO2004031211-A2.
 XX
 PD 15-APR-2004.
 XX
 PF 03-OCT-2003; 2003WO-US031308.
 XX
 PR 03-OCT-2002; 2002US-0416207P.
 PR 08-OCT-2002; 2002US-0417269P.
 XX
 PA (EPIM-) EPIMMUNE INC.
 XX
 PI Sidney J, Southwood S, Sette A;
 XX
 DR WPI; 2004-347953/32.
 XX
 PT New composition of peptides and nucleic acids capable of binding Major
 PT Histocompatibility Complex molecules, useful for diagnosing, preventing
 PT or treating viral infections or cancer, such as prostate cancer,
 PT hepatitis B or AIDS.
 XX
 PS Claim 1; SEQ ID NO 2035; 186pp; English.
 XX
 CC The invention relates to a novel composition comprising one or more
 CC peptides or nucleic acids encoding an HLA binding peptide. The
 CC composition further comprises an HTL epitope. It also comprises a spacer
 CC molecule, a carrier, an MHC targeting sequence or a lipid. The peptides
 CC are incorporated as part of a liposome. The peptide is from an antigen
 CC selected from prostate specific antigen (PSA), prostate specific membrane
 CC antigen (PSM), hepatitis B virus (HBV) antigen, hepatitis C virus (HCV)
 CC antigen, malignant melanoma antigen (MAGE), Epstein Barr virus, human
 CC immunodeficiency type-1 (HIV-1), human immunodeficiency type-2 (HIV-2),
 CC Papilloma virus, Lassa virus, Mycobacterium tuberculosis (MT), p53,
 CC mutant p53 (mp53), CEA, HER2/neu, and tyrosine kinase related protein
 CC (TKP). The composition is useful for preventing or treating viral
 CC infections or cancer, such as prostate cancer, hepatitis B, hepatitis C,
 CC AIDS, renal carcinoma, cervical carcinoma, lymphoma, CMV or chondylosa
 CC acuminatum. The composition is also be used for diagnosing such diseases.
 CC This sequence represents a peptide of the invention.
 CC
 XX
 SQ Sequence 15 AA;
 XX
 QY
 DB 4 HPTNIHKYLC 14
 5 HPQKVKFMLC 15
 32.1%; Score 35; DB 8; Length 15;
 Best Local Similarity 36.4%; Pred. No. 1.1e+02;
 Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

RESULT 24
 ADN65435
 ID ADN65435 standard; peptide; 15 AA.
 XX
 AC ADN65435;
 XX
 DT 01-JUL-2004 (first entry)
 XX
 DE HLA binding peptide #2035.
 XX
 KM cytosaratic; hepatotropic; virucide; antiinflammatory; anti-HIV;
 KM gene therapy; vaccine; HLA binding peptide; HTL epitope; liposome;
 KM prostate specific antigen; prostate specific membrane antigen;
 KM hepatitis B virus antigen; hepatitis C virus antigen;
 KM malignant melanoma antigen; MAGE; Epstein Barr virus; cancer;

RESULT 25
 AAW30783
 ID AAW30783 standard; peptide; 19 AA.
 XX
 AC AAW30783;
 XX
 DT 27-FEB-1998 (first entry)
 XX
 DE Prostate Specific Antigen (PSA) derived peptide ABT15.
 XX
 KM Prostate specific antigen; PSA; immunogenic; human glandular kallikrein;
 KM hK2; antigen; antibody; detection; diagnosis; prostate cancer.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN MO9729199-A2.

PD 14-AUG-1997.
 XX
 PF 06-FEB-1997; 97MO-US001911.
 XX
 PR 06-FEB-1996; 96US-00595945.
 XX
 PA (ABBO) ABBOTT LAB.
 XX
 PI Dowell BL, Bridon DP, Qiu X, Lilja H, Pironen T, Vihinen M;
 PI Pettersson IK;
 XX
 DR WPI; 1997-415352/38.
 XX
 PT Prostate Specific Antigen peptide(s) - useful for diagnosis of prostate
 PT cancer.
 PS Claim 2; Page 10; 42pp; English.
 XX
 CC AAW30769-84 are synthetic peptides derived from the prostate specific
 CC antigen (PSA) sequence. These peptides are identical to a highly
 CC immunogenic region of PSA, and also comprise one or more amino acids
 CC identical or non-identical to the amino acid sequence of human glandular
 CC kallikrein (hk2). The peptides are used as antigens for the production of
 CC antibodies which are used to detect PSA in a test sample (claimed). This
 CC is useful for diagnosis of prostate cancer. The peptides enable the
 CC production of antisera necessary to determine the amount of total PSA,
 CC free PSA and PSA-Act complex present in a sample and thus improve the
 CC ability of the clinician to distinguish, e.g., between BPH (benign
 CC prostatic hyperplasia) and prostatic cancer in a patient
 XX
 SQ Sequence 19 AA;

Query Match 32.1%; Score 35; DB 2; Length 19;
 Best Local Similarity 36.4%; Pred. No. 1.5e+02;
 Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 OY 4 HPTNIHKYLVLC 14
 DB 9 HFQKVTKFMLC 19

Search completed: January 26, 2006, 07:58:09
 Job time : 68.5345 secs

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OM protein - protein search, using sw model

Run on: January 26, 2006, 07:50:06 : Search time 17.8534 Seconds
(without alignments)
87.985 Million cell updates/sec

Title: US-09-662-293-11
Perfect score: 109
Sequence: 1 DIPHPNTHKYLVCESVNG 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 229350

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Issued Patents AA: *
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3: /cgn2_6/ptcodata/1/1aa/H_COMB.pep: *
4: /cgn2_6/ptcodata/1/1aa/PTUS_COMB.pep: *
5: /cgn2_6/ptcodata/1/1aa/RE_COMB.pep: *
6: /cgn2_6/ptcodata/1/1aa/backfill.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	109	100.0	20	2	US-09-292-225-3
3	35	32.1	15	2	US-08-595-945-3
4	35	32.1	19	2	US-08-595-945-15
5	35	32.1	20	2	US-09-026-276-20
6	35	32.1	20	2	US-09-964-201A-20
7	34	31.2	15	1	US-07-829-462-6
8	34	29.4	10	2	US-08-159-339A-551
9	32	29.4	15	2	US-09-009-953-109
10	31.5	28.9	21	2	US-09-962-756-51
11	31	28.4	8	1	US-08-529-190B-73
12	31	28.4	16	2	US-09-791-524A-3
13	31	28.4	17	1	US-08-370-567-1
14	31	28.4	17	1	US-08-438-759-1
15	31	28.4	17	1	US-08-538-911-20
16	31	28.4	17	2	US-09-402-641-10
17	31	28.4	17	2	US-09-411-067C-2
18	31	28.4	17	2	US-09-428-082B-196
19	31	28.4	17	2	US-09-155-260C-16
20	31	28.4	17	2	US-09-402-464-1
21	31	28.4	17	4	PCT-US94-05591-20
22	31	28.4	17	4	PCT-US94-05591-20
23	31	28.4	17	4	PCT-US94-05591-20
24	31	28.4	20	2	US-09-791-524A-9
25	31	28.4	21	2	US-09-791-524A-10
26	30	27.5	10	2	US-09-139-802-58
27	30	27.5	10	2	US-09-659-786-58

28	30	27.5	10	2	US-08-926-914-58	Sequence 58, Appl
29	30	27.5	15	2	US-09-300-410A-2	Sequence 2, Appl
30	29.5	27.1	20	1	US-08-614-935-75	Sequence 75, Appl
31	29.5	27.1	20	1	US-09-130-287-75	Sequence 75, Appl
32	29	26.6	6	1	US-08-192-243-1	Sequence 1, Appl
33	29	26.6	6	1	US-08-448-059-1	Sequence 1, Appl
34	29	26.6	6	2	US-09-295-996B-15	Sequence 15, Appl
35	29	26.6	6	2	US-09-295-996B-15	Sequence 15, Appl
36	29	26.6	6	2	US-09-551-737C-18	Sequence 18, Appl
37	29	26.6	6	2	US-09-924B-10	Sequence 10, Appl
38	29	26.6	6	2	US-09-551-738B-15	Sequence 15, Appl
39	29	26.6	11	1	US-07-942-245-195	Sequence 195, Appl
40	29	26.6	11	1	US-08-024-253-16	Sequence 16, Appl
41	29	26.6	11	2	US-09-649-063-16	Sequence 16, Appl
42	29	26.6	20	1	US-08-305-871A-11	Sequence 11, Appl
43	29	26.6	20	1	US-08-797-842-7	Sequence 7, Appl
44	29	26.6	20	2	US-09-100-409A-47	Sequence 47, Appl
45	29	26.6	20	2	US-09-009-953-195	Sequence 195, Appl
46	29	26.6	20	2	US-08-788-822A-14	Sequence 14, Appl
47	29	26.6	20	2	US-09-311-784A-150	Sequence 150, Appl
48	29	26.6	20	2	US-09-239-043D-2566	Sequence 2566, Ap
49	29	26.6	20	2	US-09-701-623C-71	Sequence 71, Appl
50	29	26.6	20	2	US-09-674-183-8	Sequence 8, Appl
51	29	26.6	20	2	US-10-666-480-5	Sequence 5, Appl
52	29	26.6	20	5	US-09-618-592-7	Sequence 7, Appl
53	29	26.6	21	2	US-09-962-756-53	Sequence 53, Appl
54	29	26.6	21	2	US-09-962-756-53	Sequence 53, Appl
55	29	26.6	21	2	US-09-962-756-510	Sequence 510, Appl
56	29	26.6	21	2	US-10-666-480-34	Sequence 34, Appl
57	28	25.7	9	2	US-08-159-339A-526	Sequence 526, Appl
58	28	25.7	11	2	US-09-119-507B-51	Sequence 51, Appl
59	28	25.7	11	2	US-08-897-556A-51	Sequence 51, Appl
60	28	25.7	11	2	US-09-547-693-51	Sequence 51, Appl
61	28	25.7	13	1	US-08-147-011-1	Sequence 1, Appl
62	28	25.7	15	2	US-09-009-953-110	Sequence 110, Appl
63	28	25.7	16	2	US-08-810-009-51	Sequence 51, Appl
64	28	25.7	16	2	US-09-776-490-51	Sequence 51, Appl
65	28	25.7	19	2	US-08-802-981-86	Sequence 86, Appl
66	28	25.7	19	2	US-09-747-287A-121	Sequence 121, Appl
67	28	25.7	19	2	US-09-394-019C-74	Sequence 74, Appl
68	28	25.7	19	2	US-09-394-019C-76	Sequence 76, Appl
69	28	25.7	19	2	US-09-394-019C-83	Sequence 83, Appl
70	28	25.7	19	2	US-09-394-019C-319	Sequence 319, Appl
71	28	25.7	19	2	US-09-394-019C-321	Sequence 321, Appl
72	28	25.7	19	2	US-09-394-019C-328	Sequence 328, Appl
73	28	25.7	21	1	US-07-851-976B-1	Sequence 1, Appl
74	28	25.7	21	1	US-08-291-609-1	Sequence 1, Appl
75	28	25.7	21	1	US-08-401-136-1	Sequence 1, Appl
76	28	25.7	21	2	US-08-850-554-1	Sequence 1, Appl
77	28	25.7	21	2	US-09-962-756-130	Sequence 130, Appl
78	28	25.7	21	6	5459061-6	Sequence 10, Appl
79	27	24.8	10	2	US-10-365-908-52	Sequence 52, Appl
80	27	24.8	11	1	US-07-847-311A-19	Sequence 19, Appl
81	27	24.8	12	1	US-09-430-221-9	Sequence 9, Appl
82	27	24.8	14	2	US-08-182-967-23	Sequence 23, Appl
83	27	24.8	14	2	US-09-069-827A-131	Sequence 131, Appl
84	27	24.8	15	2	US-09-117-860-11	Sequence 11, Appl
85	27	24.8	16	2	US-09-428-082B-565	Sequence 565, Appl
86	27	24.8	16	2	US-09-428-082B-573	Sequence 573, Appl
87	27	24.8	16	2	US-09-155-260C-7	Sequence 7, Appl
88	27	24.8	17	1	US-08-451-947-32	Sequence 32, Appl
89	27	24.8	17	1	US-08-451-947-32	Sequence 32, Appl
90	27	24.8	17	1	US-08-451-947-32	Sequence 32, Appl
91	27	24.8	17	2	US-09-928-594-32	Sequence 32, Appl
92	27	24.8	17	2	US-09-461-325-294	Sequence 294, Appl
93	27	24.8	17	2	US-08-450-842-32	Sequence 32, Appl
94	27	24.8	17	2	US-08-451-390-32	Sequence 32, Appl
95	27	24.8	17	2	US-10-012-442-294	Sequence 294, Appl
96	27	24.8	17	4	US-10-115-123-294	Sequence 294, Appl
97	27	24.8	17	4	PCT-US91-06950-32	Sequence 32, Appl
98	27	24.8	18	1	US-08-232-513A-12	Sequence 12, Appl
99	27	24.8	18	1	US-09-231-159-17	Sequence 17, Appl
100	27	24.8	18	2	US-08-611-307-17	Sequence 17, Appl
			2	2	US-09-372-425A-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1

US-09-292-225-11
; Sequence 11, Application US/09292225
; Patent No. 6455686
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/09/292,225
; CURRENT FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: 60/098,909
; EARLIER FILING DATE: 1998-09-02
; EARLIER APPLICATION NUMBER: 60/085,295
; EARLIER FILING DATE: 1998-05-13
; EARLIER APPLICATION NUMBER: 60/098,565
; EARLIER FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: 09/062,013
; EARLIER FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-09-292-225-11

Query Match 100.0%; Score 109; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 2,6e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DHPPTNHHKYLVCESVNG 19
Db 1 DHPPTNHHKYLVCESVNG 19

RESULT 2

US-09-292-225-3
; Sequence 3, Application US/09292225
; Patent No. 6455686
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/09/292,225
; CURRENT FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: 60/098,909
; EARLIER FILING DATE: 1998-09-02
; EARLIER APPLICATION NUMBER: 60/085,295
; EARLIER FILING DATE: 1998-05-13
; EARLIER APPLICATION NUMBER: 60/098,565
; EARLIER FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: 09/062,013
; EARLIER FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-09-292-225-3

Query Match 100.0%; Score 109; DB 2; Length 20;

Best Local Similarity 100.0%; Pred. No. 2,7e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DHPPTNHHKYLVCESVNG 19
Db 1 DHPPTNHHKYLVCESVNG 19

RESULT 3

US-08-595-945-3
; Sequence 3, Application US/08595945
; Patent No. 6143509
; GENERAL INFORMATION:
; APPLICANT: DOWELL, BARRY L.
; APPLICANT: BRIDON, DOMINIQUE P.
; APPLICANT: QIU, XIAOXING
; APPLICANT: LILJA, HANS
; APPLICANT: PIIRONEN, TIMO P.
; APPLICANT: VIHINEN, MAUNO A.
; APPLICANT: PETERSSON, KIM S.I.
; TITLE OF INVENTION: PROSTATE SPECIFIC ANTIGEN PEPTIDES
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/595,945
; FILING DATE: 06-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BECKER, CHERYL L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 5875-US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847-935-1729
; TELEFAX: 847-938-2623
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-595-945-3

Query Match 32.1%; Score 35; DB 2; Length 15;
Best Local Similarity 36.4%; Pred. No. 33;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Oy 4 HPTNHHKYLVC 14
Db 5 HPQKTKFMLC 15

RESULT 4

US-08-595-945-15
; Sequence 15, Application US/08595945
; Patent No. 6143509
; GENERAL INFORMATION:
; APPLICANT: DOWELL, BARRY L.
; APPLICANT: BRIDON, DOMINIQUE P.
; APPLICANT: QIU, XIAOXING
; APPLICANT: LILJA, HANS

APPLICANT: PIIRONEN, TIMO P.
APPLICANT: VIHINEN, MAURO A.
TITLE OF INVENTION: PROSTATE SPECIFIC ANTIGEN PEPTIDES
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESS: ABBOTT LABORATORIES
STREET: 100 ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/595,945
FILING DATE: 06-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BECKER, CHERYL L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 5875, US.01
TELEPHONE: 847-935-1729
TELECOMMUNICATION INFORMATION:
TELEFAX: 847-938-2623
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-595-945-15

Query Match 32.1%; Score 35; DB 2; Length 19;
Best Local Similarity 36.4%; Pred. No. 43;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 4 HPTNHHKYLVC 14
|| : ||: ||
Db 9 HPQKVTKEMLC 19

RESULT 5
US-09-026-276-20
Sequence 20, Application US/09026276
Patent No. 6319503
GENERAL INFORMATION:
APPLICANT: Kenten, John H
APPLICANT: Triontano, Alfonso
APPLICANT: Pilon, Aprille L
APPLICANT: Lohmas, Gerald L
APPLICANT: Roberts, Steven F
TITLE OF INVENTION: HEAT-SHOCK FUSION-BASED VACCINE SYSTEM
FILE REFERENCE: U.S. Patent Application No. 6319503 09\026,276
CURRENT APPLICATION NUMBER: US/09/026,276
CURRENT FILING DATE: 1998-02-19
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 20
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens
US-09-026-276-20

Query Match 32.1%; Score 35; DB 2; Length 20;
Best Local Similarity 36.4%; Pred. No. 45;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 4 HPTNHHKYLVC 14
|| : ||: ||
Db 7 HPQKVTKEMLC 17

RESULT 6
US-09-964-201A-20
Sequence 20, Application US/09964201A
Patent No. 6660271
GENERAL INFORMATION:
APPLICANT: Kenten, John H
APPLICANT: Triontano, Alfonso
APPLICANT: Pilon, Aprille L
APPLICANT: Lohmas, Gerald L
APPLICANT: Roberts, Steven F
TITLE OF INVENTION: HEAT-SHOCK FUSION-BASED VACCINE SYSTEM
FILE REFERENCE: U.S. Patent Application No. 6660271 09\026,276
CURRENT APPLICATION NUMBER: US/09/964,201A
CURRENT FILING DATE: 2002-05-21
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 20
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens
US-09-964-201A-20

Query Match 32.1%; Score 35; DB 2; Length 20;
Best Local Similarity 36.4%; Pred. No. 45;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 4 HPTNHHKYLVC 14
|| : ||: ||
Db 7 HPQKVTKEMLC 17

RESULT 7
US-07-829-462-6
Sequence 6, Application US/07829462
Patent No. 5453489
GENERAL INFORMATION:
APPLICANT: Ruoslahti, Erkki I.
APPLICANT: Morla, Alex
TITLE OF INVENTION: NOVEL FRAGMENTS OF FIBRONECTIN AND
METHODS TO MODULATE THE ROLE OF FIBRONECTIN IN
EXTRACELLULAR MATRIX ASSEMBLY
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL AND FLORES
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/829,462
FILING DATE: 19920131
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, CATRYN A.
REGISTRATION NUMBER: 31,547
REFERENCE/DOCKET NUMBER: P-LA 9179
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-535-9001
TELEFAX: 619-535-8949
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids

TYPE: AMINO ACID
TOPOLOGY: linear
US-07-829-462-6

Query Match 31.2%; Score 34; DB 1; Length 15;
Best Local Similarity 45.5%; Pred. No. 48;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 3 PHPTNHYLV 13
| : : | : : | : :
Db 3 PPSHISKYIL 13

RESULT 8

US-08-159-339A-551
Sequence 551, Application US/08159339A

Patent No. 6037135
GENERAL INFORMATION:
APPLICANT: Kubo, Ralph T.
APPLICANT: Grey, Howard M.
APPLICANT: Sette, Alessandro
APPLICANT: Celis, Esteban
TITLE OF INVENTION: HLA Binding peptides and Their
TITLE OF INVENTION: Uses
NUMBER OF SEQUENCES: 1254
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA

ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159,339A
FILING DATE: 29-NOV-1993
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,666
FILING DATE: 07-AUG-1992
APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-MAR-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993

ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-005030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
TELEX:

INFORMATION FOR SEQ ID NO: 551:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-159-339A-551

Query Match 29.4%; Score 32; DB 2; Length 10;
Best Local Similarity 55.6%; Pred. No. 66;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 IPHPNTHK 10
| : : | : : | : :
Db 2 IPHPAGLKK 10

RESULT 9
US-09-009-953-109
Sequence 109, Application US/09009953

Patent No. 6413517
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
TITLE OF INVENTION: Identification of Broadly
Reactive DR Restricted Epitopes
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA

ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,953
FILING DATE: 21-Jan-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,713
FILING DATE: 23-JAN-1997
APPLICATION NUMBER: US 60/037,432
FILING DATE: 07-FEB-1997

ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-011520US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 109:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 109:
US-09-009-953-109

Query Match 29.4%; Score 32; DB 2; Length 15;
Best Local Similarity 55.6%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 IPHPNTHK 10
| : : | : : | : :
Db 6 IPHPAGLKK 14

RESULT 10
US-09-962-756-51
Sequence 51, Application US/09962756

Patent No. 6875741
GENERAL INFORMATION:
APPLICANT: PILUTTLA, RENUKA
APPLICANT: BRISSETTE, RENEE
APPLICANT: BLUME, ARTHUR J.
APPLICANT: SCHAFFER, LAUGE
APPLICANT: BRANDT, JAKOB
APPLICANT: GOLDSTEIN, NEIL I.
APPLICANT: SPETZLER, JANE
APPLICANT: OSTERGAARD, SOREN
APPLICANT: HANSEN, PER HERTZ
TITLE OF INVENTION: INSULIN AND IGF-1 RECEPTOR AGONISTS AND ANTAGONISTS

FILE REFERENCE: 1878-4051US1
 CURRENT APPLICATION NUMBER: US/09/962,756
 CURRENT FILING DATE: 2001-09-24
 PRIOR APPLICATION NUMBER: 09/538,038
 PRIOR FILING DATE: 2000-03-29
 PRIOR APPLICATION NUMBER: 09/146,127
 PRIOR FILING DATE: 1998-09-02
 NUMBER OF SEQ ID NOS: 2227
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 51
 LENGTH: 21
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 US-09-962-756-51

Query Match 28.9%; Score 31.5; DB 2; Length 21;
 Best Local Similarity 37.5%; Pred. No. 1.8e+02;
 Matches 6; Conservative 5; Mismatches 4; Indels 1; Gaps 1;

QY 3 PHPTNHYLVCSVN 18
 ||:|:|:|:
 Db 7 PHGSNFDWV-EXIN 21

RESULT 11
 US-08-529-1908-73
 Sequence 73, Application US/085291908
 Patent No. 5833991
 GENERAL INFORMATION:
 APPLICANT: Mabucci, Maria G.
 TITLE OF INVENTION: GLYCINE-CONTAINING SEQUENCES
 TITLE OF INVENTION: CONFERRING INVISIBILITY TO THE IMMUNE SYSTEM
 NUMBER OF SEQUENCES: 76
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Banner & Witcoff, Ltd.
 STREET: One Financial Center
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 OPERATING SYSTEM: DOS
 SOFTWARE: Wordperfect 6.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/529,1908
 FILING DATE: 15-SEP-1995
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: SE9501324-9
 FILING DATE: 10-APR-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US08/522,595
 FILING DATE: 01-SEP-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Williams, Ph. D., Kathleen A
 REGISTRATION NUMBER: 34,380
 TELEPHONE/DOCKET NUMBER: 3255/53015
 TELEPHONE: 617-345-9110
 TELEFAX: 617-345-9111
 INFORMATION FOR SEQ ID NO: 73:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 8 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: unknown
 MOLECULE TYPE: peptide
 US-08-529-1908-73

Query Match 28.4%; Score 31; DB 1; Length 8;
 Best Local Similarity 71.4%; Pred. No. 4.6e+05;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 IHKYLVC 14
 ||:|:|:|:
 Db 1 IHRYLRC 7

RESULT 12
 US-09-791-524A-3
 Sequence 3, Application US/09791524A
 Patent No. 6911199
 GENERAL INFORMATION:
 APPLICANT: Aventis Pharmaceuticals Products Inc.
 TITLE OF INVENTION: Targeted Adenovirus Vectors for Delivery of Heterologous Genes
 FILE REFERENCE: P26,992-B USA
 CURRENT APPLICATION NUMBER: US/09/791,524A
 PRIOR FILING DATE: 2001-02-22
 PRIOR APPLICATION NUMBER: PCT/IB99/01524
 PRIOR FILING DATE: 1999-08-27
 PRIOR APPLICATION NUMBER: US 60/098,028
 PRIOR FILING DATE: 1998-08-27
 NUMBER OF SEQ ID NOS: 165
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO 3
 LENGTH: 16
 TYPE: PRT
 ORGANISM: Adenovirus
 US-09-791-524A-3

Query Match 28.4%; Score 31; DB 2; Length 16;
 Best Local Similarity 45.5%; Pred. No. 1.6e+02;
 Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IPHPTNHYKL 12
 ||:|:|:|:
 Db 4 MPHSLNFSQYL 14

RESULT 13
 US-08-370-567-1
 Sequence 1, Application US/08370567
 Patent No. 5656726
 GENERAL INFORMATION:
 APPLICANT: Rosenberg, Steven
 APPLICANT: Doyle, Michael
 APPLICANT: Goodson, Robert
 TITLE OF INVENTION: Peptide Inhibitors of Urokinase Receptor
 TITLE OF INVENTION: Activity
 NUMBER OF SEQUENCES: 37
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Chiron Corporation
 STREET: 4560 Horton Street
 CITY: Emeryville
 STATE: CA
 COUNTRY: USA
 ZIP: 94608
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/370,567
 FILING DATE:
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/061,514
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Green, Grant D.

REGISTRATION NUMBER: 31,259
REFERENCE/DOCKET NUMBER: 0941.001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2706
TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
US-08-370-567-1

Query Match 28.4%; Score 31; DB 1; Length 17;
Best Local Similarity 45.5%; Pred. No. 1.7e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Oy 2 IPHPTNIHKYL 12
Db 4 MPHSLNFSQYL 14

RESULT 14
US-08-438-759-1
Sequence 1, Application US/08438759
Patent No. 5675782
GENERAL INFORMATION:
APPLICANT: Rosenberg, Steven
APPLICANT: Doyle, Michael
APPLICANT: Goodson, Robert
TITLE OF INVENTION: Peptide Inhibitors of Urokinase Receptor
TITLE OF INVENTION: Activity
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESS: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,759
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/370,567
FILING DATE:
APPLICATION NUMBER: US/08/061,514
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Green, Grant D.
REGISTRATION NUMBER: 31,259
REFERENCE/DOCKET NUMBER: 0941.001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2706
TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
US-08-438-759-1

Query Match 28.4%; Score 31; DB 1; Length 17;
Best Local Similarity 45.5%; Pred. No. 1.7e+02;

Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Oy 2 IPHPTNIHKYL 12
Db 4 MPHSLNFSQYL 14

RESULT 15
US-08-538-911-20
Sequence 20, Application US/08538911
Patent No. 5750344
GENERAL INFORMATION:
APPLICANT: Doyle, Michael
APPLICANT: Winter, Jill
TITLE OF INVENTION: Method For Selection Of Biologically
TITLE OF INVENTION: Active Peptide Sequences
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESS: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/538,911
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/069,352
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Green, Grant D.
REGISTRATION NUMBER: 31,259
REFERENCE/DOCKET NUMBER: 0407.001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2706
TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
US-08-538-911-20

Query Match 28.4%; Score 31; DB 1; Length 17;
Best Local Similarity 45.5%; Pred. No. 1.7e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Oy 2 IPHPTNIHKYL 12
Db 4 MPHSLNFSQYL 14

RESULT 16
US-09-402-641-10
Sequence 10, Application US/09402641
Patent No. 6528619
GENERAL INFORMATION:
APPLICANT: BUERGLE, Markus
APPLICANT: GRAEFF, Heinrich
APPLICANT: KESSLER, Horst
APPLICANT: MAGDOLEN, Viktor Robert
APPLICANT: KOENIG, Bernhard
APPLICANT: KOPPLITZ, Marcus


```

; APPLICANT: RIEMER, Christoph
; APPLICANT: SCHMITT, Manfred
; APPLICANT: WEIDLE, Ulrich
; APPLICANT: WILHELM, Olaf
; TITLE OF INVENTION: INHIBITORS FOR UROKINASE RECEPTOR
; FILE REFERENCE: Case 20367US
; CURRENT FILING DATE: US/09/402,641
; PRIOR FILING DATE: 2000-01-10
; PRIOR APPLICATION NUMBER: EP97106024.9
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: PCT/EP98/02178
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: clone-20 peptide
US-09-402-641-10

```

```

Query Match      28.4%; Score 31; DB 2; Length 17;
Best Local Similarity 45.5%; Pred. No. 1.7e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

```

```

QY      2 IPHPTNIHKYL 12
       :||| :|||
Db      4 MPHSLNFSQYL 14

```

```

RESULT 17
US-09-411-067C-2
; Sequence 2, Application US/09411067C
; Patent No. 6576610
; GENERAL INFORMATION:
; APPLICANT: NUVAS, LLC
; APPLICANT: HOUSTON, L.L.
; TITLE OF INVENTION: USE OF A CONTEXT-DEPENDENT FUNCTIONAL ENTITY TO ENHANCE THE EFFIC
; TITLE OF INVENTION: AN AGENT
; FILE REFERENCE: NOVAS1140
; CURRENT APPLICATION NUMBER: US/09/411,067C
; CURRENT FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-411-067C-2

```

```

Query Match      28.4%; Score 31; DB 2; Length 17;
Best Local Similarity 45.5%; Pred. No. 1.7e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

```

```

QY      2 IPHPTNIHKYL 12
       :||| :|||
Db      4 MPHSLNFSQYL 14

```

```

RESULT 18
US-09-428-082B-196
; Sequence 196, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428,082B
; CURRENT FILING DATE: 1999-10-22

```

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; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 196
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: UKR ANTAGONIST PEPTIDE
US-09-428-082B-196

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Query Match      28.4%; Score 31; DB 2; Length 17;
Best Local Similarity 45.5%; Pred. No. 1.7e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

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QY      2 IPHPTNIHKYL 12
       :||| :|||
Db      4 MPHSLNFSQYL 14

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RESULT 19
US-09-155-260C-16
; Sequence 16, Application US/09155260C
; Patent No. 6794358
; GENERAL INFORMATION:
; APPLICANT: ROSENBERG, STEVE
; APPLICANT: DOYLE, MICHAEL
; APPLICANT: CHAPMAN, HAROLD
; TITLE OF INVENTION: PEPTIDE LIGANDS OF THE UROKINASE RECEPTOR
; FILE REFERENCE: 014024-0284102
; CURRENT APPLICATION NUMBER: US/09/155,260C
; CURRENT FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: PCT/US97/05199
; PRIOR FILING DATE: 1997-03-28
; PRIOR APPLICATION NUMBER: 08/623,361
; PRIOR FILING DATE: 1996-03-28
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide ligand
US-09-155-260C-16

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Query Match      28.4%; Score 31; DB 2; Length 17;
Best Local Similarity 45.5%; Pred. No. 1.7e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

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QY      2 IPHPTNIHKYL 12
       :||| :|||
Db      4 MPHSLNFSQYL 14

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RESULT 20
US-09-402-464-1
; Sequence 1, Application US/09402464
; Patent No. 6872702
; GENERAL INFORMATION:
; APPLICANT: Kessler, Horst
; APPLICANT: Graeff, Heinrich
; APPLICANT: Schmitt, Manfred
; APPLICANT: Magdolen, Viktor
; APPLICANT: Wilhelm, Olaf G.
; APPLICANT: Riemer, Christoph
; APPLICANT: Burgle, Markus
; TITLE OF INVENTION: Inhibitors for Urokinase Receptor
; FILE REFERENCE: 100564-09040
; CURRENT APPLICATION NUMBER: US/09/402,464
; CURRENT FILING DATE: 2000-01-07

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PRIOR APPLICATION NUMBER: EP 97 106 024.9
PRIOR FILING DATE: 1997-04-11
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 1
LENGTH: 17
TYPE: PRT
ORGANISM: Homo sapiens
US-09-402-464-1

Query Match 28.4%; Score 31; DB 2; Length 17;
Best Local Similarity 45.5%; Pred. No. 1.7e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 IPHPTNIHKYL 12
: || | : ||
Db 4 MPHSLNFSQYL 14

RESULT 21
US-09-791-524A-4
Sequence 4, Application US/09791524A
Patent No. 6911199
GENERAL INFORMATION:
APPLICANT: Aventis Pharmaceuticals Products Inc.
TITLE OF INVENTION: Targeted Adenovirus Vectors For Delivery Of Heterologous Genes
FILE REFERENCE: P26, 992-B USA
CURRENT APPLICATION NUMBER: US/09/791, 524A
CURRENT FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: PCT/IB99/01524
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: US 60/098, 028
PRIOR FILING DATE: 1998-08-27
NUMBER OF SEQ ID NOS: 165
SOFTWARE: Patentln version 3.2
SEQ ID NO 4
LENGTH: 17
TYPE: PRT
ORGANISM: Adenovirus
US-09-791-524A-4

Query Match 28.4%; Score 31; DB 2; Length 17;
Best Local Similarity 45.5%; Pred. No. 1.7e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 IPHPTNIHKYL 12
: || | : ||
Db 4 MPHSLNFSQYL 14

RESULT 22
PCT-US94-05591-20
Sequence 20, Application PC/TUS9405591
GENERAL INFORMATION:
APPLICANT: Doyle, Michael V.
TITLE OF INVENTION: Method For Selection Of Biologically
TITLE OF INVENTION: Active Peptide Sequences
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05591
FILING DATE: 19-MAY-1994

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Green, Grant D.
REGISTRATION NUMBER: 31,259
REFERENCE/DOCKET NUMBER: 0407.100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2706
TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
PCT-US94-05591-20

Query Match 28.4%; Score 31; DB 4; Length 17;
Best Local Similarity 45.5%; Pred. No. 1.7e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 IPHPTNIHKYL 12
: || | : ||
Db 4 MPHSLNFSQYL 14

RESULT 23
PCT-US94-05684-1
Sequence 1, Application PC/TUS9405684
GENERAL INFORMATION:
APPLICANT: Chiron Corporation
TITLE OF INVENTION: Peptide Inhibitors of Urokinase Receptor
TITLE OF INVENTION: Activity
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05684
FILING DATE: 19 MAY 1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Green, Grant D.
REGISTRATION NUMBER: 31,259
REFERENCE/DOCKET NUMBER: 0941.100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2706
TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
PCT-US94-05684-1

Query Match 28.4%; Score 31; DB 4; Length 17;
Best Local Similarity 45.5%; Pred. No. 1.7e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 IPHPTNIHKYL 12
: || | : ||

Db 4 MPHSLNFSQYL 14

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RESULT 24
US-09-791-524A-9
; Sequence 9, Application US/09791524A
; Patent No. 6911199
; GENERAL INFORMATION:
; APPLICANT: Aventis Pharmaceuticals Products Inc.
; TITLE OF INVENTION: Targeted Adenovirus Vectors For Delivery Of Heterologous Genes
; FILE REFERENCE: P26,992-B USA
; CURRENT APPLICATION NUMBER: US/09/791,524A
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: PCT/IB99/01524
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: US 60/098,028
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Adenovirus
US-09-791-524A-9

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Query Match 28.4%; Score 31; DB 2; Length 20;
 Best Local Similarity 45.5%; Pred. No. 2.1e+02;
 Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IPHPTNIHKYL 12
 :||| :|||
 Db 6 MPHSLNFSQYL 16

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RESULT 25
US-09-791-524A-10
; Sequence 10, Application US/09791524A
; Patent No. 6911199
; GENERAL INFORMATION:
; APPLICANT: Aventis Pharmaceuticals Products Inc.
; TITLE OF INVENTION: Targeted Adenovirus Vectors For Delivery Of Heterologous Genes
; FILE REFERENCE: P26,992-B USA
; CURRENT APPLICATION NUMBER: US/09/791,524A
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: PCT/IB99/01524
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: US 60/098,028
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Adenovirus
US-09-791-524A-10

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Query Match 28.4%; Score 31; DB 2; Length 21;
 Best Local Similarity 45.5%; Pred. No. 2.2e+02;
 Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IPHPTNIHKYL 12
 :||| :|||
 Db 6 MPHSLNFSQYL 16

Search completed: January 26, 2006, 08:07:03
 Job time : 19.0201 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 26, 2006, 08:04:12 ; Search time 61.75 Seconds
(without alignments)
128.563 Million cell updates/sec

Title: US-09-662-293-11

Perfect score: 109
Sequence: 1 DIHPHTIKHYLCESVNG 19

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 389445

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published Applications MA Main:*

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3: /cgn2_6/ptodata/1/pubpaa/us09_PUBSCOMB.pep:.*
4: /cgn2_6/ptodata/1/pubpaa/us10_PUBSCOMB.pep:.*
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6: /cgn2_6/ptodata/1/pubpaa/us11_PUBSCOMB.pep:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	109	100.0	19	4	US-10-218-743-11
2	109	100.0	20	4	US-10-218-743-3
3	37.5	34.4	20	3	US-09-864-761-38552
4	35	32.1	7	3	US-09-994-385-54
5	35	32.1	7	5	US-10-912-512-54
6	35	32.1	7	5	US-10-235-043-54
7	35	32.1	20	3	US-09-964-201A-20
8	35	32.1	20	4	US-10-681-389-20
9	35	32.1	20	4	US-10-681-388-20
10	33	30.3	21	4	US-10-062-710-50
11	33	29.4	10	4	US-10-200-708-47
12	32	29.4	10	4	US-10-200-708-95
13	32	29.4	10	4	US-10-200-708-117
14	32	29.4	10	4	US-10-200-708-119
15	32	29.4	10	4	US-10-200-708-671
16	32	29.4	14	4	US-10-417-895A-36
17	32	29.4	14	5	US-10-808-187-2265
18	32	29.4	14	5	US-10-808-187-2265
19	32	29.4	15	4	US-10-103-395-109
20	32	29.4	16	4	US-10-062-710-19
21	32	29.4	17	4	US-10-442-909-32
22	32	29.4	20	4	US-10-285-649A-9
23	32	29.4	20	6	US-11-008-653-128
24	31.5	28.9	17	4	US-10-430-685-95
25	31.5	28.9	21	3	US-09-962-756-51
26	31.5	28.9	21	4	US-10-253-471-51
27	31.5	28.9	21	4	US-10-253-493-51

28	31	28.4	12	4	US-10-706-391-29	Sequence 29, Appl
29	31	28.4	16	3	US-09-791-524-3	Sequence 3, Appl
30	31	28.4	17	3	US-09-791-524-4	Sequence 4, Appl
31	31	28.4	17	4	US-10-609-217-196	Sequence 196, App
32	31	28.4	17	4	US-10-632-388-196	Sequence 196, App
33	31	28.4	17	4	US-10-651-723-196	Sequence 196, App
34	31	28.4	17	4	US-10-645-761-196	Sequence 196, App
35	31	28.4	17	4	US-10-666-666-196	Sequence 196, App
36	31	28.4	17	4	US-10-653-048-196	Sequence 196, App
37	31	28.4	17	5	US-10-756-289-1	Sequence 1, Appl
38	31	28.4	17	5	US-10-821-544-16	Sequence 16, Appl
39	31	28.4	17	5	US-10-645-764-196	Sequence 196, App
40	31	28.4	18	3	US-09-864-761-44227	Sequence 44227, A
41	31	28.4	20	3	US-09-791-524-9	Sequence 9, Appl
42	31	28.4	21	3	US-10-791-524-10	Sequence 10, Appl
43	31	27.5	9	4	US-10-182-252A-787	Sequence 187, App
44	30	27.5	9	4	US-10-182-252A-830	Sequence 830, App
45	30	27.5	10	3	US-09-765-086-58	Sequence 58, Appl
46	30	27.5	10	3	US-09-573-822C-160	Sequence 160, App
47	30	27.5	10	4	US-10-264-374-58	Sequence 58, Appl
48	30	27.5	10	4	US-10-375-992-58	Sequence 58, Appl
49	30	27.5	10	4	US-10-264-374-58	Sequence 58, Appl
50	30	27.5	10	4	US-10-375-992-58	Sequence 58, Appl
51	30	27.5	10	5	US-10-838-289-549	Sequence 549, App
52	30	27.5	15	5	US-10-946-647-769	Sequence 769, App
53	30	27.5	16	4	US-10-148-671-10	Sequence 10, Appl
54	30	27.5	20	5	US-10-776-013-463	Sequence 463, App
55	29.5	27.1	9	4	US-10-062-109A-123	Sequence 123, App
56	29.5	27.1	10	4	US-10-005-480A-123	Sequence 123, App
57	29.5	27.1	10	4	US-10-062-109A-164	Sequence 164, App
58	29.5	27.1	10	4	US-10-005-480A-164	Sequence 164, App
59	29.5	27.1	17	5	US-10-485-788-89	Sequence 89, Appl
60	29	26.6	8	4	US-10-285-374-08	Sequence 408, App
61	29	26.6	9	3	US-09-826-290-41	Sequence 41, Appl
62	29	26.6	9	3	US-09-791-393-7	Sequence 7, Appl
63	29	26.6	9	3	US-09-791-389-7	Sequence 7, Appl
64	29	26.6	9	4	US-10-264-309-239	Sequence 239, App
65	29	26.6	9	4	US-10-182-252A-232	Sequence 232, App
66	29	26.6	9	4	US-10-182-252A-759	Sequence 759, App
67	29	26.6	9	4	US-10-182-252A-832	Sequence 832, App
68	29	26.6	9	4	US-10-182-252A-866	Sequence 866, App
69	29	26.6	9	5	US-10-264-309-239	Sequence 239, App
70	29	26.6	11	2	US-08-996-140-16	Sequence 16, Appl
71	29	26.6	11	4	US-10-159-351-80	Sequence 80, Appl
72	29	26.6	11	4	US-10-239-656-9	Sequence 9, Appl
73	29	26.6	11	5	US-10-879-994-59	Sequence 59, Appl
74	29	26.6	12	4	US-10-411-869A-36	Sequence 36, Appl
75	29	26.6	15	4	US-10-283-940-59	Sequence 59, Appl
76	29	26.6	15	6	US-11-022-454-59	Sequence 59, Appl
77	29	26.6	19	4	US-10-461-180-280	Sequence 280, App
78	29	26.6	20	3	US-09-466-035-84	Sequence 84, Appl
79	29	26.6	20	4	US-10-103-395-195	Sequence 195, App
80	29	26.6	20	4	US-10-225-567A-2221	Sequence 2221, A
81	29	26.6	20	4	US-10-029-386-33390	Sequence 33390, App
82	29	26.6	20	4	US-10-371-525-150	Sequence 150, App
83	29	26.6	20	4	US-10-371-069-150	Sequence 150, App
84	29	26.6	20	4	US-10-371-645-150	Sequence 150, App
85	29	26.6	20	4	US-10-371-260-150	Sequence 150, App
86	29	26.6	20	4	US-10-666-480-5	Sequence 5, Appl
87	29	26.6	20	4	US-10-732-862A-232	Sequence 232, App
88	29	26.6	20	4	US-10-481-180-283	Sequence 283, App
89	29	26.6	20	5	US-10-474-960A-403	Sequence 403, App
90	29	26.6	20	5	US-10-654-601-2566	Sequence 2566, App
91	29	26.6	20	6	US-11-127-702-5	Sequence 5, Appl
92	29	26.6	21	3	US-09-962-756-56	Sequence 56, Appl
93	29	26.6	21	3	US-09-962-756-56	Sequence 56, Appl
94	29	26.6	21	3	US-09-962-756-56	Sequence 56, Appl
95	29	26.6	21	4	US-10-253-471-53	Sequence 53, App
96	29	26.6	21	4	US-10-253-471-53	Sequence 53, App
97	29	26.6	21	4	US-10-253-471-510	Sequence 510, App
98	29	26.6	21	4	US-10-253-493-53	Sequence 53, App
99	29	26.6	21	4	US-10-253-493-76	Sequence 76, App
100	29	26.6	21	4	US-10-253-493-510	Sequence 510, App

ALIGNMENTS

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RESULT 1
US-10-218-743-11
; Sequence 11, Application US/10218743
; Publication No. US20030096779A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Weber, Eric R.
; APPLICANT: Hunter, Shirley Wu
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/10/218,743
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/292,225
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: 60/098,909
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/085,295
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/098,565
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: 09/062,013
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-10-218-743-11

Query Match      100.0%; Score 109; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.1e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 DIPHPTNIHKYLCVCSVNG 19
Db      1 DIPHPTNIHKYLCVCSVNG 19

RESULT 2
US-10-218-743-3
; Sequence 3, Application US/10218743
; Publication No. US20030096779A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/10/218,743
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/292,225
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: 60/098,909
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/085,295
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/098,565
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: 09/062,013
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 20
; TYPE: PRT
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; ORGANISM: Dermatophagoides farinae
US-10-218-743-3

Query Match      100.0%; Score 109; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 DIPHPTNIHKYLCVCSVNG 19
Db      1 DIPHPTNIHKYLCVCSVNG 19

RESULT 3
US-09-664-761-38552
; Sequence 38552, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecm1ca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
; SEQ ID NO 38552
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC005099.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.7
```

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.6
 OTHER INFORMATION: EXPRESSED IN HEPA, SIGNAL = 1.8
 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.9
 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.8
 OTHER INFORMATION: SWISSPROT HIT: P53820, EVALU8 8.80e+00
 US-09-864-761-38552

Query Match 34.4% Score 37.5; DB 3; Length 20;
 Best Local Similarity 42.9%; Pred. No. 1.2e+02;
 Matches 6; Conservative 5; Mismatches 2; Indels 1; Gaps 1;
 Qy 2 IPHPTNIRKYLVE 15
 Db 8 LPHH-HSHTHLLCQ 20

RESULT 4
 US-09-954-385-54
 Sequence 54, Application US/09954385
 Publication No. US20030100467A1
 GENERAL INFORMATION:
 APPLICANT: Aehle, Wolfgang
 APPLICANT: Baldwin, Toby L.
 APPLICANT: Van Gestel, Franciscus J.C.
 APPLICANT: Janssen, Giselle G.
 APPLICANT: Murray, Christopher J.
 APPLICANT: Wang, Huaming
 APPLICANT: Winetzk, Deborah S.
 TITLE OF INVENTION: Binding Phenol Oxidizing Enzyme-peptide
 FILE REFERENCE: GC690
 CURRENT APPLICATION NUMBER: US/09/954,385
 CURRENT FILING DATE: 2001-09-12
 NUMBER OF SEQ ID NOS: 433
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 54
 LENGTH: 7
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: binding peptide
 US-09-954-385-54

Query Match 32.1% Score 35; DB 3; Length 7;
 Best Local Similarity 83.3%; Pred. No. 1.7e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 3 PHPTNI 8
 Db 1 PHPTNL 6

RESULT 5
 US-10-912-512-54
 Sequence 54, Application US/10912512
 Publication No. US20050042684A1
 GENERAL INFORMATION:
 APPLICANT: Aehle, Wolfgang
 APPLICANT: Baldwin, Toby L.
 APPLICANT: Van Gestel, Franciscus J.C.
 APPLICANT: Janssen, Giselle G.
 APPLICANT: Murray, Christopher J.
 APPLICANT: Wang, Huaming
 APPLICANT: Winetzk, Deborah S.
 TITLE OF INVENTION: Binding Phenol Oxidizing Enzyme-peptide
 FILE REFERENCE: GC690
 CURRENT APPLICATION NUMBER: US/10/912,512
 CURRENT FILING DATE: 2004-08-05
 PRIOR APPLICATION NUMBER: US/09/954,385
 PRIOR FILING DATE: 2001-09-12
 NUMBER OF SEQ ID NOS: 433

SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 54
 LENGTH: 7
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: binding peptide
 US-10-912-512-54

Query Match 32.1% Score 35; DB 5; Length 7;
 Best Local Similarity 83.3%; Pred. No. 1.7e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 3 PHPTNI 8
 Db 1 PHPTNL 6

RESULT 6
 US-10-235-043-54
 Sequence 54, Application US/10235043
 Publication No. US20050058956A1
 GENERAL INFORMATION:
 APPLICANT: Aehle, Wolfgang
 APPLICANT: Baldwin, Toby M.
 APPLICANT: Van Gestel, Franciscus J.C.
 APPLICANT: Janssen, Giselle G.
 APPLICANT: Murray, Christopher J.
 APPLICANT: Wang, Huaming
 APPLICANT: Winetzk, Deborah S.
 TITLE OF INVENTION: Binding Phenol Oxidizing Enzyme-peptide
 FILE REFERENCE: GC690-2
 CURRENT APPLICATION NUMBER: US/10/235,043
 CURRENT FILING DATE: 2002-09-03
 NUMBER OF SEQ ID NOS: 446
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 54
 LENGTH: 7
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: binding peptide
 US-10-235-043-54

Query Match 32.1% Score 35; DB 5; Length 7;
 Best Local Similarity 83.3%; Pred. No. 1.7e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 3 PHPTNI 8
 Db 1 PHPTNL 6

RESULT 7
 US-09-964-201A-20
 Sequence 20, Application US/09964201A
 Publication No. US20030091575A1
 GENERAL INFORMATION:
 APPLICANT: Aehle, Wolfgang
 APPLICANT: Kanten, John H.
 APPLICANT: Tramontano, Alfonso
 APPLICANT: Pilon, April L.
 APPLICANT: Lohme, Gerald L.
 APPLICANT: Roberts, Steven F.
 TITLE OF INVENTION: HEAT-SHOCK FUSION-BASED VACCINE SYSTEM
 FILE REFERENCE: U.S. Patent Application No. US20030091575A1
 CURRENT APPLICATION NUMBER: US/09/964,201A
 CURRENT FILING DATE: 2002-05-21
 NUMBER OF SEQ ID NOS: 35
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 20
 LENGTH: 20
 TYPE: PRT

ORGANISM: Homo sapiens
US-09-964-201A-20

Query Match 32.1%; Score 35; DB 3; Length 20;
Best Local Similarity 36.4%; Pred. No. 2.9e+02;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 4 HPTNHHKYLVC 14
|| : ||:|
Db 7 HPQKVTKEMLC 17

RESULT 8

US-10-681-389-20
Sequence 20, Application US/10681389
Publication No. US20040115218A1
GENERAL INFORMATION:
APPLICANT: Kenten, John H
APPLICANT: Trantomano, Alfonso
APPLICANT: Pilon, Gerald L
APPLICANT: Lohnas, Gerald L
APPLICANT: Roberts, Steven F
TITLE OF INVENTION: HEAT-SHOCK FUSION-BASED VACCINE SYSTEM
FILE REFERENCE: U.S. Patent Application No. 09/026,276
CURRENT FILING DATE: 2003-10-07
PRIOR APPLICATION NUMBER: US/10/681,389
PRIOR FILING DATE: 2002-05-21
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 20
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens
US-10-681-389-20

Query Match 32.1%; Score 35; DB 4; Length 20;
Best Local Similarity 36.4%; Pred. No. 2.9e+02;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 4 HPTNHHKYLVC 14
|| : ||:|
Db 7 HPQKVTKEMLC 17

RESULT 9

US-10-681-388-20
Sequence 20, Application US/10681388
Publication No. US20040170643A1
GENERAL INFORMATION:
APPLICANT: Kenten, John H
APPLICANT: Trantomano, Alfonso
APPLICANT: Pilon, Gerald L
APPLICANT: Lohnas, Gerald L
APPLICANT: Roberts, Steven F
TITLE OF INVENTION: HEAT-SHOCK FUSION-BASED VACCINE SYSTEM
FILE REFERENCE: U.S. Patent Application No. 09/026,276
CURRENT FILING DATE: 2003-10-07
PRIOR APPLICATION NUMBER: US/10/681,388
PRIOR FILING DATE: 2002-05-21
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 20
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens
US-10-681-388-20

Query Match 32.1%; Score 35; DB 4; Length 20;
Best Local Similarity 36.4%; Pred. No. 2.9e+02;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 4 HPTNHHKYLVC 14
|| : ||:|
Db 7 HPQKVTKEMLC 17

RESULT 10
US-10-062-710-50
Sequence 50, Application US/10062710
Publication No. US20030049253A1
GENERAL INFORMATION:
APPLICANT: Li, Frank Q.
APPLICANT: Chu, Yong-Liang
APPLICANT: Qiu, Jian-Tai
TITLE OF INVENTION: Polymeric Conjugates for Delivery of
TITLE OF INVENTION: MHC-Recognized Epitopes
TITLE OF INVENTION: Via Peptide Vaccines
FILE REFERENCE: 3781-001-27
CURRENT FILING DATE: US/10/062,710
CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/310,498
PRIOR FILING DATE: 2001-08-08
NUMBER OF SEQ ID NOS: 232
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 50
LENGTH: 21
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: HIV Helper-T Cell Epitopes
US-10-062-710-50

Query Match 30.3%; Score 33; DB 4; Length 21;
Best Local Similarity 57.1%; Pred. No. 6.3e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 PHPTNHH 9
|| : ||:|
Db 1 PHPVSLH 7

RESULT 11
US-10-200-708-47
Sequence 47, Application US/10200708
Publication No. US20030180314A1
GENERAL INFORMATION:
APPLICANT: Degroot, Anne S.
TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
FILE REFERENCE: 17999-001
CURRENT APPLICATION NUMBER: US/10/200,708
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: US/09/351,036
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 60/092,346
PRIOR FILING DATE: 1998-07-10
PRIOR APPLICATION NUMBER: 60/115,145
PRIOR FILING DATE: 1999-01-08
PRIOR APPLICATION NUMBER: 60/130,677
PRIOR FILING DATE: 1999-04-23
NUMBER OF SEQ ID NOS: 672
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 47
LENGTH: 10
TYPE: PRT
ORGANISM: Human immunodeficiency virus
US-10-200-708-47

Query Match 29.4%; Score 32; DB 4; Length 10;
Best Local Similarity 55.6%; Pred. No. 4.1e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 IPHPTNHHK 10
|| : ||:|
Db 1 IPHPAGLKK 9


```

RESULT 12
US-10-200-708-95
; Sequence 95, Application US/10200708
; Publication No. US20030180314A1
; GENERAL INFORMATION:
; APPLICANT: Degroot, Anne S.
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
; FILE REFERENCE: 17999-001
; CURRENT APPLICATION NUMBER: US/10/200,708
; PRIOR FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/351,036
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/092,346
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/115,145
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 60/130,677
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 95
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-200-708-95

```

```

Query Match      29.4%; Score 32; DB 4; Length 10;
Best Local Similarity 55.6%; Pred. No. 4.1e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```

```

QY 2 IPHPTNHHK 10
DB 2 IHPHAGLKK 10

```

```

RESULT 13
US-10-200-708-117
; Sequence 117, Application US/10200708
; Publication No. US20030180314A1
; GENERAL INFORMATION:
; APPLICANT: Degroot, Anne S.
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
; FILE REFERENCE: 17999-001
; CURRENT APPLICATION NUMBER: US/10/200,708
; PRIOR FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/351,036
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/092,346
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/115,145
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 60/130,677
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 117
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-200-708-117

```

```

Query Match      29.4%; Score 32; DB 4; Length 10;
Best Local Similarity 55.6%; Pred. No. 4.1e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```

```

QY 2 IPHPTNHHK 10
DB 2 IHPHAGLKK 10

```

RESULT 14

```

US-10-200-708-119
; Sequence 119, Application US/10200708
; Publication No. US20030180314A1
; GENERAL INFORMATION:
; APPLICANT: Degroot, Anne S.
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
; FILE REFERENCE: 17999-001
; CURRENT APPLICATION NUMBER: US/10/200,708
; PRIOR FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/351,036
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/092,346
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/115,145
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 60/130,677
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 119
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-200-708-119

```

```

Query Match      29.4%; Score 32; DB 4; Length 10;
Best Local Similarity 55.6%; Pred. No. 4.1e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```

```

QY 2 IPHPTNHHK 10
DB 1 IHPHAGLKK 9

```

```

RESULT 15
US-10-200-708-671
; Sequence 671, Application US/10200708
; Publication No. US20030180314A1
; GENERAL INFORMATION:
; APPLICANT: Degroot, Anne S.
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
; FILE REFERENCE: 17999-001
; CURRENT APPLICATION NUMBER: US/10/200,708
; PRIOR FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/351,036
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/092,346
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/115,145
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 60/130,677
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 671
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-200-708-671

```

```

Query Match      29.4%; Score 32; DB 4; Length 10;
Best Local Similarity 55.6%; Pred. No. 4.1e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```

```

QY 2 IPHPTNHHK 10
DB 2 IHPHAGLKK 10

```

```

RESULT 16
US-10-417-895A-36
; Sequence 36, Application US/10417895A
; Publication No. US20040033569A1

```

```
; GENERAL INFORMATION:
; APPLICANT: Crea, Roberto
; TITLE OF INVENTION: "DOPING" IN WALK-THROUGH MUTAGENESIS
; FILE REFERENCE: 1551.2002-001
; CURRENT APPLICATION NUMBER: US/10/417,895A
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 60/373,686
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: variant peptide for second complementarity
; OTHER INFORMATION: determining region of Fv region of an
; OTHER INFORMATION: immunoglobulin
US-10-417-895A-36
```

```
Query Match      29.4%; Score 32; DB 4; Length 14;
Best Local Similarity 55.6%; Pred. No. 5.8e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
Oy      4 HPTNIHKL 12
Db      4 HPTIGHDIV 12
```

RESULT 17

```
US-10-808-187-2265
; Sequence 2265, Application US/10808187
; Publication No. US2005009009A1
; GENERAL INFORMATION:
```

```
; APPLICANT: PEIRIS, JOSEPH S. M.
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: GUAN, YI
; APPLICANT: CHAN, KWOK HUNG
```

```
; APPLICANT: NICHOLLS, JOHN
; TITLE OF INVENTION: A DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS CAUSING SEVERE ACUTE
; FILE REFERENCE: V9661.0078
; RESPIRATORY SYNDROME (SARS)
```

```
CURRENT APPLICATION NUMBER: US/10/808,187
```

```
CURRENT FILING DATE: 2004-03-24
```

```
PRIOR APPLICATION NUMBER: 60/457,031
```

```
PRIOR FILING DATE: 2003-03-24
```

```
PRIOR APPLICATION NUMBER: 60/457,730
```

```
PRIOR FILING DATE: 2003-03-26
```

```
PRIOR APPLICATION NUMBER: 60/459,931
```

```
PRIOR FILING DATE: 2003-04-02
```

```
PRIOR APPLICATION NUMBER: 60/460,357
```

```
PRIOR FILING DATE: 2003-04-03
```

```
PRIOR APPLICATION NUMBER: 60/461,265
```

```
PRIOR FILING DATE: 2003-04-08
```

```
PRIOR APPLICATION NUMBER: 60/462,805
```

```
PRIOR FILING DATE: 2003-04-14
```

```
PRIOR APPLICATION NUMBER: 60/468,139
```

```
PRIOR FILING DATE: 2003-05-05
```

```
PRIOR APPLICATION NUMBER: 60/464,886
```

```
PRIOR FILING DATE: 2003-04-23
```

```
PRIOR APPLICATION NUMBER: 60/471,200
```

```
PRIOR FILING DATE: 2003-05-16
```

```
NUMBER OF SEQ ID NOS: 2476
```

```
SOFTWARE: PatentIn ver. 3.2
```

```
SEQ ID NO 2265
```

```
LENGTH: 14
```

```
TYPE: PRT
```

```
ORGANISM: Human severe acute respiratory system virus
```

```
US-10-808-187-2265
```

```
Query Match      29.4%; Score 32; DB 5; Length 14;
```

```
Best Local Similarity 83.3%; Pred. No. 5.8e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Oy      4 HPTNIH 9
Db      9 HPTTIH 14
```

RESULT 18

```
US-10-807-807-2265
; Sequence 2265, Application US/10807807
; Publication No. US20050181357A1
; GENERAL INFORMATION:
```

```
; APPLICANT: LEUNG, FREDERICK C.
; APPLICANT: PEIRIS, JOSEPH S. M.
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: POON, LIT MAN
```

```
; APPLICANT: GUAN, YI
; APPLICANT: CHAN, KWOK HUNG
```

```
; APPLICANT: NICHOLLS, JOHN M.
```

```
; TITLE OF INVENTION: A HIGH-THROUGHPUT DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS
; CAUSING SEVERE ACUTE RESPIRATORY SYNDROME (SARS)
```

```
; FILE REFERENCE: V9661.0077
; CURRENT APPLICATION NUMBER: US/10/807,807
```

```
CURRENT FILING DATE: 2004-03-24
```

```
PRIOR APPLICATION NUMBER: 60/457,031
```

```
PRIOR FILING DATE: 2003-03-24
```

```
PRIOR APPLICATION NUMBER: 60/457,730
```

```
PRIOR FILING DATE: 2003-03-26
```

```
PRIOR APPLICATION NUMBER: 60/459,931
```

```
PRIOR FILING DATE: 2003-04-02
```

```
PRIOR APPLICATION NUMBER: 60/460,357
```

```
PRIOR FILING DATE: 2003-04-03
```

```
PRIOR APPLICATION NUMBER: 60/461,265
```

```
PRIOR FILING DATE: 2003-04-08
```

```
PRIOR APPLICATION NUMBER: 60/462,805
```

```
PRIOR FILING DATE: 2003-04-14
```

```
PRIOR APPLICATION NUMBER: 60/464,886
```

```
PRIOR FILING DATE: 2003-04-23
```

```
PRIOR APPLICATION NUMBER: 60/465,738
```

```
PRIOR FILING DATE: 2003-04-25
```

```
PRIOR APPLICATION NUMBER: 60/470,935
```

```
PRIOR FILING DATE: 2003-05-14
```

```
NUMBER OF SEQ ID NOS: 2487
```

```
SOFTWARE: PatentIn ver. 3.2
```

```
SEQ ID NO 2265
```

```
LENGTH: 14
```

```
TYPE: PRT
```

```
ORGANISM: Human severe acute respiratory system virus
```

```
US-10-807-807-2265
```

```
Query Match      29.4%; Score 32; DB 5; Length 14;
Best Local Similarity 83.3%; Pred. No. 5.8e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Oy      4 HPTNIH 9
Db      9 HPTTIH 14
```

RESULT 19

```
US-10-103-395-109
; Sequence 109, Application US/10103395
; Publication No. US20020160019A1
; GENERAL INFORMATION:
```

```
; APPLICANT: EPIMUNE, Inc.
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
```

```
; APPLICANT: Southwood, Scott
```

```
; TITLE OF INVENTION: IDENTIFICATION OF BROADLY REACTIVE DR
```

```
; FILE REFERENCE: 39963-20016.01
; CURRENT APPLICATION NUMBER: US/10/103,395
```

```
Query Match      29.4%; Score 32; DB 5; Length 14;
```

```

; CURRENT FILING DATE: 2003-01-03
; PRIOR APPLICATION NUMBER: US 09/009,953
; PRIOR FILING DATE: 1998-01-21
; PRIOR APPLICATION NUMBER: PCT/US98/01373
; PRIOR FILING DATE: 1998-01-23
; PRIOR APPLICATION NUMBER: US 60/036,713
; PRIOR FILING DATE: 1997-01-23
; PRIOR APPLICATION NUMBER: US 60/037,432
; PRIOR FILING DATE: 1997-02-07
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 109
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-103-395-109

Query Match      29.4%; Score 32; DB 4; Length 15;
Best Local Similarity 55.6%; Pred. No. 6.3e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      2 IPHPTNHHK 10
Db      6 IPHPAGLKK 14

RESULT 20
US-10-062-710-19
; Sequence 19, Application US/10062710
; Publication No. US20030049253A1
; GENERAL INFORMATION:
; APPLICANT: Li, Frank O.
; APPLICANT: Chu, Yong-Liang
; APPLICANT: Qiu, Jian-Tai
; TITLE OF INVENTION: Polymeric Conjugates for Delivery of
; TITLE OF INVENTION: MHC-Recognized Epitopes
; FILE REFERENCE: 3781-001-27
; CURRENT APPLICATION NUMBER: US/10/062,710
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: US 60/310,498
; PRIOR FILING DATE: 2001-08-08
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV Helper-T Cell Epitopes
US-10-062-710-19

Query Match      29.4%; Score 32; DB 4; Length 16;
Best Local Similarity 55.6%; Pred. No. 6.7e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      2 IPHPTNHHK 10
Db      8 IPHPAGLKK 16

RESULT 21
US-10-442-909-32
; Sequence 32, Application US/10442909
; Publication No. US20040001845A1
; GENERAL INFORMATION:
; APPLICANT: Alfeld, Marcus
; APPLICANT: Yu, Xu
; APPLICANT: Walker, Bruce
; APPLICANT: Adoo, Marylyn
; TITLE OF INVENTION: Cytotoxic T-Cell Epitopes of HIV-1 Virus
; FILE REFERENCE: 24028-010
; CURRENT APPLICATION NUMBER: US/10/442,909
```

```

; CURRENT FILING DATE: 2003-05-20
; PRIOR APPLICATION NUMBER: 60/382,120
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-10-442-909-32

Query Match      29.4%; Score 32; DB 4; Length 17;
Best Local Similarity 55.6%; Pred. No. 7.2e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      2 IPHPTNHHK 10
Db      8 IPHPAGLKK 16

RESULT 22
US-10-285-649A-9
; Sequence 9, Application US/10285649A
; Publication No. US20030106089A1
; GENERAL INFORMATION:
; APPLICANT: McBride, Kevin
; APPLICANT: Stalker, David M.
; APPLICANT: Pear, Julie
; APPLICANT: Perez-Grau, Luis
; TITLE OF INVENTION: COTTON FIBER TRANSCRIPTIONAL FACTORS
; FILE REFERENCE: 15615/03/US
; CURRENT APPLICATION NUMBER: US/10/285,649A
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 08/984,099
; PRIOR FILING DATE: 1997-12-03
; PRIOR APPLICATION NUMBER: PCT/US96/09897
; PRIOR FILING DATE: 1996-06-07
; PRIOR APPLICATION NUMBER: US 08/480,178
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: IBM PC; Windows 2000; Microsoft Word 2000
; SEQ ID NO 9
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Goseyplum Hirsutum
US-10-285-649A-9

Query Match      29.4%; Score 32; DB 4; Length 20;
Best Local Similarity 42.9%; Pred. No. 8.5e+02;
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY      2 IPHPTNHHKYLVC 15
Db      6 LPPTFTHKCLTSD 19

RESULT 23
US-11-008-653-128
; Sequence 128, Application US/11008653
; Publication No. US20050175627A1
; GENERAL INFORMATION:
; APPLICANT: Schneider, Joerg
; TITLE OF INVENTION: HIV Pharmacies
; FILE REFERENCE: 3742.1001-000
; CURRENT APPLICATION NUMBER: US/11/008,653
; CURRENT FILING DATE: 2004-12-09
; PRIOR APPLICATION NUMBER: PCT/GB2004/004038
; PRIOR FILING DATE: 2004-09-23
; PRIOR APPLICATION NUMBER: GB 0325011.5
; PRIOR FILING DATE: 2003-10-27
; PRIOR APPLICATION NUMBER: GB 0322637.0
; PRIOR FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: GB 0322402.9
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; PRIOR FILING DATE: 2003-09-24
 ; NUMBER OF SEQ ID NOS: 174
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 128
 ; LENGTH: 20
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: peptide from pol pool 2
 US-11-008-653-128

Query Match 29.4%; Score 32; DB 6; Length 20;
 Best Local Similarity 55.6%; Pred. No. 8.5e+02;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IHPPTNIHK 10
 DB 5 IHPAGLKK 13

RESULT 24
 US-10-430-685-95
 ; Sequence 95, Application US/10430685
 ; Publication No. US20040039543A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KECK, Peter
 ; TITLE OF INVENTION: COMPUTER METHOD AND APPARATUS FOR CLASSIFYING OBJECTS
 ; FILE REFERENCE: 63040-010210
 ; CURRENT APPLICATION NUMBER: US/10/430,685
 ; PRIOR FILING DATE: 2003-05-06
 ; PRIOR APPLICATION NUMBER: PCT/US01/44000
 ; PRIOR FILING DATE: 2001-11-06
 ; PRIOR APPLICATION NUMBER: 60/246,196
 ; NUMBER OF SEQ ID NOS: 240
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 95
 ; LENGTH: 17
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-430-685-95

Query Match 28.9%; Score 31.5; DB 4; Length 17;
 Best Local Similarity 66.7%; Pred. No. 8.5e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 4 HPTNIHXYL 12
 DB 1 HPTN-HAYI 8

RESULT 25
 US-09-962-756-51
 ; Sequence 51, Application US/09962756
 ; Publication No. US20030195147A1
 ; GENERAL INFORMATION:
 ; APPLICANT: PILUTTLA, RENKA
 ; APPLICANT: BRISSETTE, RENEE
 ; APPLICANT: BLUME, ARTHUR J.
 ; APPLICANT: SCHAFER, LAUDE
 ; APPLICANT: BRANDT, JAKOB
 ; APPLICANT: GOLDSTEIN, NEIL I.
 ; APPLICANT: SPETZLER, JANE
 ; APPLICANT: OSTERGAARD, SOREN
 ; APPLICANT: HANSEN, PER HERTZ
 ; TITLE OF INVENTION: INSULIN AND IGF-1 RECEPTOR AGONISTS AND ANTAGONISTS
 ; FILE REFERENCE: 1878-4051US1
 ; CURRENT APPLICATION NUMBER: US/09/962,756
 ; PRIOR FILING DATE: 2001-09-24
 ; PRIOR APPLICATION NUMBER: 09/538,038
 ; PRIOR FILING DATE: 2000-03-29
 ; PRIOR APPLICATION NUMBER: 09/146,127
 ; PRIOR FILING DATE: 1998-09-02

; NUMBER OF SEQ ID NOS: 2227
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 51
 ; LENGTH: 21
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 US-09-962-756-51

Query Match 28.9%; Score 31.5; DB 3; Length 21;
 Best Local Similarity 37.5%; Pred. No. 1.1e+03;
 Matches 6; Conservative 5; Mismatches 4; Indels 1; Gaps 1;

QY 3 PHPTNIHXYLVCESVN 18
 DB 7 PHGSNFYDFV-EAIN 21

Search completed: January 26, 2006, 08:38:39
 Job time : 63.75 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 26, 2006, 08:05:12 ; Search time 3.60345 Seconds
(without alignments)
57.099 Million cell updates/sec

Title: US-09-662-293-11
Perfect score: 109
Sequence: 1 DIPHTNHKYLCEVSNG 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 75621 seqs, 10829074 residues

Total number of hits satisfying chosen parameters: 37628

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published Applications AA New:
1: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US12_NEW_PUB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US13_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US14_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	29.4	10	7	US-11-045-024-3294
2	32	29.4	10	7	US-11-045-024-10214
3	32	29.4	10	7	US-11-045-024-12085
4	32	29.4	11	7	US-11-045-024-3376
5	32	29.4	11	7	US-11-045-024-10191
6	32	29.4	11	7	US-11-045-024-10215
7	32	29.4	11	7	US-11-045-024-12063
8	32	29.4	11	7	US-11-045-024-12086
9	32	29.4	11	7	US-11-045-024-13140
10	31	28.4	16	7	US-11-038-980-3
11	31	28.4	17	7	US-11-038-980-4
12	31	28.4	20	7	US-11-038-980-9
13	31	28.4	21	7	US-11-038-980-10
14	29.5	27.1	9	6	US-10-859-643-123
15	29.5	27.1	9	7	US-10-859-643-123
16	29.5	27.1	9	7	US-11-097-864-123
17	29.5	27.1	10	6	US-10-859-643-164
18	29.5	27.1	10	7	US-11-097-864-164
19	29.5	27.1	10	7	US-11-097-864-164
20	29.5	27.1	10	7	US-10-966-483-17
21	29.5	27.1	14	6	US-11-166-412-88
22	29.5	27.1	17	6	US-10-506-443A-18
23	29.5	27.1	20	6	US-10-723-207-71
24	28	25.7	8	7	US-11-045-024-1627
25	28	25.7	8	7	US-11-045-024-4340

26	28	25.7	9	7	US-11-045-024-1222	Sequence 3222, Ap
27	28	25.7	9	7	US-11-045-024-10229	Sequence 10229, A
28	28	25.7	9	7	US-11-045-024-12094	Sequence 12094, A
29	28	25.7	9	7	US-11-045-024-13796	Sequence 13796, A
30	28	25.7	10	7	US-11-045-024-2073	Sequence 2073, Ap
31	28	25.7	10	7	US-11-045-024-4608	Sequence 4608, Ap
32	28	25.7	10	7	US-11-045-024-10231	Sequence 10231, A
33	28	25.7	10	7	US-11-045-024-12035	Sequence 12035, A
34	28	25.7	11	7	US-11-045-024-2288	Sequence 2288, Ap
35	28	25.7	11	7	US-11-045-024-3375	Sequence 3375, Ap
36	28	25.7	11	7	US-11-045-024-10232	Sequence 10232, A
37	28	25.7	11	7	US-11-045-024-12096	Sequence 12096, A
38	28	25.7	15	7	US-11-045-024-13150	Sequence 13150, A
39	28	25.7	16	6	US-10-967-671-10	Sequence 10, Appl
40	27	24.8	13	7	US-11-033-039-792	Sequence 792, Ap
41	27	24.8	14	7	US-11-152-366-236	Sequence 236, Ap
42	27	24.8	19	6	US-10-880-238-115	Sequence 115, Ap
43	27	24.8	19	6	US-11-033-039-794	Sequence 794, Ap
44	26.5	24.3	18	7	US-11-119-581-113	Sequence 113, Ap
45	26	23.9	5	6	US-10-956-755A-55	Sequence 55, Appl
46	26	23.9	5	6	US-10-956-755A-73	Sequence 73, Appl
47	26	23.9	5	6	US-10-956-755A-91	Sequence 91, Appl
48	26	23.9	8	7	US-11-045-024-1626	Sequence 1626, Ap
49	26	23.9	8	7	US-11-045-024-10228	Sequence 10228, A
50	26	23.9	9	6	US-10-859-643-17	Sequence 17, Appl
51	26	23.9	9	7	US-11-097-864-17	Sequence 17, Appl
52	26	23.9	9	7	US-11-097-864-17	Sequence 17, Appl
53	26	23.9	9	7	US-11-045-024-1831	Sequence 1831, Appl
54	26	23.9	9	7	US-11-045-024-13806	Sequence 13806, A
55	26	23.9	9	7	US-11-041-893-64	Sequence 64, Appl
56	26	23.9	10	6	US-10-859-643-53	Sequence 53, Appl
57	26	23.9	10	7	US-11-097-812-53	Sequence 53, Appl
58	26	23.9	10	7	US-11-097-812-53	Sequence 53, Appl
59	26	23.9	10	7	US-11-045-024-1072	Sequence 1072, A
60	26	23.9	10	7	US-11-045-024-10220	Sequence 10220, A
61	26	23.9	13	6	US-10-511-559-126	Sequence 126, Ap
62	26	23.9	13	6	US-10-511-559-127	Sequence 127, Ap
63	26	23.9	13	6	US-10-511-559-128	Sequence 128, Ap
64	26	23.9	13	6	US-10-511-559-129	Sequence 129, Ap
65	26	23.9	13	7	US-11-116-144-64	Sequence 64, Appl
66	26	23.9	15	7	US-11-045-024-13137	Sequence 13137, A
67	26	23.9	20	6	US-10-623-155-247	Sequence 247, Ap
68	26	23.9	6	7	US-11-084-717-55	Sequence 55, Appl
69	25	22.9	9	7	US-11-010-748A-856	Sequence 856, Ap
70	25	22.9	9	7	US-11-010-748A-860	Sequence 860, Ap
71	25	22.9	9	7	US-11-010-748A-861	Sequence 861, Ap
72	25	22.9	9	7	US-11-010-748A-864	Sequence 864, Ap
73	25	22.9	9	7	US-11-010-748A-866	Sequence 866, Ap
74	25	22.9	9	7	US-11-010-748A-868	Sequence 868, Ap
75	25	22.9	9	7	US-11-010-748A-869	Sequence 869, Ap
76	25	22.9	17	7	US-11-010-748A-885	Sequence 885, Ap
77	25	22.9	18	7	US-11-033-039-1223	Sequence 1223, Ap
78	25	22.9	20	6	US-10-485-788A-580	Sequence 580, Ap
79	25	22.9	20	7	US-11-022-562-141	Sequence 141, Ap
80	25	22.9	20	7	US-11-022-562-142	Sequence 142, Ap
81	25	22.9	8	7	US-11-064-416-4	Sequence 4, Appl
82	25	22.9	8	7	US-11-064-416-5	Sequence 5, Appl
83	24	22.0	9	6	US-10-966-483-14	Sequence 14, Appl
84	24	22.0	10	6	US-10-614-599-26	Sequence 26, Appl
85	24	22.0	12	6	US-10-966-371-7	Sequence 7, Appl
86	24	22.0	12	7	US-11-180-897-5	Sequence 5, Appl
87	24	22.0	12	7	US-11-180-897-19	Sequence 19, Appl
88	24	22.0	12	7	US-11-180-897-19	Sequence 19, Appl
89	24	22.0	14	6	US-10-939-890-44	Sequence 44, Ap
90	24	22.0	16	7	US-11-033-039-1428	Sequence 1428, Ap
91	24	22.0	17	7	US-11-033-039-1427	Sequence 1427, Ap
92	24	22.0	17	7	US-11-041-893-132	Sequence 132, Ap
93	24	22.0	18	7	US-11-033-039-1426	Sequence 1426, Ap
94	24	22.0	19	7	US-11-033-039-1425	Sequence 1425, Ap
95	24	22.0	20	6	US-10-623-155-514	Sequence 514, Ap
96	24	22.0	20	7	US-11-022-562-173	Sequence 173, Ap
97	24	22.0	20	7	US-11-033-039-1424	Sequence 1424, Ap
98	24	22.0	21	7	US-11-033-039-1423	Sequence 1423, Ap

99 23 21.1 7 7 US-11-226-701-28
100 23 21.1 8 7 US-11-140-417-18

Sequence 28, Appl
Sequence 18, Appl

ALIGNMENTS

RESULT 1

US-11-045-024-3294
; Sequence 3294, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: EpiImmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US/11/045,024
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3294
; LENGTH: 10
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-3294

Query Match 29.4%; Score 32; DB 7; Length 10;
Best Local Similarity 55.6%; Pred. No. 11;

Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 IPHPNTIHK 10
||| : |
Db 2 IPHPAGLKK 10

RESULT 2

US-11-045-024-10214
; Sequence 10214, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph

; APPLICANT: Grey, Howard M.

; APPLICANT: EpiImmune Inc.

; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007

; CURRENT FILING DATE: 2005-01-28

; PRIOR APPLICATION NUMBER: US/11/045,024

; PRIOR FILING DATE: 1999-10-05

; PRIOR APPLICATION NUMBER: US 08/027,146

; PRIOR FILING DATE: 1993-03-05

; PRIOR APPLICATION NUMBER: US 08/073,205

; PRIOR FILING DATE: 1993-06-04

; PRIOR APPLICATION NUMBER: US 08/103,396

; PRIOR FILING DATE: 1993-08-06

; PRIOR APPLICATION NUMBER: US 08/159,184

; PRIOR FILING DATE: 1993-11-29

; PRIOR APPLICATION NUMBER: US 08/159,339

; PRIOR FILING DATE: 1993-11-29

; PRIOR APPLICATION NUMBER: US 08/205,713

; PRIOR FILING DATE: 1994-03-04

; PRIOR APPLICATION NUMBER: US 08/347,610

; PRIOR FILING DATE: 1994-12-01

; NUMBER OF SEQ ID NOS: 14528

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 10214

; LENGTH: 10

; TYPE: PRT

; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS

US-11-045-024-10214

Query Match 29.4%; Score 32; DB 7; Length 10;
Best Local Similarity 55.6%; Pred. No. 11;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 IPHPNTIHK 10
||| : |
Db 2 IPHPAGLKK 10

RESULT 3

US-11-045-024-12085
; Sequence 12085, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: EpiImmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US/11/045,024
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713

PRIOR FILING DATE: 1994-03-04
 PRIOR APPLICATION NUMBER: US 08/347,610
 PRIOR FILING DATE: 1994-12-01
 NUMBER OF SEQ ID NOS: 14528
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 12085
 LENGTH: 10
 TYPE: PRT
 ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
 US-11-045-024-12085

Query Match 29.4%; Score 32; DB 7; Length 10;
 Best Local Similarity 55.6%; Pred. No. 11;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 IPHPTNTHK 10
 Db 2 IPHPAGLKK 10

RESULT 4
 US-11-045-024-3376
 Sequence 3376, Application US/11045024
 Publication No. US20050271676A1
 GENERAL INFORMATION:
 APPLICANT: Sette, Alessandro
 APPLICANT: Sidney, John
 APPLICANT: Southwood, Scott
 APPLICANT: Livingston, Brian
 APPLICANT: Chesnut, Robert
 APPLICANT: Baker, Denise Marie
 APPLICANT: Celis, Esceban
 APPLICANT: Kubo, Ralph
 APPLICANT: Grey, Howard M.
 APPLICANT: EpiImmune Inc.
 TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
 TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
 FILE REFERENCE: 2060.0040007
 CURRENT APPLICATION NUMBER: US/11/045,024
 CURRENT FILING DATE: 2005-01-28
 PRIOR APPLICATION NUMBER: US 09/412,863
 PRIOR FILING DATE: 1999-10-05
 PRIOR APPLICATION NUMBER: US 08/027,146
 PRIOR FILING DATE: 1993-03-05
 PRIOR APPLICATION NUMBER: US 08/073,205
 PRIOR FILING DATE: 1993-06-04
 PRIOR APPLICATION NUMBER: US 08/103,396
 PRIOR FILING DATE: 1993-08-06
 PRIOR APPLICATION NUMBER: US 08/159,184
 PRIOR FILING DATE: 1993-11-29
 PRIOR APPLICATION NUMBER: US 08/159,339
 PRIOR FILING DATE: 1993-11-29
 PRIOR APPLICATION NUMBER: US 08/205,713
 PRIOR FILING DATE: 1994-03-04
 PRIOR APPLICATION NUMBER: US 08/347,610
 PRIOR FILING DATE: 1994-12-01
 NUMBER OF SEQ ID NOS: 14528
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 3376
 LENGTH: 11
 TYPE: PRT
 ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
 US-11-045-024-3376

Query Match 29.4%; Score 32; DB 7; Length 11;
 Best Local Similarity 55.6%; Pred. No. 13;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 IPHPTNTHK 10
 Db 2 IPHPAGLKK 10

RESULT 5
 US-11-045-024-10191
 Sequence 10191, Application US/11045024
 Publication No. US20050271676A1
 GENERAL INFORMATION:
 APPLICANT: Sette, Alessandro
 APPLICANT: Sidney, John
 APPLICANT: Southwood, Scott
 APPLICANT: Livingston, Brian
 APPLICANT: Chesnut, Robert
 APPLICANT: Baker, Denise Marie
 APPLICANT: Celis, Esceban
 APPLICANT: Kubo, Ralph
 APPLICANT: Grey, Howard M.
 APPLICANT: EpiImmune Inc.
 TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
 TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
 FILE REFERENCE: 2060.0040007
 CURRENT APPLICATION NUMBER: US/11/045,024
 CURRENT FILING DATE: 2005-01-28
 PRIOR APPLICATION NUMBER: US 09/412,863
 PRIOR FILING DATE: 1999-10-05
 PRIOR APPLICATION NUMBER: US 08/027,146
 PRIOR FILING DATE: 1993-03-05
 PRIOR APPLICATION NUMBER: US 08/073,205
 PRIOR FILING DATE: 1993-06-04
 PRIOR APPLICATION NUMBER: US 08/103,396
 PRIOR FILING DATE: 1993-08-06
 PRIOR APPLICATION NUMBER: US 08/159,184
 PRIOR FILING DATE: 1993-11-29
 PRIOR APPLICATION NUMBER: US 08/159,339
 PRIOR FILING DATE: 1993-11-29
 PRIOR APPLICATION NUMBER: US 08/205,713
 PRIOR FILING DATE: 1994-03-04
 PRIOR APPLICATION NUMBER: US 08/347,610
 PRIOR FILING DATE: 1994-12-01
 NUMBER OF SEQ ID NOS: 14528
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 10191
 LENGTH: 11
 TYPE: PRT
 ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
 US-11-045-024-10191

Query Match 29.4%; Score 32; DB 7; Length 11;
 Best Local Similarity 55.6%; Pred. No. 13;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 IPHPTNTHK 10
 Db 2 IPHPAGLKK 10

RESULT 6
 US-11-045-024-10215
 Sequence 10215, Application US/11045024
 Publication No. US20050271676A1
 GENERAL INFORMATION:
 APPLICANT: Sette, Alessandro
 APPLICANT: Sidney, John
 APPLICANT: Southwood, Scott
 APPLICANT: Livingston, Brian
 APPLICANT: Chesnut, Robert
 APPLICANT: Baker, Denise Marie
 APPLICANT: Celis, Esceban
 APPLICANT: Kubo, Ralph
 APPLICANT: Grey, Howard M.
 APPLICANT: EpiImmune Inc.
 TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
 TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
 FILE REFERENCE: 2060.0040007
 CURRENT APPLICATION NUMBER: US/11/045,024
 CURRENT FILING DATE: 2005-01-28

```

; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-12063
Query Match      29.4%; Score 32; DB 7; Length 11;
Best Local Similarity 55.6%; Pred. No. 13;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY      2 IPHPTNIHK 10
      ||||| : |
      3 IPHPAGLKK 11

Db

RESULT 7
US-11-045-024-12063
; Sequence 12063, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: EpiImmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12063
; LENGTH: 11
```

```

; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-12063
Query Match      29.4%; Score 32; DB 7; Length 11;
Best Local Similarity 55.6%; Pred. No. 13;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY      2 IPHPTNIHK 10
      ||||| : |
      3 IPHPAGLKK 11

Db

RESULT 8
US-11-045-024-12086
; Sequence 12086, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: EpiImmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12086
; LENGTH: 11
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-12086
Query Match      29.4%; Score 32; DB 7; Length 11;
Best Local Similarity 55.6%; Pred. No. 13;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY      2 IPHPTNIHK 10
      ||||| : |
      3 IPHPAGLKK 11

Db

RESULT 9
US-11-045-024-13140
; Sequence 13140, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
```



```
APPLICANT: Southwood, Scott
APPLICANT: Livingston, Brian
APPLICANT: Chesnut, Robert
APPLICANT: Baker, Denise Marie
APPLICANT: Cells, Esteban
APPLICANT: Kubo, Ralph
APPLICANT: Grey, Howard M.
APPLICANT: EpiImmune Inc.
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2060.0040007
CURRENT APPLICATION NUMBER: US/11/045,024
CURRENT FILING DATE: 2005-01-28
PRIOR APPLICATION NUMBER: US 09/412,863
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: US 08/027,146
PRIOR FILING DATE: 1993-03-05
PRIOR APPLICATION NUMBER: US 08/073,205
PRIOR FILING DATE: 1993-06-04
PRIOR APPLICATION NUMBER: US 08/103,396
PRIOR FILING DATE: 1993-08-06
PRIOR APPLICATION NUMBER: US 08/159,184
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/159,339
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/347,610
PRIOR FILING DATE: 1994-12-01
NUMBER OF SEQ ID NOS: 14528
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13140
LENGTH: 15
TYPE: PRT
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-13140

Query Match      29.4% Score 32; DB 7; Length 15;
Best Local Similarity 55.6% Pred. No. 17;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy      2 IPHPTNIHK 10
Db      6 IPHAGLKK 14

RESULT 10
US-11-038-980-3
Sequence 3, Application US/11038980
Publication No. US2006002893A1
GENERAL INFORMATION:
APPLICANT: Centellon SAS
APPLICANT: Emmanuelle Vigne
APPLICANT: Jean-Francois Dedieu
APPLICANT: Martine Latta
APPLICANT: Patrice Yeh
APPLICANT: Michel Perricaudet
TITLE OF INVENTION: Targeted Adenovirus Vectors For Delivery Of Heterologous Genes
FILE REFERENCE: P26,992-C USA
CURRENT APPLICATION NUMBER: US/11/038,980
CURRENT FILING DATE: 2005-01-20
PRIOR APPLICATION NUMBER: US 09/791,524
PRIOR FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: PCT/IB99/01524
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: US 60/098,028
PRIOR FILING DATE: 1998-08-27
NUMBER OF SEQ ID NOS: 165
SOFTWARE: PatentIn version 3.2
SEQ ID NO 3
LENGTH: 16
TYPE: PRT
ORGANISM: Adenovirus
```

```
US-11-038-980-3
Query Match      28.4% Score 31; DB 7; Length 16;
Best Local Similarity 45.5% Pred. No. 27;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy      2 IPHPTNIHKYL 12
Db      4 MPHSLNFSQYL 14

RESULT 11
US-11-038-980-4
Sequence 4, Application US/11038980
Publication No. US2006002893A1
GENERAL INFORMATION:
APPLICANT: Centellon SAS
APPLICANT: Emmanuelle Vigne
APPLICANT: Jean-Francois Dedieu
APPLICANT: Martine Latta
APPLICANT: Patrice Yeh
APPLICANT: Michel Perricaudet
TITLE OF INVENTION: Targeted Adenovirus Vectors For Delivery Of Heterologous Genes
FILE REFERENCE: P26,992-C USA
CURRENT APPLICATION NUMBER: US/11/038,980
CURRENT FILING DATE: 2005-01-20
PRIOR APPLICATION NUMBER: US 09/791,524
PRIOR FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: PCT/IB99/01524
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: US 60/098,028
PRIOR FILING DATE: 1998-08-27
NUMBER OF SEQ ID NOS: 165
SOFTWARE: PatentIn version 3.2
SEQ ID NO 4
LENGTH: 17
TYPE: PRT
ORGANISM: Adenovirus
US-11-038-980-4

Query Match      28.4% Score 31; DB 7; Length 17;
Best Local Similarity 45.5% Pred. No. 29;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy      2 IPHPTNIHKYL 12
Db      4 MPHSLNFSQYL 14

RESULT 12
US-11-038-980-9
Sequence 9, Application US/11038980
Publication No. US2006002893A1
GENERAL INFORMATION:
APPLICANT: Centellon SAS
APPLICANT: Emmanuelle Vigne
APPLICANT: Jean-Francois Dedieu
APPLICANT: Martine Latta
APPLICANT: Patrice Yeh
APPLICANT: Michel Perricaudet
TITLE OF INVENTION: Targeted Adenovirus Vectors For Delivery Of Heterologous Genes
FILE REFERENCE: P26,992-C USA
CURRENT APPLICATION NUMBER: US/11/038,980
CURRENT FILING DATE: 2005-01-20
PRIOR APPLICATION NUMBER: US 09/791,524
PRIOR FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: PCT/IB99/01524
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: US 60/098,028
PRIOR FILING DATE: 1998-08-27
NUMBER OF SEQ ID NOS: 165
SOFTWARE: PatentIn version 3.2
SEQ ID NO 9
```

LENGTH: 20
TYPE: PRT
ORGANISM: Adenovirus
US-11-038-980-9

Query Match 28.4%; Score 31; DB 7; Length 20;
Best Local Similarity 45.5%; Pred. No. 34;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IPHPTNIHXYL 12
: || | : ||
Db 6 MPHSLNFSQYL 16

RESULT 13
US-11-038-980-10

Sequence 10, Application US/11038980
Publication No. US20060002893A1
GENERAL INFORMATION:
APPLICANT: Cencelion SAS
APPLICANT: Emmanuelle Vigne
APPLICANT: Jean-Francois Dedieu
APPLICANT: Martine Latta
APPLICANT: Patrice Yeh
APPLICANT: Michel Perricaudet
TITLE OF INVENTION: Targeted Adenovirus Vectors for Delivery of Heterologous Genes
FILE REFERENCE: P26,992-C USA
CURRENT APPLICATION NUMBER: US/11/038,980
PRIOR FILING DATE: 2005-01-20
PRIOR APPLICATION NUMBER: US 09/791,524
PRIOR FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: PCT/IB99/01524
PRIOR FILING DATE: 1989-08-27
PRIOR APPLICATION NUMBER: US 60/098,028
PRIOR FILING DATE: 1998-08-27
NUMBER OF SEQ ID NOS: 165
SOFTWARE: PatentIn version 3.2
SEQ ID NO 10
LENGTH: 21
TYPE: PRT
ORGANISM: Adenovirus
US-11-038-980-10

Query Match 28.4%; Score 31; DB 7; Length 21;
Best Local Similarity 45.5%; Pred. No. 35;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IPHPTNIHXYL 12
: || | : ||
Db 6 MPHSLNFSQYL 16

RESULT 14
US-10-859-643-123

Sequence 123, Application US/10859643
Publication No. US20060002993A1
GENERAL INFORMATION:
APPLICANT: Chailita-Eid, Pia M.
APPLICANT: Raitano, Arthur B.
APPLICANT: Farris, Mary
APPLICANT: Hubert, Rene S.
APPLICANT: Morrison, Karen Jane Meyrick
APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
FILE REFERENCE: 511582006203
CURRENT APPLICATION NUMBER: US/10/859,643
PRIOR FILING DATE: 2004-06-02
PRIOR APPLICATION NUMBER: US 10/005,480
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 765
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 123
LENGTH: 9
TYPE: PRT
ORGANISM: Homo Sapien
US-10-859-643-123

Query Match 27.1%; Score 29.5; DB 6; Length 9;
Best Local Similarity 75.0%; Pred. No. 5.9e+04;
Matches 6; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 2 IPH-PTNI 8
||| ||| :
Db 2 IPHRPTNV 9

RESULT 15
US-11-097-864-123

Sequence 123, Application US/11097864
Publication No. US20050265924A1
GENERAL INFORMATION:
APPLICANT: Chailita-Eid, Pia M.
APPLICANT: Raitano, Arthur B.
APPLICANT: Farris, Mary
APPLICANT: Hubert, Rene S.
APPLICANT: Morrison, Karen Jane Meyrick
APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2F10B
TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 511582006205
CURRENT APPLICATION NUMBER: US/11/097,864
PRIOR FILING DATE: 2005-04-01
PRIOR APPLICATION NUMBER: US 10/062,109
PRIOR FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: US 10/005,480
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 765
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 123
LENGTH: 9
TYPE: PRT
ORGANISM: Homo Sapien
US-11-097-864-123

Query Match 27.1%; Score 29.5; DB 7; Length 9;
Best Local Similarity 75.0%; Pred. No. 5.9e+04;
Matches 6; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 2 IPH-PTNI 8
||| ||| :
Db 2 IPHRPTNV 9

RESULT 16
US-11-097-912-123

Sequence 123, Application US/11097912
Publication No. US20050265921A1
GENERAL INFORMATION:
APPLICANT: Chailita-Eid, Pia M.
APPLICANT: Raitano, Arthur B.
APPLICANT: Farris, Mary
APPLICANT: Hubert, Rene S.
APPLICANT: Morrison, Karen Jane Meyrick
APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 161P2F10B
TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 511582006204
CURRENT APPLICATION NUMBER: US/11/097,912
PRIOR FILING DATE: 2005-04-01
PRIOR APPLICATION NUMBER: US 10/062,109
PRIOR FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: US 10/005,480
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 765

```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 123
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-097-912-123
```

```
Query Match      27.1% Score 29.5; DB 7; Length 9;
Best Local Similarity 75.0%; Pred. No. 5.9e+04;
Matches 6; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
```

```
Qy      2 IPR-PTNI 8
        ||| |||:
Db      2 IPRPTNV 9
```

```
RESULT 17
US-10-859-643-164
; Sequence 164, Application US/10859643
; Publication No. US2006002993A1
; GENERAL INFORMATION:
; APPLICANT: Chaillita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; FILE REFERENCE: 511582006203
; CURRENT APPLICATION NUMBER: US/10/859,643
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 164
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-859-643-164
```

```
Query Match      27.1% Score 29.5; DB 6; Length 10;
Best Local Similarity 75.0%; Pred. No. 29;
Matches 6; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
```

```
Qy      2 IPR-PTNI 8
        ||| |||:
Db      3 IPRPTNV 10
```

```
RESULT 18
US-11-097-864-164
; Sequence 164, Application US/11097864
; Publication No. US20050265924A1
; GENERAL INFORMATION:
; APPLICANT: Chaillita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2F10B
; FILE REFERENCE: 511582006205
; CURRENT APPLICATION NUMBER: US/11/097,864
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
```

```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 164
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-097-864-164
```

```
Query Match      27.1% Score 29.5; DB 7; Length 10;
Best Local Similarity 75.0%; Pred. No. 29;
Matches 6; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
```

```
Qy      2 IPR-PTNI 8
        ||| |||:
Db      3 IPRPTNV 10
```

```
RESULT 19
US-11-097-912-164
; Sequence 164, Application US/11097912
; Publication No. US20050265921A1
; GENERAL INFORMATION:
; APPLICANT: Chaillita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 161P2F10B
; TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 511582006204
; CURRENT APPLICATION NUMBER: US/11/097,912
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 164
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-097-912-164
```

```
Query Match      27.1% Score 29.5; DB 7; Length 10;
Best Local Similarity 75.0%; Pred. No. 29;
Matches 6; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
```

```
Qy      2 IPR-PTNI 8
        ||| |||:
Db      3 IPRPTNV 10
```

```
RESULT 20
US-10-966-483-17
; Sequence 17, Application US/1096483
; Publication No. US20050281783A1
; GENERAL INFORMATION:
; APPLICANT: Kinch, Michael S.
; APPLICANT: Kiener, Peter A.
; APPLICANT: Bruckheimer, Elizabeth
; APPLICANT: Dubensky, Jf. Thomas W.
; APPLICANT: Cook, David N.
; TITLE OF INVENTION: LISTERIA-BASED Epha2 VACCINES
; FILE REFERENCE: 10271-146
; CURRENT APPLICATION NUMBER: US/10/966,483
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: US 60/511,919
; PRIOR FILING DATE: 2003-10-15
; PRIOR APPLICATION NUMBER: US 60/511,719
; PRIOR FILING DATE: 2003-10-15
; PRIOR APPLICATION NUMBER: US 60/532,666
; PRIOR FILING DATE: 2003-12-24
```

```

; PRIOR APPLICATION NUMBER: US 60/556,631
; PRIOR FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE: 2004-10-07
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 17
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-966-483-17

Query Match      26.6%; Score 29; DB 6; Length 13;
Best Local Similarity 41.7%; Pred. No. 46;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Oy      8 IHXYLVCEVNG 19
        |||||
        :|:|:|:|
Db      2 IYMSVCMVMSG 13

RESULT 21
US-11-166-412-88
; Sequence 88, Application US/11166412
; Publication No. US20060014231A1
; GENERAL INFORMATION:
; APPLICANT: Van Rompaey, Luc
; APPLICANT: Tomme, Peter H. M.
; TITLE OF INVENTION: Methods and Compositions To Promote Bone Homeostasis
; FILE REFERENCE: P27,927-D USA
; CURRENT APPLICATION NUMBER: US/11/166,412
; PRIOR FILING DATE: 2005-06-24
; PRIOR APPLICATION NUMBER: 60/582,704
; PRIOR FILING DATE: 2004-06-24
; PRIOR APPLICATION NUMBER: 60/630,449
; PRIOR FILING DATE: 2004-11-23
; PRIOR APPLICATION NUMBER: 60/673,206
; PRIOR FILING DATE: 2005-04-20
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 88
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Protein domain fragment
US-11-166-412-88

Query Match      26.6%; Score 29; DB 7; Length 14;
Best Local Similarity 36.4%; Pred. No. 50;
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Oy      4 HPTNIHKYLV 14
        |||||
        :|:|:|:|
Db      4 YSTGVHESLTC 14

RESULT 22
US-10-506-443A-18
; Sequence 18, Application US/10506443A
; Publication No. US20060013817A1
; GENERAL INFORMATION:
; APPLICANT: Sahin Dr., Ugur
; APPLICANT: Tureci Dr., Ozlem
; APPLICANT: Koslowski Dr., Michael
; TITLE OF INVENTION: Genetic Products Differentially Expressed in Tumors and Use There
; FILE REFERENCE: 342-3PCT
; CURRENT APPLICATION NUMBER: US/10/506,443A
; PRIOR FILING DATE: 2004-09-01
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: Patentin version 3.1
```

```

; SEQ ID NO 18
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-506-443A-18

Query Match      26.6%; Score 29; DB 6; Length 17;
Best Local Similarity 50.0%; Pred. No. 60;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Oy      4 HPTNIHKYLV 13
        |||||
        :|:|:|:|
Db      2 HWKNIHKQVI 11

RESULT 23
US-10-723-207-71
; Sequence 71, Application US/10723207
; Publication No. US20050250934A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Y1
; APPLICANT: Walfield, Alan M.
; TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF
; FILE REFERENCE: 1151-4153US2
; CURRENT APPLICATION NUMBER: US/10/723,207
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: 09/701,623
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US99/13959
; PRIOR FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: 09/100,287
; PRIOR FILING DATE: 1998-06-20
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 71
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide
; OTHER INFORMATION: synthesized from amino acids with no genetic
; OTHER INFORMATION: material as source
US-10-723-207-71

Query Match      26.6%; Score 29; DB 6; Length 20;
Best Local Similarity 33.3%; Pred. No. 71;
Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Oy      3 PHPTNIHKYLV 14
        |||||
        :|:|:|:|
Db      1 PHPTALRQALIC 12

RESULT 24
US-11-045-024-1627
; Sequence 1627, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Cells, Etseban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: EpiImmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
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; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1627
; LENGTH: 8
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-1627

Query Match      25.7%; Score 28; DB 7; Length 8;
Best Local Similarity 57.1%; Pred. No. 5.9e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      2 IPHPTNI 8
      |||||
      :
Db      2 IPHPAGL 8

RESULT 25
US-11-045-024-4340
; Sequence 4340, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esreban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epiimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4340
```

```
; LENGTH: 8
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-4340

Query Match      25.7%; Score 28; DB 7; Length 8;
Best Local Similarity 57.1%; Pred. No. 5.9e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      2 IPHPTNI 8
      |||||
      :
Db      2 IPHPAGL 8

Search completed: January 26, 2006, 08:39:07
Job time : 3.60345 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 26, 2006, 07:48:50 ; Search time 9.5 Seconds

(without alignments)
192.434 Million cell updates/sec

Title: US-09-662-293-11

Perfect score: 109
Sequence: 1 DIPPTNHHKLVCEVSNG 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 4071

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database : PIR 80:*

1: PIR1:*\n2: PIR2:*\n3: PIR3:*\n4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the change being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	34.9	15	2	A60929
2	38	34.9	15	2	B60929
3	27	24.8	11	2	S42587
4	27	24.8	18	2	H64711
5	26	23.9	18	2	S65454
6	25.5	23.4	16	2	S55307
7	25	22.9	19	2	PQ0548
8	24	22.9	20	2	D84716
9	24	22.0	9	2	A60108
10	24	22.0	9	2	S10930
11	24	22.0	17	2	S15728
12	24	22.0	18	2	S29264
13	24	22.0	18	2	PN0175
14	24	22.0	19	2	I50153
15	24	22.0	20	2	A45655
16	23	21.1	13	2	S38736
17	23	21.1	16	2	PH1604
18	23	21.1	17	2	S15754
19	23	21.1	17	2	S63503
20	22.5	20.6	18	1	A58589
21	22	20.2	10	2	BS9272
22	22	20.2	10	2	B37196
23	22	20.2	11	2	B60409
24	22	20.2	11	2	D60409
25	22	20.2	13	2	B47415
26	22	20.2	15	2	S60007
27	22	20.2	16	2	S00123
28	22	20.2	16	2	A41170
29	22	20.2	16	2	A11488

30	22	20.2	19	2	D44101
31	22	20.2	20	2	A38556
32	21	19.3	12	2	A54315
33	21	19.3	12	2	B47171
34	21	19.3	13	2	A54326
35	21	19.3	14	2	S41601
36	21	19.3	15	2	PQ0232
37	21	19.3	15	2	A56786
38	21	19.3	15	2	PH0136
39	21	19.3	15	2	A08416
40	21	19.3	17	2	C49255
41	21	19.3	17	2	S15064
42	21	19.3	18	2	PQ0680
43	21	19.3	18	2	S20322
44	21	19.3	20	2	A24589
45	21	19.3	20	2	A60100
46	21	19.3	20	2	C56894
47	21	19.3	20	2	B56894
48	21	19.3	20	2	S44465
49	21	19.3	20	2	AE0120
50	21	19.3	21	2	PD0015
51	20	18.3	11	2	PA0028
52	20	18.3	11	2	PH1375
53	20	18.3	11	2	PH1376
54	20	18.3	12	1	LFECPB
55	20	18.3	14	2	S48685
56	20	18.3	15	2	B56046
57	20	18.3	15	2	PH1610
58	20	18.3	18	2	PL0025
59	20	18.3	19	2	S29167
60	20	18.3	19	2	PH1352
61	20	18.3	19	2	D49404
62	20	18.3	19	2	PQ0409
63	20	18.3	20	2	PX0042
64	20	18.3	20	2	S68028
65	20	18.3	20	2	B38382
66	20	18.3	21	2	S58431
67	19.5	17.9	14	2	A58963
68	19.5	17.9	19	2	C32735
69	19.5	17.9	19	2	B32735
70	19.5	17.9	19	2	A34233
71	19.5	17.4	9	2	S55696
72	19	17.4	10	2	S77980
73	19	17.4	11	2	A26930
74	19	17.4	13	2	S15755
75	19	17.4	13	2	PT0290
76	19	17.4	14	2	A40207
77	19	17.4	14	2	G61308
78	19	17.4	15	2	PA0024
79	19	17.4	15	2	PC1317
80	19	17.4	15	2	PS0221
81	19	17.4	15	2	PH1619
82	19	17.4	15	4	I38336
83	19	17.4	17	2	A61334
84	19	17.4	17	2	I57941
85	19	17.4	17	2	B25348
86	19	17.4	18	2	S63487
87	19	17.4	18	2	A60118
88	19	17.4	19	2	A31252
89	19	17.4	19	2	C39305
90	19	17.4	20	2	S03335
91	19	17.4	20	2	S66222
92	19	17.4	20	2	C34917
93	19	17.4	20	2	A85659
94	19	17.4	21	2	PC2214
95	19	17.4	21	2	D38837
96	19	17.4	21	2	B41299
97	18.5	17.0	15	2	B41668
98	18.5	17.0	16	2	S30384
99	18.5	17.0	20	2	PQ0537
100	18	16.5	9	2	S26508

calmodulin, vasocac
GTP-binding protei
entactin/nidogen -
chondroitin sulfat
glandular kallikre
interferon alpha r
cystatin Cl-4a - m
pimeleoyl-CoA synth
T-cell receptor be
lombiricene kinase
T-cell receptor be
hypothetical prote
photosystem I 5.6K
gluten - wheat
photosystem II chl
fimbrial antigen C
intracystalline c
intracystalline c
pyrithocorcin - Py
insertion element
actin-binding prot
protein QA300042 -
T antigen variant
T antigen variant
pyrE leader peptid
extension protein
urinary tract ston
Ig H chain V-D-J r
T-cell surface gly
guinaldine oxidore
Ig heavy chain DJ
T-cell receptor be
RNA-directed RNA p
venomabin B (EC 3.4
iodothronine 5'-mo
15K protein B - ra
phosphatidylinosit
alpha-conotoxin Cn
thyroglobulin - pi
thyroglobulin - sh
trehalase inhibito
phosphoenolpyruvat
cytochrome-c oxid
emg leader peptid
actin 7 - soybean
Ig heavy chain CRD
cell surface glyco
hemocyanin chain 3
protein QA300050 -
large granule L4' c
gastrin-releasing
Ig H chain V-D-J r
hypothetical TEL/M
trypsin (EC 3.4.21
beta 3 -adrenergic
glycogen(starch) s
fibrinogenolytic p
22K protein - Lyme
metallothionein I
neurotoxin Tx3 - s
photosystem II pho
defensin AMP2 - Da
catechol 1,2-dioxy
hypothetical prote
fibrinogenolytic p
T-cell receptor be
T-cell receptor al
hypothetical prote
hypothetical prote
arylhydroxamic aci
collagen alpha 2(V)

ALIGNMENTS

RESULT 1
A:Accession: A60929
C:Species: Hyphomicrobium sp.
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C:Accession: A60929
R:Kohler-Staub, D.; Hartmann, S.; Gaelli, R.; Suter, F.; Leisinger, T.
J. Gen. Microbiol. 132, 2837-2843, 1986
A:Title: Evidence for identical dichloromethane dehalogenases in different methylotrophic
A:Reference number: A60929
A:Accession: A60929
A:Molecule type: Protein
A:Residues: 1-15 <KOH>
A:Cross-references: UNIPROT:Q7M134; UNIPARC:UPI000017A6F8
C:Keywords: carbon-halide lyase

Query Match
Best Local Similarity 34.9%; Score 38; DB 2; Length 15;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 PHPTNIH 9
|:|||||
DB 3 PHPTNIH 9

RESULT 2
B60929
dichloromethane dehalogenase (EC 4.5.1.3) - Pseudomonas sp. (fragment)
C:Species: Pseudomonas sp.
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C:Accession: B60929
R:Kohler-Staub, D.; Hartmann, S.; Gaelli, R.; Suter, F.; Leisinger, T.
J. Gen. Microbiol. 132, 2837-2843, 1986
A:Title: Evidence for identical dichloromethane dehalogenases in different methylotrophic
A:Reference number: A60929
A:Contents: DSM 1565
A:Accession: B60929
A:Molecule type: Protein
A:Residues: 1-15 <KOH>
A:Cross-references: UNIPROT:Q7M126; UNIPARC:UPI000017A6F8
C:Keywords: carbon-halide lyase

Query Match
Best Local Similarity 34.9%; Score 38; DB 2; Length 15;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 PHPTNIH 9
|:|||||
DB 3 PHPTNIH 9

RESULT 3
S42587
celF protein - Escherichia coli (fragment)
C:Species: Escherichia coli
C:Date: 25-Dec-1994 #sequence_revision 10-Nov-1995 #text_change 10-Nov-1995
C:Accession: S42587
R:Guzzo, A.; Dubow, M. S.
Mol. Gen. Genet. 242, 455-460, 1994
A:Title: A luxX transcripional fusion to the cryptic celF gene of Escherichia coli die
A:Reference number: S42587; MUID:94166755; PMID:8121401
A:Accession: S42587
A:Molecule type: DNA
A:Residues: 1-11 <GUZ>
A:Cross-references: UNIPARC:UPI000017AA33
C:Genetics: celF
A:Gene: celF

Query Match
Best Local Similarity 24.8%; Score 27; DB 2; Length 11;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 PHPTN 7
|:|||||
DB 7 PHPTN 11

RESULT 4
H64711
hypothetical protein HP1536 - Helicobacter pylori (strain 26695)
C:Species: Helicobacter pylori
C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C:Accession: H64711
R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Wattey, L.
Nature 388, 539-547, 1997
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A:Reference number: A64520; MUID:97394467; PMID:9252185
A:Accession: H64711
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-18 <TOM>
A:Cross-references: UNIPROT:O26062; UNIPARC:UPI00000C07C3; GB:A600651; GB:A6000511; NID

Query Match
Best Local Similarity 24.8%; Score 27; DB 2; Length 18;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 HPTNIHXYL 12
|:|||||
DB 10 HPSRNPXYL 18

RESULT 5
S65454
aspergillopepsin I (EC 3.4.23.18) - Aspergillus niger (fragments)
N:Alternate names: aspergillopepsinogen I
C:Species: Aspergillus niger
C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C:Accession: S65454
R:Imoue, H.; Hayaishi, T.; Huang, X.P.; Lu, J.F.; Athauda, S.B.P.; Kong, K.H.; Yamagata, I.
Eur. J. Biochem. 237, 719-725, 1996
A:Title: Heterologous expression and site-directed mutagenesis studies on the activation
A:Reference number: S65454; MUID:96235238; PMID:8647118
A:Accession: S65454
A:Molecule type: Protein
A:Residues: 1-5;6-10;11-18 <INO>
A:Cross-references: UNIPARC:UPI000017B3BC; UNIPARC:UPI000017B3BD; UNIPARC:UPI000017B3BE
A:Experimental source: strain var. macrosporus
C:Keywords: aspartic proteinase; hydrolase

Query Match
Best Local Similarity 23.9%; Score 26; DB 2; Length 18;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 PHPTNIHXY 11
|:|||||
DB 2 PAPTSLAXF 10

RESULT 6
S55307
glutathione transferase 3-3 - rat (fragments)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 07-May-1999
C:Accession: S55307
R:Cooke, R.J.; Bjornestedt, R.; Douglas, K.T.; McKie, J.H.; King, M.D.; Coles, B.; Kett
Biochem. J. 302, 383-390, 1994
A:Title: Photoaffinity labelling of the active site of the rat glutathione transferases
A:Reference number: S55307; MUID:9437965; PMID:8092989
A:Accession: S55307

A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-16 <COO>
A:Cross-references: UNIPARC:UPI000017C91E

Query Match 23.4% Score 25.5; DB 2; Length 16;
Best Local Similarity 42.9%; Pred. No. 1.1e+03;
Matches 6; Conservative 2; Mismatches 3; Indels 3; Gaps 1;

RESULT 7

P00548
capsid protein VP26 - human herpesvirus 1 (fragment)

C:Species: human herpesvirus 1

C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004

C:Accession: P00548

R:Davidson, M.D.; Rixon, F.J.; Davison, A.J.

J. Gen. Virol. 73, 2709-2713, 1992

A:Title: Identification of genes encoding two capsid proteins (VP24 and VP26) of herpes

A:Reference number: P00544; MUID:93019027; PMID:1328483

A:Accession: P00548

A:Molecule type: protein

A:Residues: 1-19 <DAV>

A:Cross-references: UNIPROT:Q7LZW5; UNIPARC:UPI000017A7C9

A:Experimental source: strain 17

C:Genetics:

A:Gene: UL35

C:Keywords: capsid protein

Query Match 22.9% Score 25; DB 2; Length 19;
Best Local Similarity 80.0%; Pred. No. 1.6e+03;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DHPH 5
DB 11 DHPH 15

RESULT 8

D84716

hypothetical protein At2g31090 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C:Accession: D84716

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Mofeit, K.S.; Cronin, L.A.; Shen, M.; Vanden, S.E.; Unayam, L.; Tallon, L.;

Neube, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: D84716

A:Molecule type: DNA

A:Status: preliminary

A:Residues: 1-20 <STO>

A:Cross-references: UNIPROT:O82275; UNIPARC:UPI000017A6CB; GB:AE002093; NID:g3746066; PI

C:Genetics:

A:Gene: At2g31090

A:Map position: 2

Query Match 22.9% Score 25; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 1.7e+03;

Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 12 LVCSVNG 19
DB 7 LVCDCTSG 14

RESULT 9

A60108

exotoxin A - Streptococcus pyogenes (strain C203.S) (fragment)

N:Alternate names: biastogen A; scarlet fever toxin

C:Species: Streptococcus pyogenes

C:Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 31-Dec-2004

C:Accession: A60108

R:Schlivert, P.M.; Gray, E.D.

Infect. Immun. 57, 1865-1867, 1989

A:Title: Group A streptococcal pyrogenic exotoxin (scarlet fever toxin) type A and blas

A:Reference number: A60108; MUID:89254013; PMID:2498210

A:Accession: A60108

A:Molecule type: protein

A:Residues: 1-9 <SCH>

A:Cross-references: UNIPROT:Q54779; UNIPROT:P97163; UNIPROT:Q9R931; UNIPROT:Q57453; UNI

C:Superfamily: enterotoxin B

C:Keywords: exotoxin

Query Match 22.0% Score 24; DB 2; Length 9;
Best Local Similarity 42.9%; Pred. No. 2.8e+05;

Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 PPHPTNH 9
DB 3 PPHSQLH 9

RESULT 10

S10920
venom protein HR-3 - oriental hornet (fragment)

C:Species: Vespa orientalis (oriental hornet)

C:Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 09-Jul-2004

C:Accession: S10920

R:Tutichbaev, M.U.; Akhmedova, N.U.; Kazakov, I.; Korneev, A.S.; Gagel'gans, A.I.

Biochemistry (N.Y.) 53, 183-190, 1988

A:Title: Low-molecular-weight peptides of venom of the giant hornet Vespa orientalis. S

A:Reference number: S06445

A:Accession: S10920

A:Molecule type: protein

A:Residues: 1-9 <TUI>

A:Cross-references: UNIPROT:Q7M471; UNIPARC:UPI000017BF07

C:Keywords: venom

Query Match 22.0% Score 24; DB 2; Length 9;
Best Local Similarity 42.9%; Pred. No. 2.8e+05;

Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 7 NHHKYL 13
DB 2 SVHFFLV 8

RESULT 11

S15778
insulin chain B - bovine (fragments)

C:Species: Bos primigenius indicus x Bos primigenius taurus (cattle)

C:Date: 19-Mar-1997 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999

C:Accession: S15778; S15779

R:Bergerman, T.; Agerberth, B.; Joernvall, H.

FEBS Lett. 283, 100-103, 1991

A:Title: Direct analysis of peptides and amino acids from capillary electrophoresis.

A:Reference number: S15778; MUID:91243852; PMID:2037061

A:Accession: S15778

A:Molecule type: protein

A:Status: preliminary

A:Residues: 1-8 <FEB1>

A:Cross-references: UNIPARC:UPI000015BC0B

A:Accession: S15779

A:Molecule type: protein

A:Status: preliminary

A:Residues: 9-17 <FEB2>

A:Cross-references: UNIPARC:UPI000015BC0B

C:Superfamily: insulin

C:Keywords: hormone; pancreas

Query Match 22.0%; Score 24; DB 2; Length 17;
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-19 <CHA>
A:Cross-references: UNIPROT:Q9PSW6; UNIPARC:UPI00000FB20E; GB:X02258; NID:9211084; PIDN:
C:Superfamily: Actin

OY 11 YLVC 14
|||
Db 3 YLVC 6

RESULT 12
S29264

ovoheymerythrin - duck leech (fragment)
N:Alternate names: 14k yolk protein
C:Species: Theromyzon tessulatatum (duck leech)
C>Date: 19-Mar-1997 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: S29264
R:Beert, J.L.; Birtel, M.; Sautiere, P.; Malecha, J.
Eur. J. Biochem. 209, 563-569, 1992
A:Title: Ovoheymerythrin, a major 14-kDa yolk protein distinct from vitellogenin in leech
A:Reference number: S29264; MUID:93049299; PMID:1425663
A:Accession: S29264
A:Molecule type: protein
A:Residues: 1-18 <BAE>
A:Cross-references: UNIPROT:P80155; UNIPARC:UPI000012C58F; PIDN:AAB23969.1; PID:G258980
C:Superfamily: hemerythrin
C:Keywords: egg yolk; oxygen carrier

Query Match 22.0%; Score 24; DB 2; Length 18;
Best Local Similarity 80.0%; Pred. No. 2.1e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 DHPH 5
|||
Db 2 DHPH 6

RESULT 13
PN0175

glutathione transferase (EC 2.5.1.18) 1 - Arabidopsis thaliana (fragment)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 22-Dec-1995 #sequence_revision 08-Feb-1996 #text_change 23-Mar-2001
C:Accession: PN0175
R:Tangita, A.; Kamo, M.; Kawakami, M.; Ohki, Y.
submitted to JIPID, December 1995
A:Description: Two dimensional electrophoresis of plant proteins and standardization of
A:Reference number: PN0173
A:Accession: PN0175
A:Molecule type: protein
A:Residues: 1-18 <TSU>
A:Cross-references: UNIPARC:UPI000017AF59
A:Experimental source: leaf
C:Keywords: transferase

Query Match 22.0%; Score 24; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 2.1e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 DHPHNT 8
|||
Db 5 DHPHNT 12

RESULT 14
I50153

alpha-actin - chicken (fragment)
C:Species: Gallus gallus (chicken)
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 05-Oct-2004
C:Accession: I50153
R:Chang, K.
Mol. Cell. Biol. 4, 2498-2508, 1984
A:Title: Isolation and characterization of six different chicken actin genes.
A:Reference number: I50153; MUID:85085956; PMID:6513927

A:Accession: I50153
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-19 <CHA>
A:Cross-references: UNIPROT:Q9PSW6; UNIPARC:UPI00000FB20E; GB:X02258; NID:9211084; PIDN:
C:Superfamily: Actin

Query Match 22.0%; Score 24; DB 2; Length 19;
Best Local Similarity 50.0%; Pred. No. 2.3e+03;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 12 LVCEVNG 19
|||
Db 10 LVCEVNG 17

RESULT 15
A45655

Crotalus atrox serine proteinase (EC 3.4.21.-) - western diamondback rattlesnake (fragment)
N:Alternate names: alpha-fibrinogenase; thrombin-like proteinase
C:Species: Crotalus atrox (western diamondback rattlesnake)
C>Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
C:Accession: A45655
R:Chou, S.H.; Hung, C.C.; Lin, C.W.
Biochem. Int. 26, 105-112, 1992
A:Title: Isolation of a crotalase-like protease with alpha-fibrinogenase activity from ti
A:Reference number: A45655; MUID:92313365; PMID:1616467
A:Accession: A45655
A:Molecule type: protein
A:Residues: 1-20 <CHI>
A:Cross-references: UNIPROT:Q9PS55; UNIPARC:UPI00000FB75C
A:Experimental source: venom
A:Note: sequence extracted from NCBI backbone (NCBI:P107297)
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; serine proteinase; venom

Query Match 22.0%; Score 24; DB 2; Length 20;
Best Local Similarity 57.1%; Pred. No. 2.4e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 7 NIKKYL 13
|||
Db 10 NIKKYL 16

RESULT 16
S38736

lipid transfer protein a1 - Arabidopsis thaliana (fragment)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 19-May-1994 #sequence_revision 19-Jan-1996 #text_change 19-Jan-1996
C:Accession: S38736
R:Segura, A.; Moreno, M.; Garcia-Olmedo, F.
FEBS Lett. 332, 243-246, 1993
A:Title: Purification and antipathogenic activity of lipid transfer proteins (LTPs) from
A:Reference number: S38736; MUID:94009709; PMID:8405465
A:Accession: S38736
A:Molecule type: protein
A:Residues: 1-13 <SEG>
A:Cross-references: UNIPARC:UPI000017AFCF

Query Match 21.1%; Score 23; DB 2; Length 13;
Best Local Similarity 71.4%; Pred. No. 2.2e+03;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 12 LVCESVN 18
|||
Db 2 LVCESVN 8

RESULT 17
PH1604

Ig H chain V-D-J region (wild-type clone 327) - mouse (fragment)
C:Species: Mus musculus (house mouse)

C>Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C/Accession: P11604
R/Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A/Title: Molecular characterization of transgene-induced immunodeficiency in B-lees mice
A/Reference number: P11580; MUID:93301609; PMID:8315387
C/Accession: P11604
A/Molecule type: DNA
A/Residues: 1-16 <LEV>
A/Cross-references: UNIPARC:UPI00001766C0
A/Experimental source: bone marrow pre-B lymphocyte
C/Keywords: immunoglobulin

Query Match 21.1%; Score 23; DB 2; Length 16;
Best Local Similarity 44.4%; Pred. No. 2.7e+03;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 PPTNIHKY 11
DB 4 PHRLHLHY 12

RESULT 18
S15754
actin 6 - soybean (fragment)
C/Species: Glycine max (soybean)
C/Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 05-Oct-2004
C/Accession: S15754; S08049
R/Pearson, L.; Meagher, R.B.
Plant Mol. Biol. 14, 513-526, 1990
A/Title: Diverse soybean actin transcripts contain a large intron in the 5' untranslated
A/Reference number: S15754; MUID:91346640; PMID:2102831
A/Accession: S15754
A/Molecule type: DNA
A/Residues: 1-17 <PEA>
A/Cross-references: UNIPROT:P15986; UNIPARC:UPI0000125427; EMBL:X17119; NID:g18525; PIDN
C/Superfamily: Actin
C/Keywords: cytoskeleton

Query Match 21.1%; Score 23; DB 2; Length 17;
Best Local Similarity 50.0%; Pred. No. 2.9e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 12 LVCSNVNG 19
DB 10 LVCDNGTG 17

RESULT 19
S63503
83K proteoln - Eubacterium acidaminophilum (fragment)
C/Species: Eubacterium acidaminophilum
C/Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C/Accession: S63503
R/Meyer, M.; Granderath, K.; Andreessen, J.R.
Eur. J. Biochem. 234, 184-191, 1995
A/Title: Purification and characterization of protein P(B) of betaine reductase and its
phylum.
A/Reference number: S63502; MUID:96096737; PMID:8529639
A/Accession: S63503
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-17 <MEY>
A/Cross-references: UNIPARC:UPI000017AD3D

Query Match 21.1%; Score 23; DB 2; Length 17;
Best Local Similarity 50.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 7 NIHKYL 12
DB 2 DLHKFL 7

RESULT 20
A58589
alpha-conotoxin EI - cone shell (Conus ermineus)
C/Species: Conus ermineus (ermine cone)
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C/Accession: A58589
R/Martinez, J.S.; Olivera, B.M.; Gray, W.R.; Craig, A.G.; Grebe, D.R.; Abramson, S.N.;
Biochemistry 34, 14519-14526, 1995
A/Title: alpha-Conotoxin EI, a new nicotinic acetylcholine receptor antagonist with nov
A/Reference number: A58589; MUID:96062516; PMID:7578057
A/Accession: A58589
A/Molecule type: protein
A/Residues: 1-18 <MAR>
A/Cross-references: UNIPROT:P50982; UNIPARC:UPI00001287C0
A/Note: sequence confirmed by chemical synthesis
C/Comment: This alpha-conotoxin, as an acetylcholine receptor inhibitor, is a postsynaf
C/Superfamily: alpha-conotoxin
C/Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; hydroxyproline; pc
F/3/Modified site: 4-hydroxyproline (Pro) #status experimental
F/4-10-5-18/Disulfide bonds: #status experimental
F/18/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 20.6%; Score 22.5; DB 1; Length 18;
Best Local Similarity 41.7%; Pred. No. 3.7e+03;
Matches 5; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

QY 4 HPT-NIHKYLVC 14
DB 7 HPTCMGNSPQIC 18

RESULT 21
B59272
peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase (EC 3.5.1.52) A, small chain
N/Alternate names: peptide N-glycosidase
C/Species: Prunus dulcis var. sativa (sweet almond)
C/Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C/Accession: B59272
R/Altman, F.; Paschinger, K.; Dalik, T.; Vorauer, K.
Eur. J. Biochem. 252, 118-123, 1998
A/Title: Characterisation of peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase
A/Reference number: A59272; MUID:98181894; PMID:9523720
A/Accession: B59272
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-10 <ALT>
A/Cross-references: UNIPROT:P81898; UNIPARC:UPI00000ABBC4
C/Keywords: hydrolase

Query Match 20.2%; Score 22; DB 2; Length 10;
Best Local Similarity 42.9%; Pred. No. 2.4e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 PTNIHKY 11
DB 2 PTPLDHF 8

RESULT 22
B37196
bradykinin-potentiating peptide 2 - island jararaca
C/Species: Bothrops insularis (island jararaca)
C/Date: 14-Feb-1992 #sequence_revision 01-Dec-1992 #text_change 09-Jul-2004
C/Accession: B37196
R/Cintre, A.C.O.; Vieira, C.A.; Giglio, J.R.
J. Protein Chem. 9, 221-227, 1990
A/Title: Primary structure and biological activity of bradykinin potentiating peptides
A/Reference number: A37196; MUID:90351557; PMID:2386615
A/Accession: B37196
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-10 <CIN>

A:Cross-references: UNIPROT:P30422; UNIPARC:UPI0000126A8F
C:Keywords: pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 20.2%; Score 22; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PHP 5
|||
Db 4 PHP 6

RESULT 23

kassinin-like peptide K-I - frog (Pseudophryne guentheri)
C:Species: Pseudophryne guentheri
C:Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 16-Aug-2004
C:Accession: B60409
R:Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melchior
Peptides 11, 299-304, 1990
A:Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Australia
A:Reference number: A60409; MUID:90287814; PMID:2356157
A:Accession: B60409
A:Molecule type: protein
A:Residues: 1-11 <SIM>
A:Cross-references: UNIPROT:P42986; UNIPARC:UPI0000136FCD
A>Note: this peptide was also found in a deamidated form
C:Keywords: amidated carboxyl end; pyroglutamic acid (Gln) #status experimental
F:1/Modified site: pyrrolidone carboxylic acid (Gln) (partial) #status experimental
F:1/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 20.2%; Score 22; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PHP 5
|||
Db 2 PHP 4

RESULT 24

D60409
kassinin-like peptide K-III - frog (Pseudophryne guentheri)
C:Species: Pseudophryne guentheri
C:Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 16-Aug-2004
C:Accession: D60409
R:Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melchior
Peptides 11, 299-304, 1990
A:Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Australia
A:Reference number: A60409; MUID:90287814; PMID:2356157
A:Accession: D60409
A:Molecule type: protein
A:Residues: 1-11 <SIM>
A:Cross-references: UNIPROT:P42988; UNIPARC:UPI0000136FD7
C:Keywords: amidated carboxyl end; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:1/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 20.2%; Score 22; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PHP 5
|||
Db 2 PHP 4

RESULT 25

B47415
mannose-1-phosphate guanylyltransferase (EC 2.7.7.13) 43K alpha chain - pig (fragment)
N:Alternate names: GDP-mannose pyrophosphorylase 43K alpha chain
C:Species: Sus scrofa domestica (domestic pig)

C:Date: 25-Feb-1994 #sequence_revision 12-Aug-1996 #text_change 12-Aug-1996
C:Accession: B47415
R:Sumiyo, T.; Drake, R.R.; York, J.L.; Elbein, A.D.
J. Biol. Chem. 268, 17943-17950, 1993
A:Title: GDP-mannose pyrophosphorylase. Purification to homogeneity, properties, and uti
A:Reference number: A47415; MUID:93352609; PMID:7688733
A:Accession: B47415
A:Molecule type: protein
A:Residues: 1-13 <SZU>

A:Cross-references: UNIPARC:UPI000017C470
A:Experimental source: liver
C:Complex: The enzyme appears to be a heterodimer of alpha and beta chains.
C:Function:

A:Description: generates GDP-mannose and pyrophosphate from mannose-1-phosphate and GTP
A>Note: also catalyzes synthesis of GDP-glucose from glucose-1-phosphate (EC 2.7.7.34 ac
C:Keywords: blocked amino end; nucleotidyltransferase

Query Match 20.2%; Score 22; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PHP 5
|||
Db 8 PHP 10

Search completed: January 26, 2006, 08:05:05
Job time : 11.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 26, 2006, 07:47:56 ; Search time 56.5086 Seconds
(without alignments)
237.221 Million cell updates/sec

Title: US-09-662-293-11
Perfect score: 109
Sequence: 1 DIHPHTINKLVCESYNG 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 70528306 residues

Total number of hits satisfying chosen parameters: 15779

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Uniprot_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	34.9	15	2	Q7M126_PSESP
2	38	34.9	15	2	Q7M134_PRRHIZ
3	37	33.9	13	2	Q00789_9DELTA
4	37	33.9	13	2	Q76R60_9DELTA
5	37	33.9	21	2	Q82439_9DELTA
6	33	30.3	19	2	Q5C123_SCHUA
7	32	29.4	13	2	Q7S901_NEUCR
8	30	27.5	10	2	Q4X4H2_PLACH
9	30	27.5	18	2	Q16244_HUMAN
10	29	26.6	6	1	TMOF_SARBU
11	29	26.6	19	2	Q5EX89_PLAMI
12	29	26.6	21	2	Q4YCP3_PLABE
13	28	25.7	19	2	Q5EX77_PLAMI
14	28	25.7	19	2	Q5EX78_PLAMI
15	28	25.7	19	2	Q5EX88_PLAMI
16	28	25.7	19	2	Q5EX90_PLAMI
17	28	25.7	19	2	Q5EX91_PLAMI
18	28	25.7	19	2	Q5EX92_PLAMI
19	28	25.7	19	2	Q5EX94_PLAMI
20	28	25.7	19	2	Q5EX95_PLAMI
21	28	25.7	19	2	Q5EX96_PLAMI
22	28	25.7	19	2	Q5EX97_PLAMI
23	28	25.7	19	2	Q5EX98_PLAMI
24	28	25.7	19	2	Q5EX99_PLAMI
25	28	25.7	19	2	Q5EXA2_PLAMI
26	28	25.7	19	2	Q5EXA3_PLAMI
27	28	25.7	19	2	Q5EXA4_PLAMI
28	28	25.7	19	2	Q5EXA5_PLAMI
29	28	25.7	19	2	Q5EXA6_PLAMI
30	28	25.7	19	2	Q5EXA7_PLAMI
31	28	25.7	19	2	Q5EXA7_PLAMI

32	28	25.7	19	2	Q5EXA8_PLAMI	O5exa8 streptocarp
33	28	25.7	19	2	Q5EXA9_PLAMI	O5exa9 saintpaulia
34	28	25.7	19	2	Q5EXB0_PLAMI	O5exb0 saintpaulia
35	28	25.7	19	2	Q5EXB1_PLAMI	O5exb1 saintpaulia
36	28	25.7	20	2	Q4YMN1_PLABE	Q4ymn1 plasmodium
37	28	25.7	21	2	Q712N7_HUMAN	Q712n7 homo sapien
38	27	24.8	18	2	Q26062_HELPY	Q26062 heliobacte
39	27	24.8	19	2	Q4XJ38_PLACH	Q4xj38 plasmodium
40	27	24.8	19	2	Q4YK87_PLABE	Q4yk87 plasmodium
41	27	24.8	20	2	Q7RR59_PLAYO	Q7rr59 plasmodium
42	26	23.9	12	2	Q9UMR0_HUMAN	Q9umr0 homo sapien
43	26	23.9	17	2	Q410W0_BACTK	Q410w0 bacillus th
44	26	23.9	19	2	Q9XN07_BOOMI	Q9xn07 boophilus m
45	26	23.9	19	2	Q5EX86_PLAMI	Q5ex86 streptocarp
46	26	23.9	20	1	PHYI4_PHYOR	PHYI4 phyliomedus
47	26	23.9	20	2	Q7RS12_PLAYO	Q7rs12 plasmodium
48	26	23.9	20	2	Q5K4V0_BOVIN	Q5k4v0 bos taurus
49	26	23.9	20	2	Q90X94_CHICK	Q90x94 gallus gall
50	25	22.9	11	2	Q8MM58_9NEOP	Q8mm58 heliconius
51	25	22.9	12	2	Q8MUN4_9NEOP	Q8mun4 heliconius
52	25	22.9	12	2	Q8MUN9_9NEOP	Q8mun9 heliconius
53	25	22.9	13	2	Q8MM57_9NEOP	Q8mm57 heliconius
54	25	22.9	14	2	Q8MUN8_9NEOP	Q8mun8 heliconius
55	25	22.9	14	2	Q8MUN0_9NEOP	Q8mun0 heliconius
56	25	22.9	15	2	Q9BZNO_HUMAN	Q9bzn0 homo sapien
57	25	22.9	15	2	Q8MUP2_9NEOP	Q8mup2 heliconius
58	25	22.9	16	2	Q8MM83_9NEOP	Q8mm83 heliconius
59	25	22.9	16	2	Q8MM84_9NEOP	Q8mm84 heliconius
60	25	22.9	16	2	Q8MM85_9NEOP	Q8mm85 heliconius
61	25	22.9	16	2	Q8MUN3_9NEOP	Q8mun3 heliconius
62	25	22.9	16	2	Q8MUN5_9NEOP	Q8mun5 heliconius
63	25	22.9	17	2	Q9TWR4_PLICD	Q9twr4 dictyosteli
64	25	22.9	18	1	PHYI2_PHYRX	PHYI2 phyliomedus
65	25	22.9	18	2	Q6VYB3_9NEOP	Q6vyb3 heliconius
66	25	22.9	18	2	Q6VYD9_9NEOP	Q6vyd9 heliconius
67	25	22.9	18	2	Q6VYE7_9NEOP	Q6vey7 heliconius
68	25	22.9	18	2	Q4YEL0_PLABE	Q4yel0 plasmodium
69	25	22.9	18	2	Q28069_BOVIN	Q28069 bos taurus
70	25	22.9	19	2	Q6VYD8_9NEOP	Q6vyd8 heliconius
71	25	22.9	19	2	Q6VYE1_9NEOP	Q6vey1 heliconius
72	25	22.9	19	2	Q7RG13_PLAYO	Q7rg13 plasmodium
73	25	22.9	19	2	Q7YK42_9FABA	Q7yk42 desmanthus
74	25	22.9	19	2	Q8CJ05_MESAU	Q8cj05 mesocricetu
75	25	22.9	19	2	Q7LZM5_HHVI	Q7lzm5 human herpe
76	25	22.9	20	1	APY3_PLECI	APY3 pleurotus c
77	25	22.9	20	1	APY3_PLECI	P33481 pleurotus c
78	25	22.9	21	2	Q6LD41_HUMAN	Q6ld41 homo sapien
79	25	22.9	21	2	Q6VYA6_9NEOP	Q6vy66 heliconius
80	25	22.9	21	2	Q4YEA9_PLABE	Q4yea9 plasmodium
81	24	22.0	9	2	Q7M471_VESOR	Q7m471 vespa oren
82	24	22.0	15	2	Q9UCU7_HUMAN	Q9ucu7 homo sapien
83	24	22.0	17	2	Q6R9U9_HUMAN	Q6r9u9 homo sapien
84	24	22.0	17	2	Q6R9P0_TRABR	Q6r9p0 crachypithe
85	24	22.0	17	2	Q6R9P1_TRABR	Q6r9p1 crachypithe
86	24	22.0	17	2	Q6R9P2_PYGNE	Q6r9p2 pygathrix n
87	24	22.0	17	2	Q6R9P3_PYGEI	Q6r9p3 pygathrix b
88	24	22.0	17	2	Q6R9P4_MACCU	Q6r9p4 macaca mula
89	24	22.0	17	2	Q6R9Q1_PONYE	Q6r9q1 pongo pygma
90	24	22.0	17	2	Q6R9Q5_9PRIM	Q6r9q5 gorilla gor
91	24	22.0	17	2	Q6R9R4_PANTR	Q6r9r4 pan troglod
92	24	22.0	18	1	HEMT0_THETS	HEMT0 theryomys
93	24	22.0	18	2	Q9ZYV9_9HYME	Q9zyv9 opus kraus
94	24	22.0	18	2	Q4XS69_PLACH	Q4xs69 plasmodium
95	24	22.0	19	2	Q5CS58_SCHISA	Q5cs58 schistosoma
96	24	22.0	19	2	Q9ZYW3_9HYME	Q9zyw3 gnampitodon
97	24	22.0	19	2	Q9ZYX2_9HYME	Q9zyx2 centistes s
98	24	22.0	19	2	Q4Y3P1_PLACH	Q4y3p1 plasmodium
99	24	22.0	19	2	Q6R9P5_PYLIE	Q6r9p5 hylobates 1
100	24	22.0	19	2	Q6R9P6_9PRIM	Q6r9p6 bunodithec

ALIGNMENTS

```

RESULT 1
ID Q7M126_PSESP PRELIMINARY; PRT; 15 AA.
AC Q7M126;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DE 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
OS Pseudomonas sp.
OC Bacteria; Proteobacteria.
NCBI_TaxID=306;
RN [1]
RP PROTEIN SEQUENCE.
RA Kohler-Staub D., Hartmans S., Gaelli R., Suter F., Leisinger T.;
RT "Evidence for identical dichloromethane dehalogenases in different
RL methylobrophic bacteria."
RL J. Gen. Microbiol. 132:2837-2843(1986).
DR PIR; B60929; B60929.
DR GO; GO:0018834; F:dichloromethane dehalogenase activity; IEA.
FT NON_TER 15
SQ SEQUENCE 15 AA; 1667 MW; 05B170EF8B3721D9 CRC64;

Query Match 34.9%; Score 38; DB 2; Length 15;
Best Local Similarity 85.7%; Pred. No. 57;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 PHPTNIH 9
Db 3 PNPTNIH 9

RESULT 2
ID Q7M134_9RHIZ PRELIMINARY; PRT; 15 AA.
AC Q7M134;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DE 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Dichloromethane dehalogenase (EC 4.5.1.3) (Fragment).
OS Hypomicrobium sp.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Hypomicrobiaceae; Hyphomicrobium.
OX NCBI_TaxID=82;
RN [1]
RP PROTEIN SEQUENCE.
RA Kohler-Staub D., Hartmans S., Gaelli R., Suter F., Leisinger T.;
RT "Evidence for identical dichloromethane dehalogenases in different
RL methylobrophic bacteria."
RL J. Gen. Microbiol. 132:2837-2843(1986).
DR PIR; A60929; A60929.
DR GO; GO:0018834; F:dichloromethane dehalogenase activity; IEA.
FT NON_TER 15
SQ SEQUENCE 15 AA; 1667 MW; 05B170EF8B3721D9 CRC64;

Query Match 34.9%; Score 38; DB 2; Length 15;
Best Local Similarity 85.7%; Pred. No. 57;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 PHPTNIH 9
Db 3 PNPTNIH 9

RESULT 3
ID Q00789_9DELA PRELIMINARY; PRT; 13 AA.
AC Q00789;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Gag protein (Fragment).
GN Name=gag;

```

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OS Human T-lymphotropic virus 1.
OC Viruses; Retroid viruses; Retroviridae; Deltaretrovirus.
OX NCBI_TaxID=11908;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=87111460; PubMed=3027244;
RA Hiramatsu K., Nishida J., Naito A., Yoshikawa H.;
RT "Molecular cloning of the closed circular provirus of human T cell
RT leukaemia virus type I: A new open reading frame in the gag-pol
RT region."
RL J. Gen. Virol. 68:213-218(1987).
DR EMBL; D10033; BAA00925.1; -; Genomic_DNA.
FT NON_TER 1
SQ SEQUENCE 13 AA; 1363 MW; 408035320911B443 CRC64;

Query Match 33.9%; Score 37; DB 2; Length 13;
Best Local Similarity 85.7%; Pred. No. 70;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DHPPTN 7
Db 1 DHPPTN 7

RESULT 4
ID Q76R60_9DELA PRELIMINARY; PRT; 13 AA.
AC Q76R60;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Gag protein (Fragment).
OS Human T-lymphotropic virus 1.
OC Viruses; Retroid viruses; Retroviridae; Deltaretrovirus.
OX NCBI_TaxID=11908;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=87111460; PubMed=3027244;
RA Hiramatsu K., Nishida J., Naito A., Yoshikawa H.;
RT "Molecular cloning of the closed circular provirus of human T cell
RT leukaemia virus type I: A new open reading frame in the gag-pol
RT region."
RL J. Gen. Virol. 68:213-218(1987).
DR EMBL; X04800; CAA28492.1; -; Genomic_DNA.
FT NON_TER 1
SQ SEQUENCE 13 AA; 1363 MW; 408035320911B443 CRC64;

Query Match 33.9%; Score 37; DB 2; Length 13;
Best Local Similarity 85.7%; Pred. No. 70;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DHPPTN 7
Db 1 DHPPTN 7

RESULT 5
ID Q82439_9DELA PRELIMINARY; PRT; 21 AA.
AC Q82439;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Gag protein (Fragment).
GN Name=gag;
OS Human T-lymphotropic virus 1.
OC Viruses; Retroid viruses; Retroviridae; Deltaretrovirus.
OX NCBI_TaxID=11908;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=85211032; PubMed=2987530;
RA Ratner L., Josephs S.F., Starcich B., Hahn B.H., Shaw G.M.,
RA Gallo R.C., Wong-Staal F.;

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RT "Nucleotide sequence analysis of a variant human T-cell leukemia virus (HTLV-Ib) provirus with a deletion in pX-I.";

RL J. Virol. 54:781-790(1985).

DR EMBL; M10977; AAA46203.1; -; Genomic DNA.

FT NON_TER 21 21

SO SEQUENCE 21 AA; 2169 MW; 7B0EB0675406840D CRC64;

Query Match 33.9%; Score 37; DB 2; Length 21;

Best Local Similarity 85.7%; Pred. No. 1.2e+02;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DIPPTN 7

DB 9 DIPPTN 15

RESULT 6

OSCI23 SCHJA PRELIMINARY; PRT; 19 AA.

ID OSCI23 SCHJA PRELIMINARY; PRT; 19 AA.

AC OSCI23

DT 10-MAY-2005 (TRENBLREL. 30, Created)

DT 10-MAY-2005 (TRENBLREL. 30, Last sequence update)

DE Hypothetical protein.

OS Schistosoma japonicum (Blood fluke).

OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;

OC Schistosomacidae; Schistosomatidae; Schistosoma.

OX NCBI_TaxID=6182;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Han Z.;

RU Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY610763; AAX26652.1; -; mRNA.

KW Hypothetical protein.

SO SEQUENCE 19 AA; 2259 MW; FE2492F8464550 CRC64;

QY 5 PTNIRKLV 13

DB 8 PMKIRNVLV 16

Query Match 30.3%; Score 33; DB 2; Length 19;

Best Local Similarity 66.7%; Pred. No. 4.8e+02;

Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

RESULT 7

Q7S901 NEUCR PRELIMINARY; PRT; 13 AA.

ID Q7S901 NEUCR PRELIMINARY; PRT; 13 AA.

AC Q7S901

DT 01-MAR-2004 (TRENBLREL. 26, Created)

DT 01-MAR-2004 (TRENBLREL. 26, Last sequence update)

DE Predicted protein.

OS Name=NCU05297.1;

OS Neurospora crassa.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.

OX NCBI_TaxID=5141;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=OR74A.

RA Galagan J.E., Galvo S.E., Borkovich K.A., Selker E.U., Read N.D.,

RA Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell S., Renman B.,

RA Elkin T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,

RA Qui D., Iankilev P., Pedersen D., Nelson M., Washburne M.,

RA Seitzemerkoff C.P., Kinsey J.A., Braun E.L., Zeller A., Schulte U.,

RA Koche G.O., Jedd G., Mewes W., Scabon C., Marotte E., Greenberg D.,

RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,

RA Kamal M., Kamyshelev M., Maucell E., Bielke C., Rudd S., Fishman D.,

RA Kryzofova S., Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S.,

RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmani S.A.,

RA Desouza C.C., Glase L., Orbach M.J., Berglund J., Voelker R.,

RA Varden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,

RA Natvig D.O., Alex L.A., Mannheim G., Ebbola D.J., Preitag M.,

RA Paulsen I., Sachs M.S., Lander E.S., Nisbaum C., Birren B.,

RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";

RL Nature 0:0-0(2003).

CC -1- CAUTION: The sequence shown here is derived from an

CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is

CC preliminary data.

DR EMBL; AABX01000220; EAA32832.1; -; Genomic DNA.

SO SEQUENCE 13 AA; 1543 MW; 09180701868D404B CRC64;

Query Match 29.4%; Score 32; DB 2; Length 13;

Best Local Similarity 36.4%; Pred. No. 4.6e+02;

Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 8 IHKYLCESVN 18

DB 3 VHTYINCTALN 13

RESULT 8

Q4X4H2 PLACH PRELIMINARY; PRT; 10 AA.

ID Q4X4H2 PLACH PRELIMINARY; PRT; 10 AA.

AC Q4X4H2

DT 13-SEP-2005 (TRENBLREL. 31, Created)

DT 13-SEP-2005 (TRENBLREL. 31, Last sequence update)

DE Hypothetical protein (fragment).

GN ORFNames=PC400586.00.0;

OS Plasmodium chabaudi.

OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.

OX NCBI_TaxID=5825;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,

RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,

RA James K., Rutherford K., Harris B., Harris D., Churcho C.,

RA Quail M.A., Ormond D., Doggett J., Truman H.E., Mendoza J.,

RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,

RA Jansz C.G., Barrett B., Turner C.M.R., Waters A.P., Sinden R.S.,

RT "A comprehensive survey of the Plasmodium life cycle by genomic,

RT transcriptomic, and proteomic analyses.";

RL Science 307:82-86(2005).

CC -1- CAUTION: The sequence shown here is derived from an

CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is

CC preliminary data.

DR EMBL; CAAD01010050; CAH88321.1; -; Genomic DNA.

KW Hypothetical protein.

FT NON_TER 10 10

SO SEQUENCE 10 AA; 1230 MW; 4C729FD7205059C3 CRC64;

Query Match 27.5%; Score 30; DB 2; Length 10;

Best Local Similarity 30.0%; Pred. No. 7.3e+02;

Matches 3; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 8 IHKYLCESV 17

DB 1 MFKRILQST 10

RESULT 9

Q16244 HUMAN PRELIMINARY; PRT; 18 AA.

ID Q16244 HUMAN PRELIMINARY; PRT; 18 AA.

AC Q16244

DT 01-NOV-1996 (TRENBLREL. 01, Created)

DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)

DE SRS protein (fragment).

GN Name=STS;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homindae;

OC Homo.

OX NCBI_TaxID=9606;

```
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95038775; PubMed=7951263;
RA Yen P.H., Ferrero G.B., Chinault A.C., Mohandas T., Ballbio A.;
RT "Characterization of the deletion breakpoints in a patient with
  steroid sulfatase deficiency."
RL Hum. Mutat. 4:76-78(1994).
DR EMBL: S74383; AAD14153.1; -; Genomic_DNA.
FT NON_TER
SQ SEQUENCE 18 AA; 1958 MW; 3B3072711330CCRA CRC64;

Query Match
Best Local Similarity 27.5%; Score 30; DB 2; Length 18;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 3 PHPNTHKYLVC 14
DB 7 PCEVNSHSYOLC 18

RESULT 10
TMOF_SARBU STANDARD; PRT; 6 AA.
AC P41495;
DT 01-NOV-1995 (Rel. 32; Created)
DT 01-NOV-1995 (Rel. 32; Last sequence update)
DT 05-JUL-2004 (Rel. 44; Last annotation update)
DE Trypsin-modulating oostatic factor (TMOF).
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Sarcophagidae; Sarcophaga; Neobellieria.
OX NCBI_TaxID=7385;
RN [1]
RP PROTEIN SEQUENCE, AND SYNTHESIS.
RX TISUE=Ovary;
RX MEDLINE=94211930; PubMed=8159807; DOI=10.1016/0167-0115(94)90192-9;
RA Bylemans D., Borovsky D., Hunt D.F., Shabanowitz J., Grauwels L.,
RA de Loof A.;
RT "Sequencing and characterization of trypsin modulating oostatic factor
  (TMOF) from the ovaries of the grey fleshfly, Neobellieria
  (Sarcophaga) bullata."
RL Regul. Pept. 50:61-72(1994).
CC -!- FUNCTION: Has an oostatic activity. Inhibits trypsin biosynthesis
  in the midgut which indirectly reduces the vitellogenin
  concentration in the hemolymph resulting in inhibition of oocyte
  development.
CC -!- DEVELOPMENTAL STAGE: Synthesized and released from follicular
  epithelium after a blood meal.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
  between the Swiss Institute of Bioinformatics and the EMBL outstation -
  the European Bioinformatics Institute. There are no restrictions on its
  use as long as its content is in no way modified and this statement is not
  removed.
CC -----
CC Direct protein sequencing; Hormone.
KW SEQUENCE 6 AA; 695 MW; 61E72451B764200 CRC64;

Query Match
Best Local Similarity 26.6%; Score 29; DB 1; Length 6;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 HPTNTH 9
DB 1 NPTNTH 6

RESULT 11
O5EX89_9LAMI PRELIMINARY; PRT; 19 AA.
AC O5EX89;
DT 10-MAY-2005 (TREMBLrel. 30; Created)
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DT 10-MAY-2005 (TREMBLrel. 30; Last sequence update)
DT 10-MAY-2005 (TREMBLrel. 30; Last annotation update)
DE STM2 protein (Fragment).
OS Streptocarpus venosus.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Lamiales; Gesneriaceae; Cyrtandroidae; Didymocarpeae;
OC Streptocarpus.
OX NCBI_TaxID=301922;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B;
RX PubMed=15659624; DOI=10.1105/lpc.104.028936;
RA Harrison J., Moller M., Langdale J., Cronk Q., Hudson A.;
RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in
  Streptocarpus."
RL Plant Cell 17:430-443(2005).
DR EMBL: AY662115; AAW33769.1; -; Genomic_DNA.
DR InterPro: IPR001356; Homeobox.
DR Prodom: PD000010; Homeobox; 1.
FT NON_TER
SQ SEQUENCE 19 AA; 2057 MW; 1069FC9782AFD64A CRC64;

Query Match
Best Local Similarity 26.6%; Score 29; DB 2; Length 19;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 3 PHPNTHKYLVCES 16
DB 1 PYPSEXOKTALAES 14

RESULT 12
O4YCP3_PLABE PRELIMINARY; PRT; 21 AA.
AC O4YCP3;
DT 13-SEP-2005 (TREMBLrel. 31; Created)
DT 13-SEP-2005 (TREMBLrel. 31; Last sequence update)
DT 13-SEP-2005 (TREMBLrel. 31; Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=PB100163.00.0;
OS Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5821;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandrem M.A., Carnucci D.J., Yates J.R., Kafatos F.C.,
RA Jansz C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
  transcriptomic, and proteomic analyses."
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
  EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
  preliminary data.
CC EMBL: CAAT01006597; CA104242.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON_TER
SQ SEQUENCE 21 AA; 2405 MW; E307CB4E71595CA4 CRC64;

Query Match
Best Local Similarity 26.6%; Score 29; DB 2; Length 21;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 6 TTHKYLVCESVNG 19
DB 8 TNSERVVISQDFNG 21
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RESULT 13
Q5EX77_9LAMI PRELIMINARY; PRT; 19 AA.
ID Q5EX77_9LAMI PRELIMINARY; PRT; 19 AA.
AC Q5EX77_9LAMI PRELIMINARY; PRT; 19 AA.
DT 10-MAY-2005 (TREMBlrel. 30, Created)
DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)
DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)
DE STM1 protein (Fragment).
OS Streptococcus thermophilus.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Lamiales; Gesneriaceae; Cyrtandroideae; Didymocarpeae;
OC Streptocarpus.
OC NCBI_TaxID=167308;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15659624; DOI=10.1105/lpc.104.028936;
RA Harrison J., Moller M., Langdale J., Cronk O., Hudson A.;
RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in
RT Streptocarpus."
RL Plant Cell 17:430-443(2005).
DR EMBL; AY662127; AAW33745.1; -; Genomic_DNA.
DR InterPro; IPR001356; Homeobox.
DR ProDom; PD000010; Homeobox; 1.
FT NON_TER 1 1
FT NON_TER 1 1
SQ SEQUENCE 19 AA; 2034 MW; 1069FC9782A6314A CRC64;

Query Match 25.7%; Score 28; DB 2; Length 19;
Best Local Similarity 35.7%; Pred. No. 3.1e+03;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 3 PHPTNKHVLCES 16
|:|:|:|:|
Db 1 PYPSESQKLALES 14

RESULT 14
Q5EX78_9LAMI PRELIMINARY; PRT; 19 AA.
ID Q5EX78_9LAMI PRELIMINARY; PRT; 19 AA.
AC Q5EX78_9LAMI PRELIMINARY; PRT; 19 AA.
DT 10-MAY-2005 (TREMBlrel. 30, Created)
DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)
DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)
DE STM1 protein (Fragment).
OS Streptococcus thermophilus.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Lamiales; Gesneriaceae; Cyrtandroideae; Didymocarpeae;
OC Streptocarpus.
OC NCBI_TaxID=167270;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15659624; DOI=10.1105/lpc.104.028936;
RA Harrison J., Moller M., Langdale J., Cronk O., Hudson A.;
RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in
RT Streptocarpus."
RL Plant Cell 17:430-443(2005).
DR EMBL; AY662126; AAW33744.1; -; Genomic_DNA.
DR InterPro; IPR001356; Homeobox.
DR ProDom; PD000010; Homeobox; 1.
FT NON_TER 1 1
FT NON_TER 1 1
SQ SEQUENCE 19 AA; 2034 MW; 1069FC9782A6314A CRC64;

Query Match 25.7%; Score 28; DB 2; Length 19;
Best Local Similarity 35.7%; Pred. No. 3.1e+03;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 3 PHPTNKHVLCES 16
|:|:|:|:|
Db 1 PYPSESQKLALES 14
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RESULT 15
Q5EX88_9LAMI PRELIMINARY; PRT; 19 AA.
ID Q5EX88_9LAMI PRELIMINARY; PRT; 19 AA.
AC Q5EX88_9LAMI PRELIMINARY; PRT; 19 AA.
DT 10-MAY-2005 (TREMBlrel. 30, Created)
DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)
DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)
DE STM2 protein (Fragment).
OS Streptococcus thermophilus.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Lamiales; Gesneriaceae; Cyrtandroideae; Didymocarpeae;
OC Streptocarpus.
OC NCBI_TaxID=167246;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15659624; DOI=10.1105/lpc.104.028936;
RA Harrison J., Moller M., Langdale J., Cronk O., Hudson A.;
RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in
RT Streptocarpus."
RL Plant Cell 17:430-443(2005).
DR EMBL; AY662116; AAW33770.1; -; Genomic_DNA.
DR InterPro; IPR001356; Homeobox.
DR ProDom; PD000010; Homeobox; 1.
FT NON_TER 1 1
FT NON_TER 1 1
SQ SEQUENCE 19 AA; 2034 MW; 1069FC9782A6314A CRC64;

Query Match 25.7%; Score 28; DB 2; Length 19;
Best Local Similarity 35.7%; Pred. No. 3.1e+03;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 3 PHPTNKHVLCES 16
|:|:|:|:|
Db 1 PYPSESQKLALES 14

RESULT 16
Q5EX90_9LAMI PRELIMINARY; PRT; 19 AA.
ID Q5EX90_9LAMI PRELIMINARY; PRT; 19 AA.
AC Q5EX90_9LAMI PRELIMINARY; PRT; 19 AA.
DT 10-MAY-2005 (TREMBlrel. 30, Created)
DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)
DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)
DE STM2 protein (Fragment).
OS Streptococcus thermophilus.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Lamiales; Gesneriaceae; Cyrtandroideae; Didymocarpeae;
OC Streptocarpus.
OC NCBI_TaxID=301922;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15659624; DOI=10.1105/lpc.104.028936;
RA Harrison J., Moller M., Langdale J., Cronk O., Hudson A.;
RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in
RT Streptocarpus."
RL Plant Cell 17:430-443(2005).
DR EMBL; AY662114; AAW33768.1; -; Genomic_DNA.
DR InterPro; IPR001356; Homeobox.
DR ProDom; PD000010; Homeobox; 1.
FT NON_TER 1 1
FT NON_TER 1 1
SQ SEQUENCE 19 AA; 2034 MW; 1069FC9782A6314A CRC64;

Query Match 25.7%; Score 28; DB 2; Length 19;
Best Local Similarity 35.7%; Pred. No. 3.1e+03;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 3 PHPTNKHVLCES 16
|:|:|:|:|
Db 1 PYPSESQKLALES 14
```

Db 1 PYPSQSOKLALAES 14

RESULT 17

Q5EX91_9LAMI PRELIMINARY; PRT; 19 AA.
AC Q5EX91;
DT 10-MAY-2005 (TREMBLrel. 30, Created)
DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
DE STW2 protein (Fragment).
OS Streptocarpus thompsonii.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Lamiales; Gesneriaceae; Cyrtandroideae; Didymocarpaceae;
OC Streptocarpus.
OX NCBI_TaxID=167307;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15659624; DOI=10.1105/lpc.104.028936;
RA Harrison J., Moller M., Langdale J., Cronk Q., Hudson A.;
RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in
Streptocarpus.";
RL Plant Cell 17:430-443(2005).
DR EMBL; AY662113; AAW33767.1; -; Genomic_DNA.
DR InterPro; IPR001356; Homeobox.
DR Prodom; PD000010; Homeobox; 1.
FT NON_TER 1
FT NON_TER 19
SQ SEQUENCE 19 AA; 2034 MW; 1069FC9782A6314A CRC64;

Query Match 25.7%; Score 28; DB 2; Length 19;

Best Local Similarity 35.7%; Pred. No. 3.1e+03;

Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 3 PHPTNIHKYLVCS 16
|:|:|:|:|
Db 1 PYPSQSOKLALAES 14

RESULT 18

Q5EX92_9LAMI PRELIMINARY; PRT; 19 AA.
AC Q5EX92;
DT 10-MAY-2005 (TREMBLrel. 30, Created)
DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
DE STW2 protein (Fragment).
OS Streptocarpus primulifolius.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Lamiales; Gesneriaceae; Cyrtandroideae; Didymocarpaceae;
OC Streptocarpus.
OX NCBI_TaxID=64018;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15659624; DOI=10.1105/lpc.104.028936;
RA Harrison J., Moller M., Langdale J., Cronk Q., Hudson A.;
RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in
Streptocarpus.";
RL Plant Cell 17:430-443(2005).
DR EMBL; AY662112; AAW33766.1; -; Genomic_DNA.
DR InterPro; IPR001356; Homeobox.
DR Prodom; PD000010; Homeobox; 1.
FT NON_TER 1
FT NON_TER 19
SQ SEQUENCE 19 AA; 2034 MW; 1069FC9782A6314A CRC64;

Query Match 25.7%; Score 28; DB 2; Length 19;

Best Local Similarity 35.7%; Pred. No. 3.1e+03;

Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 3 PHPTNIHKYLVCS 16

Db 1 PYPSQSOKLALAES 14

RESULT 19
Q5EX94_9LAMI PRELIMINARY; PRT; 19 AA.
AC Q5EX94;
DT 10-MAY-2005 (TREMBLrel. 30, Created)
DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
DE STW2 protein (Fragment).
OS Streptocarpus modestus.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Lamiales; Gesneriaceae; Cyrtandroideae; Didymocarpaceae;
OC Streptocarpus.
OX NCBI_TaxID=167287;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15659624; DOI=10.1105/lpc.104.028936;
RA Harrison J., Moller M., Langdale J., Cronk Q., Hudson A.;
RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in
Streptocarpus.";
RL Plant Cell 17:430-443(2005).
DR EMBL; AY662111; AAW33765.1; -; Genomic_DNA.
DR InterPro; IPR001356; Homeobox.
DR Prodom; PD000010; Homeobox; 1.
FT NON_TER 1
FT NON_TER 19
SQ SEQUENCE 19 AA; 2034 MW; 1069FC9782A6314A CRC64;

Query Match 25.7%; Score 28; DB 2; Length 19;

Best Local Similarity 35.7%; Pred. No. 3.1e+03;

Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 3 PHPTNIHKYLVCS 16
|:|:|:|:|
Db 1 PYPSQSOKLALAES 14

RESULT 20

Q5EX95_9LAMI PRELIMINARY; PRT; 19 AA.
AC Q5EX95;
DT 10-MAY-2005 (TREMBLrel. 30, Created)
DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
DE STW2 protein (STW1 protein) (Fragment).
OS Streptocarpus hirticarpa.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Lamiales; Gesneriaceae; Cyrtandroideae; Didymocarpaceae;
OC Streptocarpus.
OX NCBI_TaxID=167276;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15659624; DOI=10.1105/lpc.104.028936;
RA Harrison J., Moller M., Langdale J., Cronk Q., Hudson A.;
RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in
Streptocarpus.";
RL Plant Cell 17:430-443(2005).
DR EMBL; AY662109; AAW33763.1; -; Genomic_DNA.
DR EMBL; AY662122; AAW33740.1; -; Genomic_DNA.
DR InterPro; IPR001356; Homeobox.
DR Prodom; PD000010; Homeobox; 1.
FT NON_TER 1
FT NON_TER 19
SQ SEQUENCE 19 AA; 2034 MW; 1069FC9782A6314A CRC64;

Query Match 25.7%; Score 28; DB 2; Length 19;

Best Local Similarity 35.7%; Pred. No. 3.1e+03;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 3 PHPTNHXYLVCS 16
|:|:|:|:
Db 1 PYPSESQKLALES 14

RESULT 21

QSEX96_9LAMI PRELIMINARY; PRT; 19 AA.
AC QSEX96;
DT 10-MAY-2005 (TReMBLrel. 30, Created)
DT 10-MAY-2005 (TReMBLrel. 30, Last sequence update)
DE STW2 protein (STW1 protein) (Fragment).
OS Streptococcus burundianus.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Lamiales; Gesneriaceae; Cyrtandroideae; Didymocarpeae;
OC Streptocarpus.
OX NCBI_TaxId=167253;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15659624; DOI=10.1105/lpc.104.028936;
RA Harrison J., Moller M., Langdale J., Cronk Q., Hudson A.;
RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in
RT Streptocarpus."
RL Plant Cell 17:430-443(2005).
DR EMBL; AY662108; AAM33762.1; -; Genomic_DNA.
DR EMBL; AY662123; AAM33741.1; -; Genomic_DNA.
DR InterPro; IPR001356; Homeobox.
DR ProDom; PD000010; Homeobox; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 19 AA; 2034 MW; 1069FC9782A6314A CRC64;

Query Match 25.7%; Score 28; DB 2; Length 19;
Best Local Similarity 35.7%; Pred. No. 3.1e+03;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 3 PHPTNHXYLVCS 16
|:|:|:|:
Db 1 PYPSESQKLALES 14

RESULT 22

QSEX97_9LAMI PRELIMINARY; PRT; 19 AA.
AC QSEX97;
DT 10-MAY-2005 (TReMBLrel. 30, Created)
DT 10-MAY-2005 (TReMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TReMBLrel. 30, Last annotation update)
DE STW2 protein (Fragment).
OS Streptocarpus willetii.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Lamiales; Gesneriaceae; Cyrtandroideae; Didymocarpeae;
OC Streptocarpus.
OX NCBI_TaxId=167311;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15659624; DOI=10.1105/lpc.104.028936;
RA Harrison J., Moller M., Langdale J., Cronk Q., Hudson A.;
RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in
RT Streptocarpus."
RL Plant Cell 17:430-443(2005).
DR EMBL; AY662107; AAM33761.1; -; Genomic_DNA.
DR InterPro; IPR001356; Homeobox.
DR ProDom; PD000010; Homeobox; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 19 AA; 2034 MW; 1069FC9782A6314A CRC64;

Query Match 25.7%; Score 28; DB 2; Length 19;
Best Local Similarity 35.7%; Pred. No. 3.1e+03;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 3 PHPTNHXYLVCS 16
|:|:|:|:
Db 1 PYPSESQKLALES 14

RESULT 23

QSEX98_9LAMI PRELIMINARY; PRT; 19 AA.
AC QSEX98;
DT 10-MAY-2005 (TReMBLrel. 30, Created)
DT 10-MAY-2005 (TReMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TReMBLrel. 30, Last annotation update)
DE STW2 protein (Fragment).
OS Streptocarpus rexii.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Lamiales; Gesneriaceae; Cyrtandroideae; Didymocarpeae;
OC Streptocarpus.
OX NCBI_TaxId=121488;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15659624; DOI=10.1105/lpc.104.028936;
RA Harrison J., Moller M., Langdale J., Cronk Q., Hudson A.;
RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in
RT Streptocarpus."
RL Plant Cell 17:430-443(2005).
DR EMBL; AY662106; AAM33760.1; -; Genomic_DNA.
DR InterPro; IPR001356; Homeobox.
DR ProDom; PD000010; Homeobox; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 19 AA; 2034 MW; 1069FC9782A6314A CRC64;

Query Match 25.7%; Score 28; DB 2; Length 19;
Best Local Similarity 35.7%; Pred. No. 3.1e+03;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 3 PHPTNHXYLVCS 16
|:~|:~|:~|:
Db 1 PYPSESQKLALES 14

RESULT 24

QSEX99_9LAMI PRELIMINARY; PRT; 19 AA.
AC QSEX99;
DT 10-MAY-2005 (TReMBLrel. 30, Created)
DT 10-MAY-2005 (TReMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TReMBLrel. 30, Last annotation update)
DE STW2 protein (Fragment).
OS Streptocarpus wendlandii.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Lamiales; Gesneriaceae; Cyrtandroideae; Didymocarpeae;
OC Streptocarpus.
OX NCBI_TaxId=167310;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15659624; DOI=10.1105/lpc.104.028936;
RA Harrison J., Moller M., Langdale J., Cronk Q., Hudson A.;
RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in
RT Streptocarpus."
RL Plant Cell 17:430-443(2005).
DR EMBL; AY662105; AAM33759.1; -; Genomic_DNA.
DR InterPro; IPR001356; Homeobox.
DR ProDom; PD000010; Homeobox; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 19 AA; 2034 MW; 1069FC9782A6314A CRC64;

SEQ SEQUENCE 19 AA; 2034 MW; 1069FC9782A6314A CRC64;

Query Match 25.7%; Score 28; DB 2; Length 19;
 Best Local Similarity 35.7%; Pred. No. 3.1e+03;
 Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

OY 3 PPTNIHKYLVCS 16
 |:|:|:|:|:
 Db 1 PYPSQSQTALAES 14

RESULT 25

OSEXAL_9LAMI PRELIMINARY; PRT; 19 AA.
 ID OSEXAL_9LAMI
 AC OSEXAL; 10-MAY-2005 (TREMBlrel. 30. Created)
 DT 10-MAY-2005 (TREMBlrel. 30. Last sequence update)
 DT 10-MAY-2005 (TREMBlrel. 30. Last annotation update)
 DE STM2 protein (Fragment).
 OS Streptococcus dunnii.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamiales; Gentianales; Gentianaceae; Cyrtandroidae; Didymocarpaceae;
 OC Streptocarpus.
 OC NCBI_TaxID=121487;
 OX [1]
 RN NUCLEOTIDE SEQUENCE.
 RP PubMed:15659624; DOI=10.1105/lpc.104.028936;
 RX Harrison J., Moller M., Langdale J., Cronk Q., Hudson A.;
 RA "The Role of KNOX Genes in the Evolution of Morphological Novelty in
 RT Streptocarpus."
 RL Plant Cell 17:430-443(2005).
 DR EMBL; AY662103; AAW33757.1; -; Genomic_DNA.
 DR InterPro; IPR001356; Homeobox.
 DR ProDom; PD000010; Homeobox.1.
 FT NON_TER 1
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 19 AA; 2034 MW; 1069FC9782A6314A CRC64;

Query Match 25.7%; Score 28; DB 2; Length 19;
 Best Local Similarity 35.7%; Pred. No. 3.1e+03;
 Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

OY 3 PPTNIHKYLVCS 16
 |:|:|:|:|:
 Db 1 PYPSQSQTALAES 14

Search completed: January 26, 2006, 08:04:02
 Job time : 58.5086 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 26, 2006, 07:47:09 : Search time 67.931 Seconds
(without alignments)
129.360 Million cell updates/sec

Title: US-09-662-293-13

Perfect score: 105
Sequence: 1 DPAKGMSPPGFIVGEEGVLS 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 897420

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database :

1: A_GeneSeq_21: *
2: geneeqp1980s: *
3: geneeqp2000s: *
4: geneeqp2001s: *
5: geneeqp2002s: *
6: geneeqp2003as: *
7: geneeqp2003bs: *
8: geneeqp2004s: *
9: geneeqp2005s: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the change being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	105	100.0	20	3	AAV52513 House dus
2	105	100.0	20	3	AAV52522 House dus
3	105	100.0	20	5	AAU96317 Der HMW-m
4	105	100.0	20	5	AAU96326 Der HMW-m
5	37	35.2	21	8	ADR50710 Mouse/ra
6	36	34.3	16	8	ADR67576 Nitrlase
7	35	33.3	9	5	AAE28728 Human CAS
8	35	33.3	10	5	AAE28775 Human CAS
9	35	33.3	20	7	ADC99464 Cancer-re
10	34	32.4	8	2	AAW65590 Peptide #
11	34	32.4	8	4	AAE09067 Human aut
12	34	32.4	8	4	AAW97330 UI RNP wt
13	34	32.4	8	6	ABU07632 Epselin-B
14	34	32.4	11	8	ADR43749 Maximakin
15	34	32.4	12	8	ADR43750 Maximakin
16	34	32.4	13	5	ABP48137 Maximakin
17	34	32.4	18	5	ABP48137 GHR blind
18	34	32.4	18	8	ADR43748 Maximakin
19	34	32.4	19	8	ADN17072 Second ge
20	34	32.4	19	8	ADR43747 Maximakin
21	33	31.4	15	2	AAW18175 Immunodom
22	33	31.4	15	2	AAW75617 M. tuberc
23	33	31.4	15	6	ABU56381 Mycobacte
24	33	31.4	15	7	AAE39326 M. tuberc

25	33	31.4	15	7	ADP45168	Adf45168 M. tuberc
26	33	31.4	15	8	AD036853	Ad036853 Majorly a
27	33	31.4	15	8	ADU64228	ADU64228 30 KD pro
28	33	31.4	16	4	AAU07809	AAU07809 Peptide e
29	33	31.4	20	5	ABP30905	ABP30905 OER antib
30	33	31.4	20	7	ADAO8550	ADAO8550 Human OER
31	33	31.4	20	7	ADFO9099	ADFO9099 Secreted
32	33	31.4	20	7	ADFO8893	ADFO8893 Secreted
33	33	31.4	20	7	ADG46180	ADG46180 OER antib
34	33	31.4	20	7	ADK40495	ADK40495 KDR & VEG
35	33	31.4	20	8	ADR40713	ADR40713 KDR/ VEGF
36	33	31.4	20	9	ADXL1776	ADXL1776 Human ova
37	33	31.4	20	9	ADXL1782	ADXL1782 Human ova
38	33	31.4	21	8	ADR50711	ADR50711 Rat sheat
39	32	30.5	10	5	AAO14949	AAO14949 Surivivin-
40	32	30.5	10	8	ADS92606	ADS92606 Platelet
41	32	30.5	15	7	ADBA49200	ADBA49200 Biotinyla
42	32	30.5	16	5	AAU10333	AAU10333 Human PRO
43	32	30.5	16	9	AEC13757	AEC13757 Staphyloc
44	32	30.5	18	6	ABP57840	ABP57840 A. margin
45	32	30.5	20	5	AAU71011	AAU71011 M. tuberc
46	32	30.5	20	7	ADK40519	ADK40519 KDR & VEG
47	32	30.5	20	8	ADR40737	ADR40737 KDR/ VEGF
48	31	29.5	9	2	AAW49486	AAW49486 Human leu
49	31	29.5	9	8	AD068173	AD068173 Human 213
50	31	29.5	9	8	AD068472	AD068472 Human 213
51	31	29.5	9	8	AD068312	AD068312 Human 213
52	31	29.5	9	8	AD069700	AD069700 Human 213
53	31	29.5	9	8	AD071975	AD071975 Human 213
54	31	29.5	9	8	AD068215	AD068215 Human 213
55	31	29.5	9	8	AD068624	AD068624 Human 213
56	31	29.5	9	8	AD072059	AD072059 Human 213
57	31	29.5	9	8	AD068890	AD068890 Human 213
58	31	29.5	9	8	AD068347	AD068347 Human 213
59	31	29.5	9	8	AD068354	AD068354 Human 213
60	31	29.5	9	8	AD068030	AD068030 Human 213
61	31	29.5	9	8	AD068858	AD068858 Human 213
62	31	29.5	9	8	AD068100	AD068100 Human 213
63	31	29.5	9	8	AD067954	AD067954 Human 213
64	31	29.5	9	8	AD066277	AD066277 Human 213
65	31	29.5	9	8	AD068944	AD068944 Human 213
66	31	29.5	9	8	AD069211	AD069211 Human 213
67	31	29.5	9	8	AD068650	AD068650 Human 213
68	31	29.5	9	8	AD069433	AD069433 Human 213
69	31	29.5	9	8	AD069643	AD069643 Human 213
70	31	29.5	9	8	AD071860	AD071860 Human 213
71	31	29.5	9	8	AD072141	AD072141 Human 213
72	31	29.5	10	8	AD074908	AD074908 Human 213
73	31	29.5	10	8	AD067058	AD067058 Human 213
74	31	29.5	10	8	AD074471	AD074471 Human 213
75	31	29.5	10	8	AD074828	AD074828 Human 213
76	31	29.5	10	8	AD066467	AD066467 Human 213
77	31	29.5	10	8	AD075227	AD075227 Human 213
78	31	29.5	10	8	AD074526	AD074526 Human 213
79	31	29.5	10	8	AD075022	AD075022 Human 213
80	31	29.5	10	8	AD065940	AD065940 Human 213
81	31	29.5	10	8	AD074212	AD074212 Human 213
82	31	29.5	10	8	AD075255	AD075255 Human 213
83	31	29.5	10	8	AD067592	AD067592 Human 213
84	31	29.5	10	8	AD074085	AD074085 Human 213
85	31	29.5	10	8	AD074939	AD074939 Human 213
86	31	29.5	10	8	AD075094	AD075094 Human 213
87	31	29.5	10	8	AD075374	AD075374 Human 213
88	31	29.5	10	8	AD074213	AD074213 Human 213
89	31	29.5	10	8	AD075134	AD075134 Human 213
90	31	29.5	10	8	AD074599	AD074599 Human 213
91	31	29.5	11	5	ABP62415	ABP62415 Human imm
92	31	29.5	13	2	AAK13452	AAK13452 Residues
93	31	29.5	13	2	AAK13455	AAK13455 Residues
94	31	29.5	14	4	AAAB83040	AAAB83040 Human Sma
95	31	29.5	14	7	ADC22507	ADC22507 Protein b
96	31	29.5	15	7	ADP89482	ADP89482 Human E2F
97	31	29.5	15	8	ADK48864	ADK48864 C-termina

98	31	29.5	15	8	AD076533	AD076533 Human 213
99	31	29.5	15	8	AD076718	AD076718 Human 213
100	31	29.5	15	8	AD076801	AD076801 Human 213

ALIGNMENTS

RESULT 1

AAVS2513

ID AAVS2513 standard; peptide; 20 AA.

AC AAVS2513;

DT 22-FEB-2000 (first entry)

DE House dust mite allergen protein (map) A/B fragment map(3).

XX Mite allergen protein; map; high molecular weight; HMW-map; allergy;

XX house dust mite; IGE; immunoglobulin E; allergen; mapA; mapB;

XX hypersensitivity reaction; therapy; treatment; diagnosis; human; feline;

XX canine; veterinary; antibody; vaccine; immunisation.

XX Dermatophagoides farinae.

XX WO954349-A2.

XX 28-OCT-1999.

XX 16-APR-1999; 99WO-US008524.

XX 17-APR-1998; 98US-00062013.

XX 13-MAY-1998; 98US-0085295P.

XX 02-SEP-1998; 98US-0098909P.

XX (HESK-) HESKA CORP.

XX Mccall CA, Hunter SW, Weber ER;

XX WPI; 2000-052700/04.

XX Novel high molecular weight Dermatophagoides nucleic acid polypeptides

XX used to modify an animals' hypersensitivity to mite allergens.

XX Claim 3; Page 69; 154pp; English.

XX Sequences AAVS2510-Y52522 represent proteolytic fragments of

XX Dermatophagoides farinae high molecular weight mite allergen protein (HMW

XX -map) composition. The HMW-map composition was isolated from a D. farinae

XX homogenate by gel filtration, with each fraction being analysed for the

XX presence of proteins that bound to IGE present in mite-allergic dog

XX antisera. The HMW-map composition comprises mapA (a 109 kD protein) and

XX mapB (98 kD). Mite allergenic proteins and peptides, and nucleic acids

XX encoding them, may be used in therapeutic compositions to modify an

XX animal's hypersensitivity reaction to mite allergens. Animals that may be

XX treated include mammals and birds, especially felines, canines, equines,

XX humans, other pets, and work or domestic animals. The proteins or

XX fragments may also be used to diagnose allergies via a skin test. The

XX proteins and peptides can also be used to raise antibodies, which have a

XX variety of potential uses. For example, they can be used as vaccines to

XX passively immunise animals against dust mite hypersensitivity, as

XX positive controls in test kits and as tools to recover desired dust mite

XX allergens from a mixture of proteins

XX Sequence 20 AA;

SQ

Query Match 100.0%; Score 105; DB 3; Length 20;

Best Local Similarity 100.0%; Pred. No. 4,7e-09;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DPAKMSPPGFIVGEEGVLS 20

DB 1 DPAKMSPPGFIVGEEGVLS 20

XX

RESULT 2

AAVS2522

ID AAVS2522 standard; peptide; 20 AA.

AC AAVS2522;

DT 22-FEB-2000 (first entry)

DE House dust mite allergen protein (map) A/B fragment map(12).

XX Mite allergen protein; map; high molecular weight; HMW-map; allergy;

XX house dust mite; IGE; immunoglobulin E; allergen; mapA; mapB;

XX hypersensitivity reaction; therapy; treatment; diagnosis; human; feline;

XX canine; veterinary; antibody; vaccine; immunisation.

XX Dermatophagoides farinae.

XX WO954349-A2.

XX 28-OCT-1999.

XX 16-APR-1999; 99WO-US008524.

XX 17-APR-1998; 98US-00062013.

XX 13-MAY-1998; 98US-0085295P.

XX 02-SEP-1998; 98US-0098909P.

XX (HESK-) HESKA CORP.

XX Mccall CA, Hunter SW, Weber ER;

XX WPI; 2000-052700/04.

XX Novel high molecular weight Dermatophagoides nucleic acid polypeptides

XX used to modify an animals' hypersensitivity to mite allergens.

XX Claim 3; Page 70; 154pp; English.

XX Sequences AAVS2510-Y52522 represent proteolytic fragments of

XX Dermatophagoides farinae high molecular weight mite allergen protein (HMW

XX -map) composition. The HMW-map composition was isolated from a D. farinae

XX homogenate by gel filtration, with each fraction being analysed for the

XX presence of proteins that bound to IGE present in mite-allergic dog

XX antisera. The HMW-map composition comprises mapA (a 109 kD protein) and

XX mapB (98 kD). Mite allergenic proteins and peptides, and nucleic acids

XX encoding them, may be used in therapeutic compositions to modify an

XX animal's hypersensitivity reaction to mite allergens. Animals that may be

XX treated include mammals and birds, especially felines, canines, equines,

XX humans, other pets, and work or domestic animals. The proteins or

XX fragments may also be used to diagnose allergies via a skin test. The

XX proteins and peptides can also be used to raise antibodies, which have a

XX variety of potential uses. For example, they can be used as vaccines to

XX passively immunise animals against dust mite hypersensitivity, as

XX positive controls in test kits and as tools to recover desired dust mite

XX allergens from a mixture of proteins

XX Sequence 20 AA;

SQ

Query Match 100.0%; Score 105; DB 3; Length 20;

Best Local Similarity 100.0%; Pred. No. 4,7e-09;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DPAKMSPPGFIVGEEGVLS 20

DB 1 DPAKMSPPGFIVGEEGVLS 20

XX

RESULT 3

AAU96317

ID AAU96317 standard; peptide; 20 AA.

XX

AC AAU96317;
 XX
 DT 15-JUL-2002 (first entry)
 XX
 DE Der HMW-map polypeptide #4.
 XX
 XX Der HMW-map; American house dust mite; antiallergic; mite; IgE;
 KM mite allergenic protein; immunoglobulin E; hypersensitivity;
 KM immunocomplex formation.
 XX
 OS Dermatophagoides farinae.
 XX
 PN WO200222807-A2.
 XX
 PD 21-MAR-2002.
 XX
 PF 14-SEP-2001; 2001WO-US028730.
 XX
 PR 14-SEP-2000; 2000US-00662293.
 XX
 PA (HESK-) HESKA CORP.
 XX
 PI Mccall CA, Hunter SW, Weber ER;
 XX
 DR WPI; 2002-351888/38.
 XX
 PT New mite allergenic protein isolated from Dermatophagoides, designated
 XX Der HMW-map protein, useful as a vaccine for treating mite allergy.
 PS Claim 12; Page 70; 161pp; English.
 XX
 CC The invention relates to an isolated mite allergenic protein of
 CC Dermatophagoides, designated Der HMW-map protein, and its related nucleic
 CC acid. The Der HMW-map protein is useful for eliciting an immune response
 CC against Der HMW-map protein. The protein or a reagent comprising a non-
 CC proteinaceous epitope is useful for identifying an animal (e.g., dog,
 CC cat) susceptible to or having an allergic response to a mite. A
 CC therapeutic composition is useful for desensitizing a host animal to an
 CC allergic response to a mite. The DNA and protein can be used in the
 CC detection of anti-Der HMW-map antibodies in animal fluids, and inhibition
 CC of immunoglobulin (Ig)E or Der HMW-map protein activity associated with a
 CC disease. Antibodies that bind to Der HMW-map are useful for inhibiting
 CC binding of proteins to IgE, to prevent immunocomplex formation, thus
 CC reducing hypersensitivity responses to mite allergens, and as vaccines
 CC against mite allergen hypersensitivity. Sequences AAU96314-AAU96342
 CC represent Der HMW-map polypeptides of the invention
 XX
 SO Sequence 20 AA;
 Query Match 100.0%; Score 105; DB 5; Length 20;
 Best Local Similarity 100.0%; Pred. No. 4.7e-09;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DPAKMSPPGFIVGEGVLS 20
 DB 1 DPAKMSPPGFIVGEGVLS 20
 XX
 RESULT 4
 AAU96326
 ID AAU96326 standard; peptide: 20 AA.
 XX
 AC AAU96326;
 XX
 DT 15-JUL-2002 (first entry)
 XX
 DE Der HMW-map polypeptide #13.
 XX
 KM Der HMW-map; American house dust mite; antiallergic; mite; IgE;
 KM mite allergenic protein; immunoglobulin E; hypersensitivity;
 KM immunocomplex formation.
 XX
 OS Dermatophagoides farinae.
 XX

XX
 PN WO200222807-A2.
 XX
 PD 21-MAR-2002.
 XX
 PF 14-SEP-2001; 2001WO-US028730.
 XX
 PR 14-SEP-2000; 2000US-00662293.
 XX
 PA (HESK-) HESKA CORP.
 XX
 PI Mccall CA, Hunter SW, Weber ER;
 XX
 DR WPI; 2002-351888/38.
 XX
 PT New mite allergenic protein isolated from Dermatophagoides, designated
 XX Der HMW-map protein, useful as a vaccine for treating mite allergy.
 PS Claim 12; Page 71; 161pp; English.
 XX
 CC The invention relates to an isolated mite allergenic protein of
 CC Dermatophagoides, designated Der HMW-map protein, and its related nucleic
 CC acid. The Der HMW-map protein is useful for eliciting an immune response
 CC against Der HMW-map protein. The protein or a reagent comprising a non-
 CC proteinaceous epitope is useful for identifying an animal (e.g., dog,
 CC cat) susceptible to or having an allergic response to a mite. A
 CC therapeutic composition is useful for desensitizing a host animal to an
 CC allergic response to a mite. The DNA and protein can be used in the
 CC detection of anti-Der HMW-map antibodies in animal fluids, and inhibition
 CC of immunoglobulin (Ig)E or Der HMW-map protein activity associated with a
 CC disease. Antibodies that bind to Der HMW-map are useful for inhibiting
 CC binding of proteins to IgE, to prevent immunocomplex formation, thus
 CC reducing hypersensitivity responses to mite allergens, and as vaccines
 CC against mite allergen hypersensitivity. Sequences AAU96314-AAU96342
 CC represent Der HMW-map polypeptides of the invention
 XX
 SO Sequence 20 AA;
 Query Match 100.0%; Score 105; DB 5; Length 20;
 Best Local Similarity 100.0%; Pred. No. 4.7e-09;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DPAKMSPPGFIVGEGVLS 20
 DB 1 DPAKMSPPGFIVGEGVLS 20
 XX
 RESULT 5
 ADR50710
 ID ADR50710 standard; peptide: 21 AA.
 XX
 AC ADR50710;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Mouse/ rat sheathlin peptide SegID 6.
 XX
 KM sheathlin; ameljin; ameloblastin; enamel matrix protein;
 KM proliferation promoter; differentiation promoter; periodontitis;
 KM fracture; bone defect; osteoporosis; osteoarthritis; bone grafting;
 KM bone fenestration; bone cartilage transplantation; bone supplementation;
 KM antiinflammatory; osteopathic.
 XX
 OS Murinae.
 XX
 PN WO2004074319-A1.
 XX
 PD 02-SEP-2004.
 XX
 PF 20-FEB-2004; 2004WO-JP002009.
 XX
 PR 21-FEB-2003; 2003JP-00045166.
 XX
 PA 21-MAY-2003; 2003JP-00142845.
 XX

XX (SEKG) SEIKAGAKU CORP.
XX Takata T, Kitagawa S, Kaneda Y;
XX WPI; 2004-642493/62.
XX Novel partial peptide of sheathlin, useful for treating periodontitis,
PT fracture, osteoporosis, osteoarthritis and useful in bone grafting after
PT surgical removal of tumor.
XX
XX Claim 3; SEQ ID NO 6; 72pp; Japanese.
XX
XX This invention relates to novel partial peptides of the sheathlin protein
CC (also known as amelotin and ameloblastin), which is an enamel matrix
CC protein. Specifically, it refers to physiologically active peptides that
CC can be employed as promoters of proliferation and differentiation in
CC various cells including osteoblasts, chondroblasts, cementoblasts, bone
CC marrow-origin mesenchymal stem cells and periodontal membrane cells. The
CC present invention describes peptides that when used as cell growth
CC promoters sequences can be useful for the treatment of periodontitis,
CC fracture, bone defect, osteoporosis, osteoarthritis, as well as in bone
CC grafting after surgical removal of tumour, bone fenestration, bone
CC cartilage transplantation and bone supplementation. Accordingly, they
CC exhibit antiinflammatory and osteopathic activities. This peptide sequence
CC is a mouse/ rat sheathlin peptide of the invention.
XX
XX Sequence 21 AA;
SQ
Query Match 35.2%; Score 37; DB 8; Length 21;
Best Local Similarity 75.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 3 AKGMSPPG 10
Db 10 AQGMAPG 17
RESULT 6
ID ADR67576 standard; peptide; 16 AA.
XX ADR67576;
XX 02-DEC-2004 (first entry)
XX Nitriclase peptide fragment #165.
XX Nitriclase; carboxylic acid; enzyme; nitrile.
XX Unidentified.
XX WO2004076655-A1.
XX 10-SEP-2004.
XX 24-FEB-2004; 2004WO-EP001804.
XX 27-FEB-2003; 2003US-0450470P.
XX (BADI) BASF AG.
XX Zejinski T, Kesseler M, Hauer B, Friedrich T;
XX WPI; 2004-653416/63.
XX New modified nitriclase polypeptides, useful for preparing carboxylic
PT acids, preferably substituted chiral carboxylic acids.
XX
XX Disclosure: Page 13; 96pp; English.
XX The present invention relates to modified nitriclase proteins, which are
CC useful for preparing carboxylic acids, preferably substituted chiral

CC carboxylic acids. Nitriclases are enzymes which catalyse the hydrolysis of
CC nitriles into the corresponding carboxylic acids and ammonium ions. The
CC modified nitriclases of the invention have a modification at position 296
CC and exhibit a modulated acceptance in comparison to wild-type nitriclase.
CC The substitution of tyrosine at position 296 in wild-type Alcaligenes
CC faecalis nitriclase comprising a sequence of 356 amino acids (ADR67405)
CC was realized by site-directed mutagenesis utilizing overlap-extension
CC PCR. The present sequence is a fragment of a nitriclase used in a sequence
CC alignment to illustrate the invention.
XX
XX Sequence 16 AA;
SQ
Query Match 34.3%; Score 36; DB 8; Length 16;
Best Local Similarity 58.3%; Pred. No. 1.9e+02;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 DPAKMSPPGPT 12
Db 1 DPAGHYSTPGFL 12
RESULT 7
ID AAE28728 standard; peptide; 9 AA.
XX AAE28728;
XX 27-DEC-2002 (first entry)
XX Human CASB88 antigenic epitope #19.
XX CASB88 protein; Crohn's disease; Colitis ulcerosa; preneoplastic lesion;
XX colorectal cancer; Wilms tumor; retinoblastoma; cancer; gene therapy;
XX rhabdomyosarcoma; leiomyosarcoma; synovial sarcoma; vaccine; human;
XX epitope.
XX Homo sapiens.
XX WO200205103-A2.
XX 27-JUN-2002.
XX 18-SEP-2001; 2001WO-EP010980.
XX 20-DEC-2000; 2000GB-00031095.
XX 27-MAR-2001; 2001GB-00007632.
XX 02-AUG-2001; 2001GB-00018926.
XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
XX Cassart J, Coche T, Gaulis SRJ, Orncoft T, Vinals Y De Bassolac;
XX WPI; 2002-691493/74.
XX Novel CASB88 polypeptide and polynucleotide useful for treating cancer,
PT Crohn's disease, colitis ulcerosa, colorectal cancer, lung cancer and
PT preneoplastic lesions, Wilms tumor, retinoblastoma and rhabdomyosarcoma.
XX
XX Claim 6; Page 77; 122pp; English.
XX The invention relates to novel CASB88 polypeptides and polynucleotides.
CC Sequences of the invention are used for the treatment of diseases e.g.
CC Crohn's disease, Colitis ulcerosa, colorectal cancer, lung cancer and
CC preneoplastic lesions, breast, brain, uterus, muscle, eye and germ cell
CC cancers, Wilms tumor, retinoblastoma, rhabdomyosarcoma, leiomyosarcoma
CC and synovial sarcoma. They are useful in gene therapy and as vaccines.
CC The present sequence is human CASB88 antigenic epitope
XX
XX Sequence 9 AA;
SQ
Query Match 33.3%; Score 35; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 GMSPPG 10
 DB 1 GMSPPG 6

RESULT 9
 AAE28775 ID AAE28775 standard; peptide; 10 AA.
 AC AAE28775;
 DT 27-DEC-2002 (first entry)
 DE Human CASB88 antigenic epitope #66.
 XX CASB88 protein; Crohn's disease; Colitis ulcerosa; preneoplastic lesion;
 KM colorectal cancer; Wilm's tumour; retinoblastoma; cancer; gene therapy;
 KM rhabdomyosarcoma; leiomyosarcoma; synovial sarcoma; vaccine; human;
 KM epitope.
 OS Homo sapiens.
 XX WO200250103-A2.
 XX 27-JUN-2002.
 XX 18-SEP-2001; 2001WO-EP010980.
 XX 20-DEC-2000; 2000GB-00031095.
 PR 27-MAR-2001; 2001GB-00007632.
 PR 02-AUG-2001; 2001GB-00018926.
 XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
 XX CASBart J, Coche T, Gaulis SRJ, Orntoft T, Vinals Y De Bassolac;
 PI WPI; 2002-691493/74.
 XX Novel CASB88 polypeptide and polynucleotide useful for treating cancer,
 PT Crohn's disease, colitis ulcerosa, colorectal cancer, lung cancer and
 PT preneoplastic lesions, Wilm's tumor, retinoblastoma and rhabdomyosarcoma.
 XX Claim 6; Page 81; 122pp; English.
 PS The invention relates to novel CASB88 polypeptides and polynucleotides.
 CC Sequences of the invention are used for the treatment of diseases e.g.
 CC Crohn's disease, Colitis ulcerosa, colorectal cancer, lung cancer and
 CC preneoplastic lesions, breast, brain, uterus, muscle, eye and germ cell
 CC cancers, Wilm's tumour, retinoblastoma, rhabdomyosarcoma, leiomyosarcoma
 CC and synovial sarcoma. They are useful in gene therapy and as vaccines.
 CC The present sequence is human CASB88 antigenic epitope
 XX
 SQ Sequence 10 AA;

Query Match 33.3%; Score 35; DB 5; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 GMSPPG 10
 DB 3 GMSPPG 8

RESULT 9
 ADC99464 ID ADC99464 standard; peptide; 20 AA.
 AC ADC99464;
 DT 01-JAN-2004 (first entry)
 DE Cancer-related DGI-5-binder peptide - SEQ ID 302.

XX cyrostatic; cancer; gene therapy; DGI-2; DGI-5; DGI-7; DGI-9; Hras;
 KM Leptin; VEGF; vascular endothelial growth factor receptor; VEGF-R1;
 KM VEGF-R2; VEGF-R3; FLT1; FMS-related tyrosine kinase 1; FLK1; KDR;
 KM kinase insert domain protein receptor; EGFR; epidermal growth factor;
 KM FGFR1; fibroblast growth factor; Tie-1.
 XX Unidentified.
 OS
 XX WO2003035839-A2.
 XX 01-MAY-2003.
 XX 24-OCT-2002; 2002WO-US034021.
 XX 24-OCT-2001; 2001US-0345471P.
 PR (DGI-5) DGI BIOTECHNOLOGIES INC.
 XX Piliulita RC, Brissette R, Spruyt M, Dedova O, Blume A;
 PI Prendergast J, Goldstein N;
 XX WPI; 2003-457332/43.
 DR Selecting target and target binder pairs for preparing a composition for
 XX treating cancer by mixing in a reaction vessel phage expressing
 PT biological targets and phage expressing target binders.
 PT
 XX Claim 26; SEQ ID NO 302; 172pp; English.
 PS The invention relates to a novel method of selecting target and target
 CC binder pairs comprising mixing in a reaction vessel phage expressing
 CC biological targets and phage expressing target binders, each having
 CC distinguishable selection markers and selecting target and target binder
 CC pairs based on the selection markers. The molecules of the invention
 CC demonstrate cyrostatic activity whilst the method may be useful for
 CC selecting target and target binder pairs for preparing a composition for
 CC treating cancer. Furthermore, the method may be utilised during gene
 CC therapy procedures. The current sequence is that of the cancer-related
 CC DGI-5-binder peptide of the invention.
 XX
 SQ Sequence 20 AA;

Query Match 33.3%; Score 35; DB 7; Length 20;
 Best Local Similarity 53.3%; Pred. No. 3.4e+02;
 Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

OY 5 GMSPPGRIVEGVL 19
 DB 2 GRUPEMGLVGERGL 16

RESULT 10
 AAM65590 ID AAM65590 standard; peptide; 8 AA.
 XX AAM65590;
 AC AAM65590;
 DT 15-OCT-1998 (first entry)
 DE Peptide #6.
 XX Epstein-Barr virus; diagnostic test; autoimmune disease; vaccine;
 KM infection; antibody; screening; genetic marker.
 XX Synthetic.
 OS
 XX WO9830586-A2.
 XX 16-JUL-1998.
 PD 13-JAN-1998; 98WO-US000342.

PR 13-JAN-1997; 97US-00781296.
 XX (OKLA-) OKLAHOMA MEDICAL RES FOUND.
 PA
 PI Harley JB, James JA;
 XX WPI; 1998-399062/34.
 DR
 XX Use of Epstein-Barr virus or component(s) - for developing product(s)
 PT which can be used for preventing, diagnosing, treating or determining
 PT risk of developing autoimmune disease.
 PS
 XX Disclosure; Page 54; 81pp; English.
 XX The invention relates to a vaccine for alleviating or preventing
 CC autoimmune disorders induced by infection with Epstein-Barr virus (EBV).
 CC It comprises EBV or a component in a carrier for administration of the
 CC virus or viral component to alleviate or prevent the autoimmune disorder.
 CC Also claimed are: (1) a diagnostic test kit comprising: (a) reagents
 CC which can be used to detect levels of antibodies to EBV, indicators of
 CC EBV infection of cells, or levels of EBV DNA or protein in a patient; (b)
 CC control samples from individuals not at risk of developing an autoimmune
 CC disease; and (c) a device for determining the differences in levels of a
 CC patient and control samples to distinguish individuals at higher risk of
 CC developing an autoimmune disease from those at lower risk of developing
 CC an autoimmune disease; and (2) a method for screening for genetic markers
 CC or risk factors for development of autoimmune disorders induced by
 CC infection with EBV comprising comparing the responses of different
 CC strains of the same species of an animal vaccinated with EBV or a
 CC component to induce an autoimmune response in at least one of the strains
 CC and comparing the differences in the genetics of the different strains to
 CC identify potential genetic markers or risk factors. The methods can be
 CC used for the prevention, diagnosis, and treatment of autoimmune diseases
 CC having EBV as an etiological agent. The autoimmune diseases may be e.g.
 CC systemic lupus erythematosus, Sjogren's syndrome, rheumatoid arthritis,
 CC juvenile onset diabetes mellitus, Wegener's granulomatosis, etc. The
 CC present sequence is shown in the specification
 CC
 XX Sequence 8 AA:
 SQ
 Query Match 32.4%; Score 34; DB 2; Length 8;
 Best Local Similarity 75.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 PAKMSPP 9
 Db 1 PAPGMRP 8

RESULT 11
 AAE09067 standard; peptide: 8 AA.
 ID AAE09067
 AC AAE09067;
 XX
 DT 15-NOV-2001 (first entry)
 XX
 XX Human autoantigen Sm B/B' octapeptide #3 used in the invention.
 DE
 XX Vaccine; therapy; autoimmune disorder; Epstein-Barr virus; EBV; anaemia;
 KM polymyositis; systemic lupus erythematosus; SLE; rheumatoid arthritis;
 KM Sjogren's syndrome; diabetes mellitus; adrenalitis; multiple sclerosis;
 KM demyelinating disease; Hashimoto's thyroiditis; autoimmune infertility;
 KM hypoparathyroidism; primary biliary cirrhosis; ankylosing spondylitis;
 KM inflammatory bowel disease; Addison's disease; thyroiditis; filariasis;
 KM Graves' disease; ulcerative colitis; dermatomyositis; myasthenia gravis;
 KM Crohn's disease; CRST syndrome; autoimmune cystitis; glomerulonephritis;
 KM polyarteritis nodosa; hepatitis; atopic rhinitis; Goodpasture's syndrome;
 KM sarcoidosis; rheumatic fever; anti-phospholipid syndrome; farmer's lung;
 KM Cushing's syndrome; bird-fancier's lung; alveolitis; erythema nodosum;
 KM pyoderma gangrenosum; fibromyalgia; Kawasaki's disease; cardiomyopathy;
 KM Sampter's syndrome; asthma; polymyalgia rheumatica; psoriasis; arteritis;
 KM erythroblastosis foetalis; cystitis; IGA nephropathy; Hodgkin's lymphoma;

KM renal cell carcinoma; eosinophilia; immunosuppressive; ophthalmological;
 KM thymometric; neuroprotective; cytostatic; nephrotropic; antiallergic;
 KM dengue; antileuk; vasotropic; antipyretic; hepatotropic; human.
 XX
 OS Homo sapiens.
 XX
 PN MO200158481-A2.
 XX
 PD 16-AUG-2001.
 XX
 PD 09-FEB-2001; 2001MO-US004191.
 XX
 PP 09-FEB-2000; 2000US-00500904.
 XX
 PR
 XX (OKLA-) OKLAHOMA MEDICAL RES FOUND.
 PA
 PI Harley JB, James JA, Kaufman KM;
 XX WPI; 2001-522437/57.
 DR
 XX Novel vaccine for alleviating or preventing autoimmune disorders induced
 PT Epstein-Barr virus (EBV) infection e.g. systemic lupus erythematosus,
 PT juvenile onset diabetes mellitus, comprises EBV virus or its component.
 XX
 XX Example 1; Fig 3; 114pp; English.
 PS
 XX The present invention relates to a vaccine for alleviating or preventing
 CC autoimmune disorders induced by infection with Epstein-Barr virus (EBV),
 CC comprising EBV or its component in a carrier. The vaccine is useful for
 CC preventing or alleviating autoimmune disorders induced by EBV, e.g.
 CC systemic lupus erythematosus (SLE), Sjogren's syndrome, juvenile onset
 CC diabetes mellitus, rheumatoid arthritis, Wegener's granulomatosis,
 CC inflammatory bowel disease, polymyositis, dermatomyositis, multiple
 CC endocrine failure, Schmidt's syndrome, autoimmune uveitis, Addison's
 CC disease, adrenalitis, primary biliary cirrhosis, Graves' disease,
 CC thyroiditis, Hashimoto's thyroiditis, autoimmune thyroid disease,
 CC pernicious and haemolytic anaemia, lupoid hepatitis, demyelinating
 CC disease, multiple sclerosis, subacute cutaneous lupus erythematosus,
 CC hypoparathyroidism, Dressler's syndrome, myasthenia gravis, autoimmune
 CC idiopathic thrombocytopenic purpura, autoimmune pemphigus vulgaris,
 CC pemphigus, bullous pemphigoid, dermatitis herpetiformis, alopecia areata,
 CC autoimmune cystitis, pemphigoid, scleroderma, progressive systemic
 CC sclerosis, CRST syndrome (calcinosis, Raynaud's oesophageal dysmotility,
 CC sclerodactyly and telangiectasia), adult onset diabetes mellitus (Type II
 CC diabetes), male or female autoimmune infertility, ankylosing spondylitis,
 CC ulcerative colitis, Crohn's disease, mixed connective tissue disease,
 CC polyarteritis nodosa, systemic necrotizing vasculitis,
 CC glomerulonephritis, atopic dermatitis, atopic rhinitis, Goodpasture's
 CC syndrome, Chagas' disease, sarcoidosis, rheumatic fever, asthma,
 CC recurrent abortion, anti-phospholipid syndrome, farmer's lung, erythema
 CC multiforme, postcardiomy syndrome, Cushing's syndrome, autoimmune
 CC chronic active hepatitis, bird-fancier's lung, allergic
 CC encephalomyelitis, toxic necrodermal lysis, alopecia, Alport's syndrome,
 CC allergic alveolitis, fibrosing alveolitis, interstitial lung disease,
 CC erythema nodosum, pyoderma gangrenosum, transfusion reaction, chronic
 CC fatigue syndrome, fibromyalgia, Takayasu's arteritis, Kawasaki's disease,
 CC polymyalgia rheumatica, temporal arteritis, giant cell arteritis, dengue,
 CC Sampter's syndrome (triaditis, nasal polyps, eosinophilia) and Behcet's
 CC disease, Caplan's syndrome, encephalomyositis, erythema elevatum et
 CC ditinum, psoriasis, erythroblastosis foetalis, Shulman's syndrome, IGA
 CC nephropathy, Felty's syndrome, fascitis with eosinophilia, filariasis,
 CC chronic cystitis, heterochromic cystitis, Fuchs's cystitis, Hodgkin's and
 CC non-Hodgkin's lymphoma, cardiomyopathy, Henoch-Schönlein purpura, post
 CC vaccination syndromes, renal cell carcinoma, Eaton-Lambert syndrome or
 CC relapsing polychondritis. The present sequence is human autoantigen Sm
 CC B/B' octapeptide used in the invention
 CC
 XX Sequence 8 AA:
 SQ
 Query Match 32.4%; Score 34; DB 4; Length 8;
 Best Local Similarity 75.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PAKGMSPP 9
DB 1 PAPGMRPP 8

RESULT 12
AAB97330 standard; peptide; 8 AA.

AAB97330;

13-AUG-2001 (first entry)

UI RNP with A and C proteins epitope peptide.

B cell; toxin; antigen specific; antibody mediated disease; virucide;
immunosuppressive; antitubercular; antiallergic; antidiabetic;
thyromimetic; antihypertensive; vasotropic; cardiant; antitumor;
neuroprotective; antirheumatic; antiallergic; dermatological;
ophthalmological; nephrotoxic; allergy; autoimmune disorder;
skin diseases; autoimmune endocrinopathy; vasculitic syndrome;
cardiovascular disease; immunohaematologic disorder; neurologic disease;
gastrointestinal disease; collagen vascular disease; renal disease;
pulmonary disease; infertility disorder; UI-U6 RNP;
systemic lupus erythematosus.

Unidentified.

WO200132853-A1.

10-MAY-2001.

12-OCT-2000; 2000WO-US028157.

29-OCT-1999; 99US-0162464P..

(BIOM-) INST APPLIED BIOMEDICINE.

Chaplin JW;

WPI; 2001-316435/33.

B cell clonal toxin useful for treating autoimmune disorders such as
Grave's disease, myocardial infarction, Crohn's disease, multiple
sclerosis, comprises a group that causes toxin to be internalized by B
cell.

Disclosure; Page 33; 46pp; English.

This invention relates to a B cell clonal toxin. The toxin is made from
two moieties, the first causes the toxin to be internalized by a B cell,
and the second is a biologically acceptable toxin. The invention includes
a method for inactivating/killing an antigen specific B cell. A target B
cell is contacted with an effective amount of a B cell clonal toxin. The
method is useful for selective immunosuppression in conditions
characterized by the presence of an unwanted or deleterious immune
response, e.g. in the treatment of antigen specific antibody mediated
disease conditions. Use of the B cell clonal toxin can result in
immunosuppressive; antitubercular; antiallergic; virucide; antidiabetic
; thyromimetic; antihypertensive; vasotropic; cardiant; antitumor;
neuroprotective; antirheumatic; antiallergic; dermatological;
ophthalmological; and nephrotoxic activity. The toxin is particularly
useful for treating a host suffering from an antigen specific antibody
mediated disease condition, where the antigen specific antibody is
produced by an antigen-reactive B cell population present in a host. The
toxin is useful for treating allergies, viral disease conditions, and
autoimmune disorders. Also treated are skin diseases; autoimmune
endocrinopathies; vasculitic syndromes; cardiovascular disease;
immunohaematologic disorders; gastrointestinal diseases; neurologic
diseases; collagen vascular diseases; renal diseases; pulmonary diseases;
and infertility disorders. The present sequence represents a UI RNP with
A and C protein epitope. An antibody response to this antigen is
implicated in systemic lupus erythematosus, a disorder which may be

CC created using the toxin of the invention
XX
SQ Sequence 8 AA;

Query Match 32.4%; Score 34; DB 4; Length 8;
Best Local Similarity 75.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PAKGMSPP 9
DB 1 PAPGMRPP 8

RESULT 13
ABU07632 standard; peptide; 8 AA.

ABU07632;

23-OCT-2003 (revised)

10-MAY-2003 (first entry)

Epstein-Barr virus nuclear antigen peptide #6.

EBV; viral; Epstein-Barr virus nuclear antigen; vaccine;
autoimmune disorder; Epstein-Barr virus infection; diabetes mellitus;
arthritis; multiple sclerosis; dermatitis; psoriasis; asthma; anaemia;
allergy.

Human herpesvirus 4.

US2002164355-A1.

07-NOV-2002.

24-OCT-2001; 2001US-00012756.

30-NOV-1993; 93US-00160604.

16-MAY-1996; 96US-0019053P.

13-JAN-1997; 97US-00781296.

(HARL/) HARLEY J B.
(JAME/) JAMES J A.

Harley JB, James JA;

WPI; 2003-298686/29.

New vaccine preventing or alleviating autoimmune disorders induced by the
Epstein-Barr virus, such as diabetes mellitus, rheumatoid arthritis, and
multiple sclerosis, systemic lupus erythematosus, atopic dermatitis and
psoriasis.

Example 1; Fig 3; 41pp; English.

The invention relates to a vaccine for alleviating or preventing
autoimmune disorders induced by infection with Epstein-Barr virus,
comprising an Epstein-Barr virus or a component in a carrier for
administration to alleviate or prevent the autoimmune disorders. The
methods and compositions of the present invention are useful for
diagnosing, preventing, treating and/or alleviating autoimmune disorders,
such as diabetes mellitus, rheumatoid arthritis, juvenile rheumatoid
arthritis, osteoarthritis, psoriatic arthritis, multiple sclerosis,
encephalomyelitis, myasthenia gravis, systemic lupus erythematosus,
autoimmune thyroiditis, atopic dermatitis, eczematous dermatitis,
psoriasis, Sjogren's Syndrome, Crohn's disease, aphthous ulcer, iritis,
conjunctivitis, keratoconjunctivitis, ulcerative colitis, asthma,
allergic asthma, cutaneous lupus erythematosus, scleroderma, vaginitis,
proctitis, drug eruptions, leprosy reversal reactions, erythema
nodosum/erythema multiforme, autoimmune uveitis, allergic encephalomyelitis, acute
necrotizing haemorrhagic encephalopathy, idiopathic bilateral progressive
sensorineural hearing loss, aplastic anaemia, pure red cell anaemia,
idiopathic thrombocytopenia, polychondritis, Wegener's granulomatosis,

CC chronic active hepatitis, Stevens-Johnson syndrome, idiopathic sprue,
 CC lichen planus, Graves' disease, sarcoidosis, primary biliary cirrhosis,
 CC uveitis posterior, interstitial lung fibrosis, graft-versus-host disease,
 CC and allergy. The present sequence represents an Epstein-Barr virus
 CC nuclear antigen peptide used in the method of the invention. (updated on
 CC 23-Oct-2003 to standardise OS field)
 CC XX
 SQ Sequence 8 AA;
 Query Match 32.4%; Score 34; DB 6; Length 8;
 Best Local Similarity 75.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 PAKGSP 9
 DB 1 PAKGRPP 8
 RESULT 14
 ID ADR43749 standard; peptide; 11 AA.
 XX ADR43749;
 AC ADR43749;
 DT 04-NOV-2004 (first entry)
 XX
 DE Maximakinin 8-18 as a bradykinin agonist.
 XX
 KW bradykinin; Cardiovascular; Vasotropic; Hypotensive; Cytostatic;
 KW vascular stenosis; hypertension; tumour; cancer; Maximakinin.
 XX
 OS Unidentified.
 XX
 PN WO2004069857-A2.
 XX
 PD 19-AUG-2004.
 XX
 PF 06-FEB-2004; 2004WO-GB000470.
 XX
 PR 06-FEB-2003; 2003GB-00002623.
 XX
 PR 06-JUN-2003; 2003GB-00012992.
 XX
 PA (UUTE-) UUTECH LTD.
 XX
 PI Shaw C, Hirst D, Chen T, O'Rourke M, Rao P;
 XX
 DR WPI; 2004-604409/58.
 XX
 PT Bradykinin agonists comprising maximakinin and its fragments, useful for
 PT selectively stimulating arterial smooth muscle bradykinin receptors and
 PT for treating cardiovascular disease e.g. ischemic heart disease.
 XX
 PS Claim 7; SEQ ID NO 3; 67bp; English.
 XX
 CC The present invention relates to a bradykinin agonist, useful in the
 CC selective stimulation of arterial smooth muscle bradykinin receptors or
 CC treatment of cardiovascular disease comprises maximakinin, its analogue
 CC or fragment or their encoding nucleic acids. Maximakinin derivatives are
 CC used in the preparation of a medicament for selectively stimulating
 CC arterial smooth muscle bradykinin receptors; for treating cardiovascular
 CC disease (claimed) e.g. ischemic heart disease, ischemic disease of other
 CC organs or organ systems, vascular stenosis, occlusion to peripheral
 CC vessels (such as limb), hypertension; and on the treatment of a condition
 CC or disorder that can be ameliorated with the selective bradykinin
 CC receptor agonist. Also useful for treatment of a condition for which
 CC dilation of vessels is required e.g. treatment of tumours and cancers,
 CC and for gene therapy. Maximakinin is a selective bradykinin receptor
 CC agonist and exhibits both tissue and receptor specific targeting. This
 CC tissue selectivity enables the use of the peptides in the treatment of
 CC diseases of the cardiovascular system while minimizing the side effects
 CC associated with the use of less selective agents. The present sequence
 CC represents a maximakinin derivative as a bradykinin agonist

SQ Sequence 11 AA;
 Query Match 32.4%; Score 34; DB 8; Length 11;
 Best Local Similarity 75.0%; Pred. No. 2.6e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 4 KGMSPPGF 11
 DB 1 KGPRPPGF 8
 RESULT 15
 ID ADR43750 standard; peptide; 12 AA.
 XX ADR43750
 AC ADR43750;
 DT 04-NOV-2004 (first entry)
 XX
 DE Maximakinin 8-19 as a bradykinin agonist.
 XX
 KW bradykinin; Cardiovascular; Vasotropic; Hypotensive; Cytostatic;
 KW vascular stenosis; hypertension; tumour; cancer; Maximakinin.
 XX
 OS Unidentified.
 XX
 PN WO2004069857-A2.
 XX
 PD 19-AUG-2004.
 XX
 PF 06-FEB-2004; 2004WO-GB000470.
 XX
 PR 06-FEB-2003; 2003GB-00002623.
 XX
 PR 06-JUN-2003; 2003GB-00012992.
 XX
 PA (UUTE-) UUTECH LTD.
 XX
 PI Shaw C, Hirst D, Chen T, O'Rourke M, Rao P;
 XX
 DR WPI; 2004-604409/58.
 XX
 PT Bradykinin agonists comprising maximakinin and its fragments, useful for
 PT selectively stimulating arterial smooth muscle bradykinin receptors and
 PT for treating cardiovascular disease e.g. ischemic heart disease.
 XX
 PS Claim 7; SEQ ID NO 4; 67bp; English.
 XX
 CC The present invention relates to a bradykinin agonist, useful in the
 CC selective stimulation of arterial smooth muscle bradykinin receptors or
 CC treatment of cardiovascular disease comprises maximakinin, its analogue
 CC or fragment or their encoding nucleic acids. Maximakinin derivatives are
 CC used in the preparation of a medicament for selectively stimulating
 CC arterial smooth muscle bradykinin receptors; for treating cardiovascular
 CC disease (claimed) e.g. ischemic heart disease, ischemic disease of other
 CC organs or organ systems, vascular stenosis, occlusion to peripheral
 CC vessels (such as limb), hypertension; and on the treatment of a condition
 CC or disorder that can be ameliorated with the selective bradykinin
 CC receptor agonist. Also useful for treatment of a condition for which
 CC dilation of vessels is required e.g. treatment of tumours and cancers,
 CC and for gene therapy. Maximakinin is a selective bradykinin receptor
 CC agonist and exhibits both tissue and receptor specific targeting. This
 CC tissue selectivity enables the use of the peptides in the treatment of
 CC diseases of the cardiovascular system while minimizing the side effects
 CC associated with the use of less selective agents. The present sequence
 CC represents a maximakinin derivative as a bradykinin agonist
 SQ Sequence 12 AA;
 Query Match 32.4%; Score 34; DB 8; Length 12;
 Best Local Similarity 75.0%; Pred. No. 2.8e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 4 KGMSPPGF 11

Db 1 KGRPPGPF 8

RESULT 16
ID ADR43752 standard; peptide: 13 AA.

AC ADR43752;

DT 04-NOV-2004 (first entry)

XX Maximakinin 7-19 as a bradykinin agonist.

XX bradykinin; Cardiovascular; Vasotropic; Hypotensive; Cytostatic;
KM vascular stenosis; hypertension; tumour; cancer; Maximakinin.

OS Unidentified.

XX WO2004069857-A2.

XX 19-AUG-2004.

XX 06-FEB-2004; 2004WO-GB000470.

XX 06-FEB-2003; 2003GB-00002623.

XX 06-JUN-2003; 2003GB-00012992.

XX (UUTE-) UUTECH LTD.

PI Shaw C, Hirst D, Chen T, O'Rourke M, Rao P;

DR WPI; 2004-604409/58.

PT Bradykinin agonists comprising maximakinin and its fragments, useful for
selectively stimulating arterial smooth muscle bradykinin receptors and
for treating cardiovascular disease e.g. ischemic heart disease.

XX Claim 7; SEQ ID NO 6; 67pp; English.

CC The present invention relates to a bradykinin agonist, useful in the
selective stimulation of arterial smooth muscle bradykinin receptors or
treatment of cardiovascular disease comprises maximakinin, its analogue
or fragment or their encoding nucleic acids. Maximakinin derivatives are
used in the preparation of a medicament for selectively stimulating
arterial smooth muscle bradykinin receptors; for treating cardiovascular
disease (claimed) e.g. ischemic heart disease, ischemic disease of other
organs or organ systems, vascular stenosis, occlusion to peripheral
vessels (such as limb), hypertension; and on the treatment of a condition
or disorder that can be ameliorated with the selective bradykinin
receptor agonist. Also useful for treatment of a condition for which
dilation of vessels is required e.g. treatment of tumours and cancers,
and for gene therapy. Maximakinin is a selective bradykinin receptor
agonist and exhibits both tissue and receptor specific targeting. This
tissue selectivity enables the use of the peptides in the treatment of
diseases of the cardiovascular system while minimizing the side effects
associated with the use of less selective agents. The present sequence
represents a maximakinin derivative as a bradykinin agonist

XX Sequence 13 AA;

Query Match 32.4%; Score 34; DB 8; Length 13;
Best Local Similarity 75.0%; Pred. No. 3.1e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 KGMSPGPF 11

Db 2 KGRPPGPF 9

RESULT 17
ID ABR48137 standard; peptide: 18 AA.

XX ABR48137;

AC 23-AUG-2002 (first entry)

DT GHR binding H5 peptide secondary library sequence #13.

XX Growth hormone; receptor; osteopathic; endocrine; hormonal; dwarfism;
KM acromegaly; animal husbandry; milk production; GHR.

OS Synthetic.

XX US6387879-B1.

XX 14-MAY-2002.

XX 15-DEC-1997; 97US-00990888.

XX 15-DEC-1997; 97US-00990888.

XX (DGIB-) DGI BIOTECHNOLOGIES INC.

PI Blume AJ, Brissette R, Carcamo J, Manddecki WS, Tang PM;

DR WPI; 2002-478462/51.

PT New amino acid sequences fully defined in the specification mimic growth
hormones and are useful to treat conditions such as dwarfism and
acromegaly, and to promote growth and milk production in cows.

XX Claim 1; Fig 15A; 46pp; English.

CC The invention relates to novel amino acid sequences which bind
specifically to growth hormone receptor (GHR). The peptides of the
invention have osteopathic, endocrine; and hormonal activity. The amino
acid sequences are useful to treat dwarfism and acromegaly, and in animal
husbandry to promote growth and milk production in cows. The sequence
represents a growth hormone receptor binding peptide of the invention

XX Sequence 18 AA;

Query Match 32.4%; Score 34; DB 5; Length 18;
Best Local Similarity 60.0%; Pred. No. 4.4e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 5 GMSPPGPIV 14

Db 6 GVSYPGLVVG 15

RESULT 18
ID ADR43748 standard; peptide: 18 AA.

AC ADR43748;

DT 04-NOV-2004 (first entry)

XX Maximakinin 1-18 as a bradykinin agonist.

XX bradykinin; Cardiovascular; Vasotropic; Hypotensive; Cytostatic;
KM vascular stenosis; hypertension; tumour; cancer; Maximakinin.

OS Unidentified.

XX WO2004069857-A2.

XX 19-AUG-2004.

XX 06-FEB-2004; 2004WO-GB000470.

XX 06-FEB-2003; 2003GB-00002623.

XX 06-JUN-2003; 2003GB-00012992.

XX (UUTE-) UUTECH LTD.
XX
XX Shaw C, Hirst D, Chen T, O'Rourke M, Rao P;
XX WPI; 2004-604409/58.
XX
XX Bradykinin agonists comprising maximakinin and its fragments, useful for
PT selectively stimulating arterial smooth muscle bradykinin receptors and
PT for treating cardiovascular disease e.g. ischemic heart disease.
XX
XX Claim 7; SEQ ID NO 2; 67pp; English.
XX
XX The present invention relates to a bradykinin agonist, useful in the
CC selective stimulation of arterial smooth muscle bradykinin receptors or
CC treatment of cardiovascular disease comprises maximakinin, its analogue
CC or fragment or their encoding nucleic acids. Maximakinin derivatives are
CC used in the preparation of a medicament for selectively stimulating
CC arterial smooth muscle bradykinin receptors, for treating cardiovascular
CC disease (claimed) e.g. ischemic heart disease, ischemic disease of other
CC organs or organ systems, vascular stenosis, occlusion to peripheral
CC vessels (such as limb), hypertension; and on the treatment of a condition
CC or disorder that can be ameliorated with the selective bradykinin
CC receptor agonist. Also useful for treatment of a condition for which
CC dilation of vessels is required e.g. treatment of tumours and cancers,
CC and for gene therapy. Maximakinin is a selective bradykinin receptor
CC agonist and exhibits both tissue and receptor specific targeting. This
CC tissue selectivity enables the use of the peptides in the treatment of
CC diseases of the cardiovascular system while minimizing the side effects
CC associated with the use of less selective agents. The present sequence
CC represents a maximakinin derivative as a bradykinin agonist
XX
XX Sequence 18 AA;
SQ

Query Match 32.4%; Score 34; DB 8; Length 18;
Best Local Similarity 75.0%; Pred. No. 4,4e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 KGMSPPGF 11
|||
|||
Db 8 KGPRPPGF 15

RESULT 19
ADN17072
ID ADN17072 standard; peptide; 19 AA.
XX
XX ADN17072;
AC
XX
XX 15-JUL-2004 (first entry)
DT
XX
XX Second generation G protein library g-alpha peptide, SEQ ID No 81.
DE
XX
XX G alpha subunit; G protein; G protein coupled receptor; GPCR;
KW
XX
XX allosteric modulator; g-alpha.
OS
XX
XX Unidentified.
XX
XX WO2004035614-A1.
PN
XX
XX 29-APR-2004.
PD
XX
XX 15-JAN-2003; 2003WO-BP000352.
PF
XX
XX 18-OCT-2002; 2002US-0419143P.
PR
XX
XX (KARO-) KARO BIO AB.
PA
XX
XX Fowlkes DM, Christensen DJ, Hamilton PT, Blasius R, Ramer JK;
PI Hyde-Derjyscher R, Duffin D, Fredericks Z,
XX
XX WPI; 2004-365151/34.
DR
XX

PT New synthetic or partially purified peptides that can bind to specific
PT subunits of G proteins, useful for detecting the activation or
PT deactivation of a G protein-coupled receptor (GPCR) or for identifying
PT allosteric modulators of GPCR.
XX
XX Example 300d; SEQ ID NO 81; 242pp; English.
XX

XX The invention relates to a novel non-naturally occurring and/or at least
CC partially purified peptide, which does not comprise a V-H or V-L homology
CC unit of an antibody and specifically binds to an activated G alpha
CC subunit of a G protein. The invention further comprises: an assay kit for
CC the identification of the activation state of a G protein coupled
CC receptor (GPCR), the kit comprising a first peptide cited above labeled
CC with a first label; methods of identifying the activation state of a GPCR
CC; a method of identifying a modulator of a GPCR; a method of determining
CC the presence or amount of a modulator of a GPCR in a sample; methods of
CC identifying a substance as an agonist or antagonist of GPCR; and a method
CC of identifying a G-alpha subunit which interacts with a GPCR. The
CC composition and methods are useful in detecting the activation or
CC deactivation of a G protein-coupled receptor or in monitoring the
CC activation state of a GPCR within a cell. These may also be used for
CC identifying allosteric modulators of GPCRs. This sequence represents a G
CC protein library g-alpha peptide oligo of the invention.
XX
XX Sequence 19 AA;
SQ

Query Match 32.4%; Score 34; DB 8; Length 19;
Best Local Similarity 72.7%; Pred. No. 4,4e+02;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 GFIVGEGVLS 20
|||||
|||
Db 8 GIWVGEGRLS 18

RESULT 20
ADR43747
ID ADR43747 standard; peptide; 19 AA.
XX

AC ADR43747;
XX

DT 04-NOV-2004 (first entry)
XX

DE Maximakinin 1-19 as a bradykinin agonist.
XX

KW bradykinin; Cardiovascular; Vasotropic; Hypotensive; Cytostatic;
XX

KW vascular stenosis; hypertension; tumour; cancer; Maximakinin.
XX

OS Unidentified.
XX

PN WO2004069857-A2.
XX

PD 19-AUG-2004.
XX

PF 06-FEB-2004; 2004WO-GB000470.
XX

PR 06-FEB-2003; 2003GB-00002623.
XX

PR 06-JUN-2003; 2003GB-00012992.
XX

PA (UUTE-) UUTECH LTD.
XX

PI Shaw C, Hirst D, Chen T, O'Rourke M, Rao P;
XX

DR WPI; 2004-604409/58.
XX

XX Bradykinin agonists comprising maximakinin and its fragments, useful for
PT selectively stimulating arterial smooth muscle bradykinin receptors and
PT for treating cardiovascular disease e.g. ischemic heart disease.
XX

PS Disclosure; SEQ ID NO 1; 67pp; English.
XX

XX The present invention relates to a bradykinin agonist, useful in the
CC selective stimulation of arterial smooth muscle bradykinin receptors or

```

CC extracellular product 30 kD protein. The vaccinating agents are used to
CC protect against (or to treat existing) infections by Mycobacterium
CC: (especially M. tuberculosis) while the epitopes can also be used to
CC detect presence of an immune response to a Mycobacterium pathogen. The
CC vectors, containing the DNA for the extracellular proteins, are used to
CC transform cells for production of recombinant DNA molecules. More
CC generally the DNA from other pathogens can be used in vaccines, e.g.
CC against other bacteria, viruses, fungi and protozoa. Since different
CC combinations of DNA can be used, a wide range of effective compositions
CC can be produced. They generate a response against the antigens most often
CC found on infected cells during the infection, regardless of the strength
CC or specificity of the immune response. The vaccines are easy to produce
CC and less toxic than known killed or attenuated vaccines, so can be given
CC to immunocompromised subjects, e.g. those with HIV infection
CC
XX
SQ Sequence 15 AA;
.
Query Match 31.4%; Score 33; DB 2; Length 15;
Best Local Similarity 62.5%; Pred. No. 5.1e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0.
.
Qy 1 DPAKGMSP 8
Db 4 DPQGMGMP 11
.
RESULT 22
AAW75617
ID AAW75617 standard; peptide; 15 AA.
AC AAW75617;
AD
AE
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ZW
ZX
ZY
ZZ

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XX ADF45168;
AC
XX 12-FEB-2004 (first entry)
XX
XX DT
XX
XX DE M. tuberculosis 30kDa extracellular protein fragment seq id 67.
XX
XX KW antibacterial; vaccine; immune response; extracellular product;
XX Mycobacterium; 30kD; extracellular protein.
XX
XX OS Mycobacterium tuberculosis.
XX
XX EN US2003152584-A1.
XX
XX PD 14-AUG-2003.
XX
XX PF 15-MAY-2002; 2002US-00147255.
XX
XX PR 23-NOV-1993; 93US-00156358.
XX 12-AUG-1994; 94US-00289667.
XX 23-MAY-1995; 95US-00447398.
XX 31-OCT-1995; 95US-00551149.
XX 23-MAY-1996; 96US-00652842.
XX 06-DEC-1996; 96US-00568357.
XX 21-SEP-1998; 98US-00157689.
XX 06-JAN-1999; 99US-00226539.
XX
XX PA (HORWITZ) HORWITZ M A.
XX
XX PI Horwitz MA;
XX
XX DR WPI; 2003-897688/82.
XX
XX PT Vaccinating agent useful for promoting an immune response in a mammalian
XX host against Mycobacterium, comprises an immunodominant epitope of a
XX PT majorly abundant extracellular product comprising an M. tuberculosis 30
XX PT kD protein.
XX
XX PS Claim 3; SEQ ID NO 67; 83pp; English.
XX
XX CC The invention describes a new vaccinating agent for promoting an immune
XX CC response in a mammalian host against Mycobacterium comprising at least
XX CC one immunodominant epitope of at least one majorly abundant extracellular
XX CC product comprising M. tuberculosis 110, 80, 71, 58, 45, 32A, 32B, 30, 24,
XX CC 23.5, 23, 16, 14 or 12 kD protein, or its analogue, homologue or subunit.
XX CC The bacterium is M. tuberculosis. The vaccinating agent is useful for
XX CC promoting an immune response in a mammalian host against Mycobacterium.
XX CC This is the amino acid sequence of a Mycobacterium tuberculosis 30kD
XX CC extracellular protein fragment that can be used to illicit and immune
XX CC response.
XX
XX SO Sequence 15 AA;

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Query Match 31.4%; Score 33; DB 7; Length 15;
Best Local Similarity 62.5%; Pred. No. 5.1e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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QY 1 DPAKGMSP 8
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Db 4 DPGQGMGP 11

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Search completed: January 26, 2006, 07:58:12
 Job time : 70.931 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 26, 2006, 07:50:06 ; Search time 18.7931 Seconds
(without alignments)
87.985 Million cell updates/sec

Title: US-09-662-293-13

Perfect score: 105

Sequence: 1 DPAKMSPPGRTVGEGLVS 20

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 229350

Minimum DB seq length: 0

Maximum DB seq length: 21

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

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6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	105	100.0	20	2	US-09-293-225-4
2	105	100.0	20	2	US-09-293-225-13
3	35	33.3	21	2	US-09-270-767-58368
4	34	32.4	8	2	US-08-475-955-116
5	34	32.4	8	2	US-07-867-819D-116
6	34	32.4	9	2	US-08-475-955-100
7	34	32.4	9	2	US-07-867-819D-100
8	34	32.4	18	2	US-08-990-888-28
9	33	31.4	15	2	US-09-157-689-67
10	33	31.4	15	2	US-09-953-510-67
11	33	31.4	20	2	US-09-667-857-397
12	33	31.4	20	2	US-10-198-053-397
13	33	31.4	20	2	US-10-198-053-603
14	33	31.4	20	2	US-09-827-271-397
15	33	29.5	16	1	US-08-483-142-185
16	31	29.5	16	1	US-08-478-572-185
17	31	29.5	18	2	US-08-484-286-185
18	31	29.5	18	2	US-08-990-888-36
19	31	29.5	18	2	US-09-570-022-13
20	31	29.5	20	2	US-09-635-501-29
21	31	29.5	20	2	US-10-007-700-463
22	30	28.6	8	2	US-08-475-955-12
23	30	28.6	8	2	US-08-475-955-205
24	30	28.6	8	2	US-08-475-955-206
25	30	28.6	8	2	US-07-867-819D-112
26	30	28.6	8	2	US-07-867-819D-112
27	30	28.6	8	2	US-07-867-819D-113

28	30	28.6	10	2	US-08-476-509B-32	Sequence 32, App1
29	30	28.6	10	2	US-08-476-509B-35	Sequence 35, App1
30	30	28.6	10	2	US-08-988-242-11	Sequence 11, App1
31	30	28.6	11	1	US-08-526-764-1	Sequence 1, App1
32	30	28.6	12	2	US-08-988-242-10	Sequence 10, App1
33	30	28.6	12	2	US-07-867-819D-14	Sequence 14, App1
34	30	28.6	14	2	US-08-630-916A-53	Sequence 53, App1
35	30	28.6	14	2	US-08-630-916A-54	Sequence 54, App1
36	30	28.6	14	2	US-09-509-355B-20	Sequence 20, App1
37	30	28.6	18	2	US-08-990-888-55	Sequence 25, App1
38	30	28.6	18	2	US-08-990-888-55	Sequence 65, App1
39	30	28.6	19	2	US-09-010-999-9	Sequence 9, App1
40	30	28.6	19	2	US-09-470-830A-27	Sequence 27, App1
41	30	28.6	20	2	US-08-928-213B-128	Sequence 128, App
42	30	28.6	20	2	US-08-928-213B-129	Sequence 129, App
43	30	28.6	21	1	US-08-325-071-16	Sequence 16, App1
44	30	28.6	21	1	US-08-325-071-32	Sequence 32, App1
45	30	28.6	21	2	US-08-461-004A-16	Sequence 16, App1
46	30	28.6	21	2	US-08-461-004A-32	Sequence 32, App1
47	29.5	28.1	14	1	US-07-721-761A-17	Sequence 17, App1
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50	29.5	28.1	17	1	US-07-721-761A-10	Sequence 10, App1
51	29.5	28.1	17	1	US-07-978-687-10	Sequence 10, App1
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54	29	27.6	8	2	US-08-475-955-123	Sequence 123, App
55	29	27.6	8	2	US-09-718-693A-3	Sequence 3, App1
56	29	27.6	8	2	US-07-867-819D-147	Sequence 147, App
57	29	27.6	8	2	US-07-867-819D-149	Sequence 149, App
58	29	27.6	8	2	US-07-867-819D-157	Sequence 157, App
59	29	27.6	11	2	US-08-475-955-10	Sequence 10, App1
60	29	27.6	11	2	US-07-867-819D-10	Sequence 10, App1
61	29	27.6	12	2	US-08-475-955-14	Sequence 14, App1
62	29	27.6	16	1	US-07-994-469A-21	Sequence 21, App1
63	29	27.6	16	1	US-08-482-142-186	Sequence 186, App
64	29	27.6	16	1	US-08-478-572-186	Sequence 186, App
65	29	27.6	16	2	US-08-484-286-186	Sequence 186, App
66	29	27.6	18	2	US-08-990-888-46	Sequence 24, App1
67	29	27.6	18	2	US-08-990-888-46	Sequence 46, App1
68	29	27.6	18	2	US-08-990-888-52	Sequence 62, App1
69	29	27.6	19	2	US-09-010-999-8	Sequence 8, App1
70	29	27.6	20	2	US-09-980-177A-77	Sequence 77, App1
71	29	27.6	20	2	US-10-007-700-413	Sequence 413, App
72	29	27.6	21	1	US-08-325-071-31	Sequence 31, App1
73	29	27.6	21	2	US-08-461-004A-31	Sequence 31, App1
74	28.5	27.1	18	2	US-10-394-880-140	Sequence 140, App
75	28	26.7	5	1	US-08-488-470A-7	Sequence 7, App1
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78	28	26.7	5	2	US-08-383-766-3	Sequence 3, App1
79	28	26.7	5	2	US-09-151-467-15	Sequence 15, App1
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81	28	26.7	5	2	US-09-256-838-15	Sequence 15, App1
82	28	26.7	5	2	US-09-261-718-3	Sequence 3, App1
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84	28	26.7	8	2	US-08-475-955-117	Sequence 117, App
85	28	26.7	8	2	US-07-867-819D-117	Sequence 117, App
86	28	26.7	9	2	US-09-769-180-11	Sequence 11, App1
87	28	26.7	10	2	US-08-476-609B-30	Sequence 30, App1
88	28	26.7	11	2	US-08-915-498B-22	Sequence 22, App1
89	28	26.7	12	2	US-10-394-880-15	Sequence 15, App1
90	28	26.7	13	2	US-08-630-916A-6	Sequence 6, App1
91	28	26.7	14	2	US-08-630-916A-85	Sequence 85, App1
92	28	26.7	14	2	US-08-630-915A-141	Sequence 141, App
93	28	26.7	14	2	US-09-879-957-141	Sequence 141, App
94	28	26.7	15	6	5187078-4	Patent No. 5187078
95	28	26.7	18	2	US-08-630-916A-9	Sequence 9, App1
96	28	26.7	18	2	US-08-990-888-30	Sequence 30, App1
97	28	26.7	18	2	US-08-990-888-69	Sequence 69, App1
98	28	26.7	18	2	US-09-292-225-12	Sequence 12, App1
99	28	26.7	18	2	US-09-570-022-12	Sequence 12, App1
100	28	26.7	19	2	US-09-068-624-2	Sequence 2, App1

ALIGNMENTS

RESULT 1

US-09-292-225-4
; Sequence 4, Application US/09292225
; Patent No. 6455686
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/09/292,225
; CURRENT FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: 60/098,909
; EARLIER FILING DATE: 1998-09-02
; EARLIER APPLICATION NUMBER: 60/085,295
; EARLIER FILING DATE: 1998-05-13
; EARLIER APPLICATION NUMBER: 60/098,565
; EARLIER FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: 09/062,013
; EARLIER FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-09-292-225-4

Query Match 100.0%; Score 105; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DPAKMSPPGFIVEGVLS 20
Db 1 DPAKMSPPGFIVEGVLS 20

RESULT 2

US-09-292-225-13
; Sequence 13, Application US/09292225
; Patent No. 6455686
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/09/292,225
; CURRENT FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: 60/098,909
; EARLIER FILING DATE: 1998-09-02
; EARLIER APPLICATION NUMBER: 60/085,295
; EARLIER FILING DATE: 1998-05-13
; EARLIER APPLICATION NUMBER: 60/098,565
; EARLIER FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: 09/062,013
; EARLIER FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-09-292-225-13

Query Match 100.0%; Score 105; DB 2; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DPAKMSPPGFIVEGVLS 20
Db 1 DPAKMSPPGFIVEGVLS 20

RESULT 3

US-09-270-767-58368
; Sequence 58368, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 58368
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-58368

Query Match 33.3%; Score 35; DB 2; Length 21;
Best Local Similarity 54.5%; Pred. No. 49;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 6 MSPPGFVIGER 16
Db 11 IAPGGRFIDGE 21

RESULT 4

US-08-475-955-116
; Sequence 116, Application US/08475955
; Patent No. 6641813
; GENERAL INFORMATION:
; APPLICANT: Harley, John
; TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
; NUMBER OF SEQUENCES: 218
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center, 1250 West Peachtree Street
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,955
; FILING DATE: June 7, 1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/867,819
; FILING DATE: April 13, 1992
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/648,205
; FILING DATE: January 31, 1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/472,947
; FILING DATE: January 31, 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284

REFERENCE/DOCKET NUMBER: OMRf114CIP(2)DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-873-8794
TELEFAX: (404)-873-8795
INFORMATION FOR SEQ ID NO: 116:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-475-955-116

Query Match 32.4%; Score 34; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PAKGMSPP 9
Db 1 PAKGMRPP 8

RESULT 5
US-07-867-819D-116
Sequence 116, Application US/07867819D
Patent No. 6897287
GENERAL INFORMATION:
APPLICANT: Harley, John
FILE OF INVENTION: Methods and Reagents for Diagnosis of Autoantibodies
FILE REFERENCE: OMRf 114 CIP (2)
CURRENT APPLICATION NUMBER: US/07/867,819D
CURRENT FILING DATE: 1992-04-13
PRIOR APPLICATION NUMBER: 07/472,947
PRIOR FILING DATE: 1990-01-31
PRIOR APPLICATION NUMBER: 07/648,205
PRIOR FILING DATE: 1991-01-31
NUMBER OF SEQ ID NOS: 161
SOFTWARE: PatentIn version 3.1
SEQ ID NO 116
LENGTH: 8
TYPE: PRT
ORGANISM: homo sapien
US-07-867-819D-116

Query Match 32.4%; Score 34; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PAKGMSPP 9
Db 1 PAKGMRPP 8

RESULT 6
US-08-475-955-100
Sequence 100, Application US/084755955
Patent No. 6641813
GENERAL INFORMATION:
APPLICANT: Harley, John
FILE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
TITLE OF INVENTION: AUTOANTIBODIES
NUMBER OF SEQUENCES: 218
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patricia L. Pabst
STREET: 2800 One Atlantic Center, 1250 West Peachtree Street
CITY: Atlanta
STATE: GA
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,955
FILING DATE: June 7, 1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/867,819
FILING DATE: April 13, 1992
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/648,205
FILING DATE: January 31, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/472,947
FILING DATE: January 31, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patricia L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRf114CIP(2)DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-873-8794
TELEFAX: (404)-873-8795
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Binding-site
LOCATION: 1..8
US-08-475-955-100

Query Match 32.4%; Score 34; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PAKGMSPP 9
Db 2 PAKGMRPP 9

RESULT 7
US-07-867-819D-100
Sequence 100, Application US/07867819D
Patent No. 6897287
GENERAL INFORMATION:
APPLICANT: Harley, John
FILE OF INVENTION: Methods and Reagents for Diagnosis of Autoantibodies
FILE REFERENCE: OMRf 114 CIP (2)
CURRENT APPLICATION NUMBER: US/07/867,819D
CURRENT FILING DATE: 1992-04-13
PRIOR APPLICATION NUMBER: 07/472,947
PRIOR FILING DATE: 1990-01-31
PRIOR APPLICATION NUMBER: 07/648,205
PRIOR FILING DATE: 1991-01-31
NUMBER OF SEQ ID NOS: 161
SOFTWARE: PatentIn version 3.1
SEQ ID NO 100
LENGTH: 9
TYPE: PRT
ORGANISM: homo sapien
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (1)-(8)
OTHER INFORMATION: Binding site
US-07-867-819D-100

Query Match 32.4%; Score 34; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 PAKGMSP 9
Db 2 PAKGMSP 9

RESULT 8

US-08-990-888-28
Sequence 28, Application US/08990888B
Patent No. 6387879
GENERAL INFORMATION:
APPLICANT: Blume, Arthur J.
APPLICANT: Bissette, Renee
APPLICANT: Carcamo, Juan
APPLICANT: Mandeck, Mlodeck S.
APPLICANT: Tang, Pauline M.
TITLE OF INVENTION: Assays For Compounds Which Bind Growth Hormone Receptor
FILE REFERENCE: 2598-4002
CURRENT APPLICATION NUMBER: US/08/990,888B
CURRENT FILING DATE: 1997-12-15
NUMBER OF SEQ ID NOS: 81
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 28
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: H5 peptide secondary library sequence
US-08-990-888-28

Query Match 32.4%; Score 34; DB 2; Length 18;
Best Local Similarity 60.0%; Pred. No. 60;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 5 GMSPPGTVG 14
Db 6 GVSYPGWLVG 15

RESULT 9

US-09-157-689-67
Sequence 67, Application US/09157689
Patent No. 6599510
GENERAL INFORMATION:
APPLICANT: Horwitz, Marcus A.
APPLICANT: Harth, Gunter
TITLE OF INVENTION: Abundant Extracellular Products and
TITLE OF INVENTION: Methods for Their Production and Use
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kurt A. Maclean
STREET: 2029 Century Park East, Suite 3800
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/157,689
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/568,357
FILING DATE: 06-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/551,149
FILING DATE: 31-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/447,398
FILING DATE: 23-MAY-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/289,667
FILING DATE: 12-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/156,358
FILING DATE: 23-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Maclean, Kurt A.
REGISTRATION NUMBER: 31,118
TELECOMMUNICATION INFORMATION:
TELEPHONE: (310) 788-5000
TELEFAX: (310) 277-1297
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS:
MOLECULE TYPE: linear
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Mycobacterium tuberculosis
STRAIN: Erdman
US-09-157-689-67

Query Match 31.4%; Score 33; DB 2; Length 15;
Best Local Similarity 62.5%; Pred. No. 71;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 DPAKMGSP 8
Db 4 DPGQMGSP 11

RESULT 10

US-09-953-510-67
Sequence 67, Application US/09953510
Patent No. 6818223
GENERAL INFORMATION:
APPLICANT: Horwitz, Marcus A.
TITLE OF INVENTION: Products and Methods for Their Production and Use
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kurt A. Maclean
STREET: 2029 Century Park East, Suite 3800
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/953,510
FILING DATE: 14-Sep-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/447,398
FILING DATE: 23-MAY-1995
APPLICATION NUMBER: US 08/289,667
FILING DATE: 12-AUG-1994
APPLICATION NUMBER: US 08/156,358
FILING DATE: 23-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Maclean, Kurt A.
REGISTRATION NUMBER: 31,118

```
REFERENCE/DOCKET NUMBER: 112-272
TELECOMMUNICATION INFORMATION:
TELEPHONE: (310) 788-5000
TELEFAX: (310) 277-1997
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Mycobacterium tuberculosis
STRAIN: Erdman
SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-09-353-510-67

Query Match      31.4%; Score 33; DB 2; Length 15;
Best Local Similarity 62.5%; Pred. No. 71;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 DPAKMSP 8
Db      4 DPGQMGP 11

RESULT 11
US-09-667-857-397
Sequence 397, Application US/09667857
Patent No. 6699864
GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary Richard
APPLICANT: Reed, Steven G.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darick
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C5
CURRENT APPLICATION NUMBER: US/09/667,857
CURRENT FILING DATE: 2000-09-20
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 397
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens
US-09-667-857-397

Query Match      31.4%; Score 33; DB 2; Length 20;
Best Local Similarity 62.5%; Pred. No. 99;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      13 VGEQGVLS 20
Db      3 IGEDGILS 10

RESULT 12
US-10-198-053-397
Sequence 397, Application US/10198053
Patent No. 6858710
GENERAL INFORMATION:
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary R.
```

```
APPLICANT: Hill, Paul
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C9
CURRENT APPLICATION NUMBER: US/10/198,053
CURRENT FILING DATE: 2002-07-17
NUMBER OF SEQ ID NOS: 624
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 397
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens
US-10-198-053-397

Query Match      31.4%; Score 33; DB 2; Length 20;
Best Local Similarity 62.5%; Pred. No. 99;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      13 VGEQGVLS 20
Db      3 IGEDGILS 10

RESULT 13
US-10-198-053-603
Sequence 603, Application US/10198053
Patent No. 6858710
GENERAL INFORMATION:
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary R.
APPLICANT: Hill, Paul
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C9
CURRENT APPLICATION NUMBER: US/10/198,053
CURRENT FILING DATE: 2002-07-17
NUMBER OF SEQ ID NOS: 624
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 603
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens
US-10-198-053-603

Query Match      31.4%; Score 33; DB 2; Length 20;
Best Local Similarity 62.5%; Pred. No. 99;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      13 VGEQGVLS 20
Db      3 IGEDGILS 10

RESULT 14
US-09-827-271-397
Sequence 397, Application US/09827271
Patent No. 6962980
GENERAL INFORMATION:
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C6
CURRENT APPLICATION NUMBER: US/09/827,271
CURRENT FILING DATE: 2001-04-04
NUMBER OF SEQ ID NOS: 461
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 397
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens
US-09-827-271-397
```

Query Match 31.4%; Score 33; DB 2; Length 20;
Best Local Similarity 62.5%; Pred. No. 99;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 13 VGESEGVLS 20
:|:|:|:
Db 3 IGEDGILS 10

RESULT 15

US-08-482-142-185
; Sequence 185, Application US/08482142
; Patent No. 5820862

GENERAL INFORMATION:

APPLICANT: Garman, Richard
APPLICANT: Greenstein, Julia

APPLICANT: Kuo, Mei-chang
APPLICANT: Rogers, Bruce

APPLICANT: Franzen, Henry
APPLICANT: Chen, Xian

APPLICANT: Evans, Sean
APPLICANT: Shaked, Ze'ev

TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS
FROM DERMATOPHAGOIDES (HOUSE DUST MITE)

NUMBER OF SEQUENCES: 207
CORRESPONDENCE ADDRESS:

ADDRESSEE: IMMUNOLOGIC PHARMACEUTICAL CORPORATION
STREET: 610 LINCOLN STREET

CITY: WALTHAM
STATE: MA

COUNTRY: USA
ZIP: 02154

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/482,142
FILING DATE: 07-JUN-1995

CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/445,307
FILING DATE: 07 June 1995

ATTORNEY/AGENT INFORMATION:
NAME: CRAIG, ANNE I.

REGISTRATION NUMBER: 32,976
REFERENCE/DOCKET NUMBER: 017.6US

TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 466-6000

TELEFAX: (617) 466-6040
INFORMATION FOR SEQ ID NO: 185:

SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids

TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: peptide
FRAGMENT TYPE: internal

US-08-482-142-185

Query Match 29.5%; Score 31; DB 1; Length 16;
Best Local Similarity 55.6%; Pred. No. 1.6e+02;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 12 IVGSEGVLS 20
:|:|:|:
Db 6 LVGDDGVLA 14

RESULT 16

US-08-478-572-185
; Sequence 185, Application US/08478572

Patent No. 5968526

GENERAL INFORMATION:
APPLICANT: Garman, Richard

APPLICANT: Greenstein, Julia
APPLICANT: Kuo, Mei-chang

APPLICANT: Rogers, Bruce
APPLICANT: Franzen, Henry

APPLICANT: Chen, Xian
APPLICANT: Evans, Sean

APPLICANT: Shaked, Ze'ev
TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS

FROM DERMATOPHAGOIDES (HOUSE DUST MITE)

NUMBER OF SEQUENCES: 207
CORRESPONDENCE ADDRESS:

ADDRESSEE: IMMUNOLOGIC PHARMACEUTICAL CORPORATION
STREET: 610 LINCOLN STREET

CITY: WALTHAM
STATE: MA

COUNTRY: USA
ZIP: 02154

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/478,572
FILING DATE: 07-June-1995

CLASSIFICATION:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/445,307
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: CRAIG, ANNE I.

REGISTRATION NUMBER: 32,976
REFERENCE/DOCKET NUMBER: 017.6US

TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 466-6000

TELEFAX: (617) 466-6040
INFORMATION FOR SEQ ID NO: 185:

SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids

TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: peptide
FRAGMENT TYPE: internal

US-08-478-572-185

Query Match 29.5%; Score 31; DB 1; Length 16;
Best Local Similarity 55.6%; Pred. No. 1.6e+02;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 12 IVGSEGVLS 20
:|:|:|:
Db 6 LVGDDGVLA 14

RESULT 17

US-08-484-296-185
; Sequence 185, Application US/08484296
; Patent No. 6268491

GENERAL INFORMATION:
APPLICANT: Garman, Richard

APPLICANT: Greenstein, Julia
APPLICANT: Kuo, Mei-chang

APPLICANT: Rogers, Bruce
APPLICANT: Franzen, Henry

APPLICANT: Chen, Xian
APPLICANT: Evans, Sean

APPLICANT: Shaked, Ze'ev
TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS

FROM DERMATOPHAGOIDES (HOUSE DUST MITE)

NUMBER OF SEQUENCES: 207

CORRESPONDENCE ADDRESS:
 ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
 STREET: 610 LINCOLN STREET
 CITY: WALTHAM
 STATE: MA
 COUNTRY: USA
 ZIP: 02154
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII TEXT
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/484,296
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/445,307
 FILING DATE: 07 June 1995
 ATTORNEY/AGENT INFORMATION:
 NAME: CRAIG, ANNE I.
 REGISTRATION NUMBER: 32,976
 REFERENCE/DOCKET NUMBER: 017.6US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 466-6000
 TELEFAX: (617) 466-6040
 INFORMATION FOR SEQ ID NO: 185:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 16 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FRAGMENT TYPE: internal
 US-08-484-296-185

Query Match 29.5%; Score 31; DB 2; Length 16;
 Best Local Similarity 55.6%; Pred. No. 1.9e+02;
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 12 IVEEGVLS 20
 DB 6 LVGDGVLA 14

RESULT 18
 US-08-990-888-36
 Sequence 36, Application US/08990888B
 Patent No. 6387879
 GENERAL INFORMATION:
 APPLICANT: Blume, Arthur J.
 APPLICANT: Brissette, Renee
 APPLICANT: Carcamo, Juan
 APPLICANT: Mandeck, Wlodek S.
 APPLICANT: Tang, Pauline M.
 TITLE OF INVENTION: Assays For Compounds Which Bind Growth Hormone Receptor
 FILE REFERENCE: 2598-4002
 CURRENT APPLICATION NUMBER: US/08/990,888B
 CURRENT FILING DATE: 1997-12-15
 NUMBER OF SEQ ID NOS: 81
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 36
 LENGTH: 18
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: H5 peptide secondary library sequence
 US-08-990-888-36

Query Match 29.5%; Score 31; DB 2; Length 18;
 Best Local Similarity 50.0%; Pred. No. 1.9e+02;
 Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 5 GMSPPGIVG 14

DB 6 GVTYFGWLIVG 15

RESULT 19
 US-09-570-022-13
 Sequence 13, Application US/09570022
 Patent No. 6573244
 GENERAL INFORMATION:
 APPLICANT: GORDON, RICHARD K.
 APPLICANT: MOORAD, DEBORAH R.
 APPLICANT: DOCTOR, BHUPENDRA P.
 APPLICANT: GARCIA, GREGORY E.
 TITLE OF INVENTION: PREVINS AS SPECIFIC INHIBITORS AND THERAPEUTIC AGENTS
 FILE REFERENCE: 38644-170531
 CURRENT APPLICATION NUMBER: US/09/570,022
 CURRENT FILING DATE: 2000-05-12
 PRIOR APPLICATION NUMBER: 60/134,446
 PRIOR FILING DATE: 1999-05-17
 NUMBER OF SEQ ID NOS: 26
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 13
 LENGTH: 18
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 US-09-570-022-13

Query Match 29.5%; Score 31; DB 2; Length 18;
 Best Local Similarity 54.5%; Pred. No. 1.9e+02;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 AKGMSPPGIV 13
 DB 5 AKGLQFGLMV 15

RESULT 20
 US-09-635-501-29
 Sequence 29, Application US/09635501
 Patent No. 6884771
 GENERAL INFORMATION:
 APPLICANT: Accon, Susan L. et al.
 TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOGY AND THERAPEUTIC
 FILE REFERENCE: MNI-132CP3
 CURRENT APPLICATION NUMBER: US/09/635,501
 CURRENT FILING DATE: 2000-08-09
 PRIOR APPLICATION NUMBER: 09/407,427
 PRIOR FILING DATE: 1999-09-29
 PRIOR APPLICATION NUMBER: 09/163,648
 PRIOR FILING DATE: 1998-09-30
 PRIOR APPLICATION NUMBER: 08/989,299
 PRIOR FILING DATE: 1997-12-11
 NUMBER OF SEQ ID NOS: 107
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 29
 LENGTH: 18
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: motifs
 US-09-635-501-29

Query Match 29.5%; Score 31; DB 2; Length 18;
 Best Local Similarity 54.5%; Pred. No. 1.9e+02;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DPAKMSPPGF 11

Db 1 DISKENNPGF 11

RESULT 21

US-10-007-700-463

Sequence 463, Application US/10007700

Patent No. 6960570

GENERAL INFORMATION:

APPLICANT: Wang, Tongfong

APPLICANT: Wang, Aijun

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Li, Samuel X.

APPLICANT: Kalos, Michael D.

APPLICANT: Henderson, Robert A.

APPLICANT: McNeill, Patricia D.

APPLICANT: Fanger, Neil

APPLICANT: Retter, Marc W.

APPLICANT: Durham, Margalita

APPLICANT: Fanger, Gary R.

APPLICANT: Vedvick, Thomas S.

APPLICANT: Carter, Derrick

APPLICANT: Matanabe, Yoshihiro

APPLICANT: Peckman, David W.

APPLICANT: Cai, Feng

APPLICANT: Foy, Teresa M.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.455C17

CURRENT APPLICATION NUMBER: US/10/007,700

CURRENT FILING DATE: 2001-11-30

NUMBER OF SEQ ID NOS: 469

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 463

LENGTH: 20

TYPE: PRT

ORGANISM: Homo sapiens

US-10-007-700-463

Query Match 29.5%; Score 31; DB 2; Length 20;

Best Local Similarity 62.5%; Pred. No. 2.1e+02;

Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 PAKGMSPP 9

Db 9 PTSGMPP 16

RESULT 22

US-08-475-955-12

Sequence 12, Application US/08475955

Patent No. 6641813

GENERAL INFORMATION:

APPLICANT: Harley, John

TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF

TITLE OF INVENTION: AUTOANTIBODIES

NUMBER OF SEQUENCES: 218

CORRESPONDENCE ADDRESS:

ADDRESSEE: Patrea L. Pabst

STREET: 2800 One Atlantic Center, 1250 West Peachtree Street

CITY: Atlanta

STATE: GA

COUNTRY: USA

ZIP: 30309-3450

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/475,955

FILING DATE: June 7, 1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/867,819

FILING DATE: April 13, 1992

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/648,205

FILING DATE: January 31, 1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/472,947

FILING DATE: January 31, 1990

ATTORNEY/AGENT INFORMATION:

NAME: Pabst, Patrea L.

REGISTRATION NUMBER: 31,284

REFERENCE/DOCKET NUMBER: OMR114CIP(2)DIV

TELECOMMUNICATION INFORMATION:

TELEPHONE: (404)-873-8794

TELEFAX: (404)-873-8795

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: Binding-site

LOCATION: 1..8

US-08-475-955-12

Query Match 28.6%; Score 30; DB 2; Length 8;

Best Local Similarity 83.3%; Pred. No. 4.6e+05;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GMSPPG 10

Db 3 GMPPPG 8

RESULT 23

US-08-475-955-205

Sequence 205, Application US/08475955

Patent No. 6641813

GENERAL INFORMATION:

APPLICANT: Harley, John

TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF

TITLE OF INVENTION: AUTOANTIBODIES

NUMBER OF SEQUENCES: 218

CORRESPONDENCE ADDRESS:

ADDRESSEE: Patrea L. Pabst

STREET: 2800 One Atlantic Center, 1250 West Peachtree Street

CITY: Atlanta

STATE: GA

COUNTRY: USA

ZIP: 30309-3450

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/475,955

FILING DATE: June 7, 1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/867,819

FILING DATE: April 13, 1992

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/648,205

FILING DATE: January 31, 1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/472,947

FILING DATE: January 31, 1990

ATTORNEY/AGENT INFORMATION:

NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRP114CIP(2)DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-873-8794
TELEFAX: (404)-873-8795
INFORMATION FOR SEQ ID NO: 205:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-475-955-205

Query Match
Best Local Similarity 83.3%; Score 30; DB 2; Length 8;
Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GMSPPG 10
DB 2 GMPPEPG 7

RESULT 24
US-08-475-955-206
Sequence 206, Application US/08475955
Patent No. 6641813
GENERAL INFORMATION:
APPLICANT: Harley, John
TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
TITLE OF INVENTION: AUTOANTIBODIES
NUMBER OF SEQUENCES: 218
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center, 1250 West Peachtree Street
CITY: Atlanta
STATE: GA
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,955
FILING DATE: June 7, 1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/867,819
FILING DATE: April 13, 1992
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/648,205
FILING DATE: January 31, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/472,947
FILING DATE: January 31, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRP114CIP(2)DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-873-8794
TELEFAX: (404)-873-8795
INFORMATION FOR SEQ ID NO: 206:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-475-955-206

Query Match
Best Local Similarity 83.3%; Score 30; DB 2; Length 8;
Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GMSPPG 10
DB 1 GMPPEPG 6

RESULT 25
US-07-867-819D-12
Sequence 12, Application US/07867819D
Patent No. 6897287
GENERAL INFORMATION:
APPLICANT: Harley, John
TITLE OF INVENTION: Methods and Reagents for Diagnosis of Autoantibodies
FILE REFERENCE: OMRP 114 CIP (2)
CURRENT APPLICATION NUMBER: US/07/867,819D
CURRENT FILING DATE: 1992-04-13
PRIOR APPLICATION NUMBER: 07/472,947
PRIOR FILING DATE: 1990-01-31
PRIOR APPLICATION NUMBER: 07/648,205
PRIOR FILING DATE: 1991-01-31
NUMBER OF SEQ ID NOS: 161
SOFTWARE: Patentin Version 3.1
SEQ ID NO 12
LENGTH: 8
TYPE: PRT
ORGANISM: homo sapien
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (1)..(8)
OTHER INFORMATION: Binding site
US-07-867-819D-12

Query Match
Best Local Similarity 83.3%; Score 30; DB 2; Length 8;
Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GMSPPG 10
DB 3 GMPPEPG 8

Search completed: January 26, 2006, 08:07:04
Job time : 19.9598 secs

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OM protein - protein search, using sw model

Run on: January 26, 2006, 08:04:12 : Search time 65 Seconds
(without alignments)
128.563 Million cell updates/sec

Title: US-09-662-293-13
Perfect score: 105
Sequence: 1 DPAKGMPPGFIVCEGVLS 20

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues
Total number of hits satisfying chosen parameters: 369445

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published Applications_AA_Main:*
1: /cgn2_6/ptodata/1/pubppaa/US07_PUBSCOMB.pep:*
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3: /cgn2_6/ptodata/1/pubppaa/US09_PUBSCOMB.pep:*
4: /cgn2_6/ptodata/1/pubppaa/US10A_PUBSCOMB.pep:*
5: /cgn2_6/ptodata/1/pubppaa/US10B_PUBSCOMB.pep:*
6: /cgn2_6/ptodata/1/pubppaa/US11_PUBSCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	105	100.0	20	4	US-10-218-743-4
2	105	100.0	20	4	US-10-218-743-13
3	35	33.3	20	4	US-10-280-066-302
4	34	32.4	8	4	US-10-012-756-6
5	34	32.4	8	4	US-10-376-121A-116
6	34	32.4	9	4	US-10-376-121A-100
7	33	31.4	15	3	US-09-953-510-67
8	33	31.4	15	3	US-09-953-413-67
9	33	31.4	15	4	US-10-147-255-67
10	33	31.4	15	5	US-10-655-155-67
11	33	31.4	20	3	US-08-884-441-397
12	33	31.4	20	3	US-09-907-969-397
13	33	31.4	20	3	US-09-827-271-397
14	33	31.4	20	4	US-10-198-053-397
15	33	31.4	20	4	US-10-198-053-603
16	33	31.4	20	5	US-10-860-790-397
17	33	31.4	20	5	US-10-860-790-603
18	33	31.4	20	5	US-10-661-156-146
19	32	30.5	15	4	US-10-328-916-58
20	32	30.5	16	3	US-09-838-785-26
21	32	30.5	16	5	US-10-953-901-593
22	32	30.5	20	5	US-10-661-156-170
23	31	29.5	14	4	US-10-307-956-35
24	31	29.5	15	4	US-10-211-088-356
25	31	29.5	17	5	US-10-950-163-8
26	31	29.5	18	3	US-09-999-781-10
27	31	29.5	18	5	US-10-854-646-13

28	31	29.5	18	6	US-11-059-218-29	Sequence 29, Appl
29	31	29.5	20	3	US-09-897-778-463	Sequence 463, App
30	31	29.5	20	4	US-10-007-700-463	Sequence 463, App
31	31	29.5	20	4	US-10-117-982-463	Sequence 463, App
32	31	29.5	20	4	US-10-313-986-463	Sequence 463, App
33	31	29.5	20	4	US-10-313-986-541	Sequence 541, App
34	31	29.5	20	5	US-10-775-972-463	Sequence 463, App
35	31	29.5	20	5	US-10-775-972-541	Sequence 541, App
36	31	29.5	20	5	US-10-922-124-463	Sequence 463, App
37	31	29.5	20	5	US-10-922-124-541	Sequence 541, App
38	31	29.5	21	3	US-09-945-825-13	Sequence 13, Appl
39	31	29.5	21	5	US-10-319-315-45	Sequence 45, Appl
40	31	29.5	21	5	US-10-895-359-13	Sequence 13, Appl
41	30	28.6	8	4	US-10-376-121A-12	Sequence 12, Appl
42	30	28.6	8	4	US-10-376-121A-123	Sequence 123, App
43	30	28.6	8	4	US-10-376-121A-205	Sequence 205, App
44	30	28.6	8	4	US-10-376-121A-206	Sequence 206, App
45	30	28.6	10	3	US-09-572-404B-272	Sequence 272, App
46	30	28.6	10	3	US-09-572-404B-274	Sequence 274, App
47	30	28.6	12	4	US-10-376-121A-14	Sequence 14, Appl
48	30	28.6	13	5	US-10-972-236A-27	Sequence 27, Appl
49	30	28.6	14	4	US-10-185-050-53	Sequence 53, Appl
50	30	28.6	14	4	US-10-185-050-54	Sequence 54, Appl
51	30	28.6	15	5	US-10-434-906-3	Sequence 3, Appl
52	30	28.6	15	5	US-10-972-236A-28	Sequence 28, Appl
53	30	28.6	16	4	US-10-285-194-376	Sequence 376, App
54	30	28.6	18	4	US-10-029-186-32096	Sequence 32096, App
55	30	28.6	18	5	US-10-862-195-907	Sequence 907, App
56	30	28.6	19	4	US-10-714-212-27	Sequence 27, Appl
57	29.5	28.1	14	4	US-10-307-956-24	Sequence 24, Appl
58	29	27.6	7	3	US-09-990-832C-57	Sequence 57, Appl
59	29	27.6	8	4	US-10-012-756-4	Sequence 4, Appl
60	29	27.6	8	5	US-10-646-132-3	Sequence 3, Appl
61	29	27.6	9	4	US-10-224-999A-2893	Sequence 2893, App
62	29	27.6	10	3	US-09-572-404B-1350	Sequence 1352, App
63	29	27.6	10	3	US-09-572-404B-1352	Sequence 1352, App
64	29	27.6	10	3	US-09-573-822C-684	Sequence 684, App
65	29	27.6	10	4	US-10-224-999A-2899	Sequence 2899, App
66	29	27.6	10	4	US-10-224-999A-2900	Sequence 2900, App
67	29	27.6	11	4	US-10-224-999A-2906	Sequence 2906, App
68	29	27.6	11	4	US-10-224-999A-2907	Sequence 2907, App
69	29	27.6	11	4	US-10-224-999A-2908	Sequence 2908, App
70	29	27.6	11	4	US-10-376-121A-10	Sequence 10, Appl
71	29	27.6	11	4	US-10-285-194-140	Sequence 140, App
72	29	27.6	12	4	US-10-286-457-50	Sequence 50, Appl
73	29	27.6	12	4	US-10-224-999A-2914	Sequence 2914, App
74	29	27.6	12	4	US-10-224-999A-2915	Sequence 2915, App
75	29	27.6	12	4	US-10-224-999A-2916	Sequence 2916, App
76	29	27.6	12	4	US-10-224-999A-2917	Sequence 2917, App
77	29	27.6	13	4	US-10-224-999A-2923	Sequence 2923, App
78	29	27.6	13	4	US-10-224-999A-2924	Sequence 2924, App
79	29	27.6	13	4	US-10-224-999A-2925	Sequence 2925, App
80	29	27.6	13	4	US-10-224-999A-2926	Sequence 2926, App
81	29	27.6	13	4	US-10-224-999A-2927	Sequence 2927, App
82	29	27.6	13	5	US-10-948-707-1350	Sequence 1350, App
83	29	27.6	14	4	US-10-224-999A-2933	Sequence 2933, App
84	29	27.6	14	4	US-10-224-999A-2934	Sequence 2934, App
85	29	27.6	14	4	US-10-224-999A-2935	Sequence 2935, App
86	29	27.6	14	4	US-10-224-999A-2936	Sequence 2936, App
87	29	27.6	14	4	US-10-224-999A-2937	Sequence 2937, App
88	29	27.6	14	4	US-10-224-999A-2938	Sequence 2938, App
89	29	27.6	14	4	US-10-149-240-12	Sequence 12, Appl
90	29	27.6	15	4	US-10-224-999A-2944	Sequence 2944, App
91	29	27.6	15	4	US-10-224-999A-2945	Sequence 2945, App
92	29	27.6	15	4	US-10-224-999A-2946	Sequence 2946, App
93	29	27.6	15	4	US-10-224-999A-2947	Sequence 2947, App
94	29	27.6	15	4	US-10-224-999A-2948	Sequence 2948, App
95	29	27.6	15	4	US-10-224-999A-2949	Sequence 2949, App
96	29	27.6	15	4	US-10-224-999A-2950	Sequence 2950, App
97	29	27.6	15	4	US-10-128-520-38	Sequence 38, Appl
98	29	27.6	16	4	US-10-225-567A-1513	Sequence 1513, Appl
99	29	27.6	16	4	US-10-224-999A-2956	Sequence 2956, App
100	29	27.6	16	4	US-10-224-999A-2957	Sequence 2957, App

ALIGNMENTS

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RESULT 1
US-10-218-743-4
; Sequence 4, Application US/10218743
; Publication No. US20030096779A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/10/218,743
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/292,225
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: 60/098,909
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/085,295
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/098,565
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: 09/062,013
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-10-218-743-4

Query Match          100.0%; Score 105; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1,1e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DPAKMSPPGFIVGEGVLS 20
        |||||
DB      1 DPAKMSPPGFIVGEGVLS 20

RESULT 2
US-10-218-743-13
; Sequence 13, Application US/10218743
; Publication No. US20030096779A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/10/218,743
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/292,225
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: 60/098,909
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/085,295
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/098,565
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: 09/062,013
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 20
; TYPE: PRT
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; ORGANISM: Dermatophagoides farinae
US-10-218-743-13

Query Match          100.0%; Score 105; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1,1e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DPAKMSPPGFIVGEGVLS 20
        |||||
DB      1 DPAKMSPPGFIVGEGVLS 20

RESULT 3
US-10-280-066-302
; Sequence 302, Application US/10280066
; Publication No. US20030180718A1
; GENERAL INFORMATION:
; APPLICANT: Pillutia, Renuka C.
; APPLICANT: Brissette, Renee
; APPLICANT: Spruyt, Michael
; APPLICANT: Degova, Olga
; APPLICANT: Blume, Arthur J.
; APPLICANT: Prendergast, John
; APPLICANT: Goldstein, Neil I.
; TITLE OF INVENTION: TARGET SPECIFIC SCREENING AND ITS USE FOR IDENTIFYING TARGET BIND
; FILE REFERENCE: 2598-4009US1
; CURRENT APPLICATION NUMBER: US/10/280,066
; PRIOR FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 60/345,471
; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 537
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 302
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Eschericia coli
; FEATURE:
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: DGIS-20M-4-E4
US-10-280-066-302

Query Match          33.3%; Score 35; DB 4; Length 20;
Best Local Similarity 53.3%; Pred. No. 3,7e+02;
Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY      5 GMSPPGFIVGEGVL 19
        |||||
DB      2 GRPPMGIVGERGGL 16

RESULT 4
US-10-012-756-6
; Sequence 6, Application US/10012756
; Publication No. US20020164355A1
; GENERAL INFORMATION:
; APPLICANT: John B. Harley and Judith A. James
; TITLE OF INVENTION: Diagnostics And Therapy Of Epstein-Barr
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30306-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/10/012,756
FILING DATE: 24-Oct-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/781,296
FILING DATE: 13-JAN-1997
APPLICATION NUMBER: 60/019,053
FILING DATE: 16-MAY-1996
APPLICATION NUMBER: 08/160,604
FILING DATE: 30-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRF161
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)873-8794
TELEFAX: (404)873-8795
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-012-756-6

Query Match 32.4%; Score 34; DB 4; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PAKMSPP 9
Db 1 PAPCMRPP 8

RESULT 5
US-10-376-121A-116
Sequence 116, Application US/10376121A
Publication No. US20030216544A1
GENERAL INFORMATION:
APPLICANT: Harley, John
TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
AUTOANTIBODIES
NUMBER OF SEQUENCES: 218
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: Suite 2000, 1201 West Peachtree Street, N.E.
CITY: Atlanta
STATE: GA
COUNTRY: USA
ZIP: 30309-3400
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/376,121A
FILING DATE: 27-Mar-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/867,819
FILING DATE: April 13, 1992
APPLICATION NUMBER: 07/648,205
FILING DATE: January 31, 1991
APPLICATION NUMBER: 07/472,947
FILING DATE: January 31, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284

REFERENCE/DOCKET NUMBER: OMRF114CIP(2)DIV(2)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-817-8473
TELEFAX: (404)-817-8588
INFORMATION FOR SEQ ID NO: 116:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 116:
US-10-376-121A-116

Query Match 32.4%; Score 34; DB 4; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PAKMSPP 9
Db 1 PAPCMRPP 8

RESULT 6
US-10-376-121A-100
Sequence 100, Application US/10376121A
Publication No. US20030216544A1
GENERAL INFORMATION:
APPLICANT: Harley, John
TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
AUTOANTIBODIES
NUMBER OF SEQUENCES: 218
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: Suite 2000, 1201 West Peachtree Street, N.E.
CITY: Atlanta
STATE: GA
COUNTRY: USA
ZIP: 30309-3400
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/376,121A
FILING DATE: 27-Mar-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/867,819
FILING DATE: April 13, 1992
APPLICATION NUMBER: 07/648,205
FILING DATE: January 31, 1991
APPLICATION NUMBER: 07/472,947
FILING DATE: January 31, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRF114CIP(2)DIV(2)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-817-8473
TELEFAX: (404)-817-8588
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Binding-site
LOCATION: 1..8
SEQUENCE DESCRIPTION: SEQ ID NO: 100:

US-10-376-121A-100

Query Match 32.4%; Score 34; DB 4; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PAKGMSP 9
2 PAKGMSP 9

DB 2 PAKGMSP 9

RESULT 7

US-09-953-510-67
Sequence 67, Application US/09953510
Patent No. US20020131975A1

GENERAL INFORMATION:

APPLICANT: Horwitz, Marcus A.

TITLE OF INVENTION: Abundant Extracellular

Products and Methods for Their Production and Use

NUMBER OF SEQUENCES: 91

CORRESPONDENCE ADDRESS:

ADDRESSEE: Kurt A. Maclean

STREET: 2029 Century Park East, Suite 3800

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90067

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0,

Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/953,510

FILING DATE: 14-Sep-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/447,398

FILING DATE: 23-MAY-1995

APPLICATION NUMBER: US 08/289,667

FILING DATE: 12-AUG-1994

APPLICATION NUMBER: US 08/156,358

FILING DATE: 23-NOV-1993

ATTORNEY/AGENT INFORMATION:

NAME: Maclean, Kurt A.

REGISTRATION NUMBER: 31,118

REFERENCE/DOCKET NUMBER: 112-272

TELECOMMUNICATION INFORMATION:

TELEPHONE: (310) 788-5000

TELEFAX: (310) 277-1297

INFORMATION FOR SEQ ID NO: 67:

SEQUENCE CHARACTERISTICS:

LENGTH: 15 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: linear

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: internal

ORIGINAL SOURCE:

ORGANISM: Mycobacterium tuberculosis

STRAIN: Erdman

SEQUENCE DESCRIPTION: SEQ ID NO: 67:

US-09-953-510-67

DB 4 DPSCGMSP 11

Query Match 31.4%; Score 33; DB 3; Length 15;
Best Local Similarity 62.5%; Pred. No. 5.4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DPAGMSP 8
1 DPAGMSP 8

DB 4 DPSCGMSP 11

RESULT 8

US-09-953-413-67
Sequence 67, Application US/09953413
Publication No. US20040018209A1

GENERAL INFORMATION:

APPLICANT: Horwitz, Marcus A.

TITLE OF INVENTION: Abundant Extracellular

Products and Methods for Their Production and Use

NUMBER OF SEQUENCES: 91

CORRESPONDENCE ADDRESS:

ADDRESSEE: Kurt A. Maclean

STREET: 2029 Century Park East, Suite 3800

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90067

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0,

Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/953,413

FILING DATE: 14-Sep-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/447,398

FILING DATE: 23-MAY-1995

APPLICATION NUMBER: US 08/289,667

FILING DATE: 12-AUG-1994

APPLICATION NUMBER: US 08/156,358

FILING DATE: 23-NOV-1993

ATTORNEY/AGENT INFORMATION:

NAME: Maclean, Kurt A.

REGISTRATION NUMBER: 31,118

REFERENCE/DOCKET NUMBER: 112-272

TELECOMMUNICATION INFORMATION:

TELEPHONE: (310) 788-5000

TELEFAX: (310) 277-1297

INFORMATION FOR SEQ ID NO: 67:

SEQUENCE CHARACTERISTICS:

LENGTH: 15 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: linear

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: internal

ORIGINAL SOURCE:

ORGANISM: Mycobacterium tuberculosis

STRAIN: Erdman

SEQUENCE DESCRIPTION: SEQ ID NO: 67:

US-09-953-413-67

DB 4 DPSCGMSP 11

Query Match 31.4%; Score 33; DB 3; Length 15;
Best Local Similarity 62.5%; Pred. No. 5.4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DPAGMSP 8
1 DPAGMSP 8

DB 4 DPSCGMSP 11

RESULT 9

US-10-147-255-67
Sequence 67, Application US/10147255
Publication No. US20030152584A1

GENERAL INFORMATION:

APPLICANT: Horwitz, Marcus A.

TITLE OF INVENTION: Abundant Extracellular

Products and Methods for Their Production and Use

NUMBER OF SEQUENCES: 91

CORRESPONDENCE ADDRESS:

ADDRESSEE: Kurt A. Maclean

STREET: 2029 Century Park East, Suite 3800

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90067

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0,

Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/953,413

FILING DATE: 14-Sep-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/447,398

FILING DATE: 23-MAY-1995

APPLICATION NUMBER: US 08/289,667

FILING DATE: 12-AUG-1994

APPLICATION NUMBER: US 08/156,358

FILING DATE: 23-NOV-1993

ATTORNEY/AGENT INFORMATION:

NAME: Maclean, Kurt A.

REGISTRATION NUMBER: 31,118

REFERENCE/DOCKET NUMBER: 112-272

TELECOMMUNICATION INFORMATION:

TELEPHONE: (310) 788-5000

TELEFAX: (310) 277-1297

INFORMATION FOR SEQ ID NO: 67:

SEQUENCE CHARACTERISTICS:

LENGTH: 15 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: linear

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: internal

ORIGINAL SOURCE:

ORGANISM: Mycobacterium tuberculosis

STRAIN: Erdman

SEQUENCE DESCRIPTION: SEQ ID NO: 67:

US-09-953-413-67


```

; APPLICANT: Horwitz, Marcue A.
; TITLE OF INVENTION: Abundant Extracellular
; Products and Methods for Their Production and Use
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kurt A. Maclean
; STREET: 2029 Century Park East, Suite 3800
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0,
; Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/147,255
; FILING DATE: 15-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/226,539A
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/447,398
; FILING DATE: 23-MAY-1995
; APPLICATION NUMBER: US 08/289,667
; FILING DATE: 12-AUG-1994
; APPLICATION NUMBER: US 08/156,358
; FILING DATE: 23-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Maclean, Kurt A.
; REGISTRATION NUMBER: 31,118
; REFERENCE/DOCKET NUMBER: 112-272
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (310) 788-5000
; TELEFAX: (310) 277-1297
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: Internal
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium tuberculosis
; STRAIN: Erdman
; SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-10-147-255-67

Query Match 31.4% Score 33; DB 4; Length 15;
Best Local Similarity 62.5%; Pred. NO. 5.4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DPAKMSF 8
Db 4 DPGQMGF 11

RESULT 10
US-10-695-155-67
; Sequence 67, Application US/10695155
; Publication No. US20040228873A1
; GENERAL INFORMATION:
; APPLICANT: HORWITZ, MARCUS A.
; APPLICANT: HARTH, GUNTER
; TITLE OF INVENTION: ABUNDANT EXTRACELLULAR PRODUCTS AND METHODS FOR THEIR PRODUCTION
; TITLE OF INVENTION: AND USE
; FILE REFERENCE: 51326-00004
```

```

; CURRENT APPLICATION NUMBER: US/10/695,155
; CURRENT FILING DATE: 2003-10-27
; PRIOR APPLICATION NUMBER: 08/652,842
; PRIOR FILING DATE: 1996-03-23
; PRIOR APPLICATION NUMBER: 08/568,357
; PRIOR FILING DATE: 1995-12-06
; PRIOR APPLICATION NUMBER: 08/551,149
; PRIOR FILING DATE: 1995-10-31
; PRIOR APPLICATION NUMBER: 08/447,398
; PRIOR FILING DATE: 1995-05-23
; PRIOR APPLICATION NUMBER: 08/289,667
; PRIOR FILING DATE: 1994-08-12
; PRIOR APPLICATION NUMBER: 08/156,358
; PRIOR FILING DATE: 1993-11-23
; PRIOR APPLICATION NUMBER: 08/545,926
; PRIOR FILING DATE: 1995-10-20
; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: Patentin version 3.2
; SEQ ID NO: 67
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-695-155-67

Query Match 31.4% Score 33; DB 5; Length 15;
Best Local Similarity 62.5%; Pred. NO. 5.4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DPAKMSF 8
Db 4 DPGQMGF 11

RESULT 11
US-09-884-441-397
; Sequence 397, Application US/09884441
; Patent No. US20020119158A1
; GENERAL INFORMATION:
; APPLICANT: Algate, Paul A.
; APPLICANT: Carter, Darick
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C7
; CURRENT APPLICATION NUMBER: US/09/884,441
; CURRENT FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 397
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-884-441-397

Query Match 31.4% Score 33; DB 3; Length 20;
Best Local Similarity 62.5%; Pred. NO. 7.4e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 13 VGEQVLS 20
Db 3 IGEDGILS 10

RESULT 12
US-09-907-969-397
; Sequence 397, Application US/09907969
; Publication No. US20030091580A1
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; APPLICANT: Flinn, Steven P.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary Richard
```

```

: APPLICANT: Reed, Steven G.
: APPLICANT: Vedvick, Thomas S.
: APPLICANT: Carter, Darrick
: APPLICANT: Hill, Paul
: APPLICANT: Albome, Earl
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
: FILE REFERENCE: 210121.4622G
: CURRENT APPLICATION NUMBER: US/09/907,969
: CURRENT FILING DATE: 2001-07-17
: NUMBER OF SEQ ID NOS: 596
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 397
: LENGTH: 20
: TYPE: prt
: ORGANISM: Homo sapiens
: US-09-907-969-397

```

Query Match	31.4%	Score 33	DB 3	Length 20
Best Local Similarity	62.5%	Pred. No. 7.4e+02		
Matches	5	Conservative	3	Mismatches 0
				Indels 0
				Gaps 0
Oy	13	VGEBCVLS	20	
	:	:		
db	3	IGEDBLS	10	

```

RESULT 13
US-09-827-271-397
; Sequence 397, Application US/09827271
; Publication No. US20030165504A1
; GENERAL INFORMATION:
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C6
; CURRENT APPLICATION NUMBER: US/09/827,271
; CURRENT FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 397
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-827-271-397

```

Query Match	31.4%	Score 33	DB 3	Length 20
Best Local Similarity	62.5%	Pred. No. 7	4e+02	
Matches	5	Conservative	3	Mismatches 0
				Indels 0
				Gaps 0
QY	13	VGGEGVLS	20	
	:	:		
db	3	IGEDGILS	10	

```

RESULT 14
US-10-198-053-397
; Sequence 397, Application US/10198053
; Publication No. US20030124140A1
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Hill, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C9
; CURRENT APPLICATION NUMBER: US/10/198,053
; CURRENT FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 624
; SOFTWARE: FaSTSeq for Windows Version 4.0
; SEQ ID NO 397

```

```

; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-198-053-397

```

```

Query Match      31.4%; Score 33; DB 4; Length 20;
Best Local Similarity 62.5%;
Matches      5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY      13 VGEQGVL 20
      :|:|:|:|
Db      3 IGEQGL 10

```

```

RESULT 15
US-10-198-053-603
; Sequence 603, Application US/10198053
; Publication No. US2003012410A1
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Hill, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C9
; CURRENT APPLICATION NUMBER: US/10/198.053
; CURRENT FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 624
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 603
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-198-053-603

```

Query Match	31.4%	Score 33	DB 4	Length 20
Best Local Similarity	62.5%	Pred. No. 7	4e+02	
Matches	5	Conservative	3	Mismatches 0
				Indels 0
				Gaps 0
QY	13	VGEBCVLS	20	
	:	:		
db	3	IGEDGILS	10	

```

RESULT 16
US-10-860-790-397
; Sequence 397, Application US/10860790
; Publication No. US20050031634A1
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Hill, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; OF OVARIAN CANCER
; FILE REFERENCE: 210.121.462C11
; CURRENT APPLICATION NUMBER: US/10/860,790
; CURRENT FILING DATE: 2004-06-02
; NUMBER OF SEQ ID NOS: 624
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 397
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-860-790-397

```

Query Match	31.4%	Score 33	DB 5	Length 20
Best Local Similarity	62.5%	Pred. NO. 7.4e+02		
Matches	5	Conservative	3	Mismatches 0
				Indels 0
				Gaps 0
QY	13	VGEQCVLS	20	
	:	:		

Db 3 IGEDGILS 10

RESULT 17

US-10-860-790-603
Sequence 603, Application US/10860790
Publication No. US20050031634A1

GENERAL INFORMATION:

APPLICANT: Bangur, Chaitanya S.

APPLICANT: Reiter, Marc W.

APPLICANT: Fanger, Gary R.

APPLICANT: Hill, Paul

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

FILE REFERENCE: 210121.462C11

CURRENT APPLICATION NUMBER: US/10/860.790

CURRENT FILING DATE: 2004-06-02

NUMBER OF SEQ ID NOS: 624

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 603

LENGTH: 20

TYPE: PRT

ORGANISM: Homo sapiens

Query Match 31.4%; Score 33; DB 5; Length 20;
Best Local Similarity 62.5%; Pred. No. 7.4e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 13 VGESEVLS 20

Db 3 IGEDGILS 10

RESULT 18

US-10-661-156-146

Sequence 146, Application US/10661156

Publication No. US20050100963A1

GENERAL INFORMATION:

APPLICANT: Sato, Aaron K.

APPLICANT: Sexton, Daniel J.

APPLICANT: Drenthfield, Daniel T.

APPLICANT: Ladner, Robert C.

APPLICANT: Arbogast, Christophe

APPLICANT: Bussat, Philippe

APPLICANT: Fan, Hong

APPLICANT: Khurana, Sudha

APPLICANT: Lindner, Karen E.

APPLICANT: Marinelli, Edmund R.

APPLICANT: Nanjappan, Palaniappa

APPLICANT: Nunn, Adrian

APPLICANT: Pillai, Radhakrishna

APPLICANT: Pochon, Sibylle

APPLICANT: Ramalingam, Kondareddiar

APPLICANT: Shrivastava, Ajay

APPLICANT: Song, Bo

APPLICANT: Swenson, Rolf E.

APPLICANT: Von Wronski, Mathew A.

TITLE OF INVENTION: KDR and VEGF/KDR Binding Peptides and

FILE REFERENCE: 0617.70012US00

CURRENT APPLICATION NUMBER: US/10/661.156

CURRENT FILING DATE: 2003-09-11

PRIOR APPLICATION NUMBER: US 10/382,082

PRIOR FILING DATE: 2003-03-03

PRIOR APPLICATION NUMBER: PCT/US03/06731

PRIOR FILING DATE: 2003-03-03

PRIOR APPLICATION NUMBER: US 60/440,411

PRIOR FILING DATE: 2003-01-15

PRIOR APPLICATION NUMBER: US 60/360,851

PRIOR FILING DATE: 2002-03-01

NUMBER OF SEQ ID NOS: 617

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 146

LENGTH: 20

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Library Isolate

US-10-661-156-146

Query Match 31.4%; Score 33; DB 5; Length 20;
Best Local Similarity 58.3%; Pred. No. 7.4e+02;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 8 PGCFVGEVGL 19

Db 2 PGCFVGEVGL 13

RESULT 19

US-10-328-916-58

Sequence 58, Application US/10328916

Publication No. US20040002114A1

GENERAL INFORMATION:

APPLICANT: Gregoire, Francine M.

APPLICANT: Johnson, Jeffrey D.

APPLICANT: Blume, John E.

TITLE OF INVENTION: Nucleic Acids Encoding a G-Protein Coupled Receptor

FILE REFERENCE: 016325-00721US

CURRENT APPLICATION NUMBER: US/10/328.916

CURRENT FILING DATE: 2003-01-06

PRIOR APPLICATION NUMBER: US 60/345,697

PRIOR FILING DATE: 2002-01-04

NUMBER OF SEQ ID NOS: 59

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 58

LENGTH: 15

TYPE: PRT

ORGANISM: Artificial Sequence

OTHER INFORMATION: Description of Artificial Sequence:C-terminal

OTHER INFORMATION: peptide of human IC-GPCR for raising antibody

US-10-328-916-58

Query Match 30.5%; Score 32; DB 4; Length 15;
Best Local Similarity 54.5%; Pred. No. 7.6e+02;
Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 6 MSPRGIVGER 16

Db 4 MEPPGLPTGAE 14

RESULT 20

US-09-838-785-26

Sequence 26, Application US/09838785

Patent No. US2002009455A1

GENERAL INFORMATION:

APPLICANT: Lau, Ted

APPLICANT: Lin, Rick

APPLICANT: Parkes, Debbie

APPLICANT: Parry, Gordon

APPLICANT: Schneider, Douglas

APPLICANT: Steindreich, Renate

APPLICANT: Van Heult, Pam T

APPLICANT: Wu, John

TITLE OF INVENTION: DNA Encoding a No. US2002009455A1el PROST 03

FILE REFERENCE: 51831AUSM1

CURRENT APPLICATION NUMBER: US/09/838.785

CURRENT FILING DATE: 2001-04-20

PRIOR APPLICATION NUMBER: 60/200,065

PRIOR FILING DATE: 2000-04-27

NUMBER OF SEQ ID NOS: 26

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 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 26
 ; LENGTH: 16
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-838-785-26
```

```
Query Match      30.5%; Score 32; DB 3; Length 16;
Best Local Similarity 55.6%; Pred. NO. 8.2e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1 DPAKMSP 9
        :|||:|
Db      3 EPAEGLSAP 11
```

```
RESULT 21
US-10-953-901-593
; Sequence 593, Application US/10953901
; Publication No. US20050181464A1
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, ALED
; APPLICANT: DHARAKSI, AKIL
; APPLICANT: VEDADI, MASOUD
; APPLICANT: ALAM, MUHAMMAD ZAHoor
; APPLICANT: ARROWSMITH, CHERYL
; APPLICANT: AMREY, DONALD E.
; APPLICANT: BEATTIE, BRYAN
; APPLICANT: BUZADZIOA, KRISTINA
; APPLICANT: CLARKE, TERESA
; APPLICANT: DOMAGALA, MEGAN
; APPLICANT: HOUSTON, SIMON
; APPLICANT: KANAGARAJAH, DHUSHY
; APPLICANT: LI QIN
; APPLICANT: MANSOURY, KAMRAN
; APPLICANT: McDONALD, MERRY-LYNN
; APPLICANT: NETHERY, KATHLEEN
; APPLICANT: NG, IVY
; APPLICANT: OUYANG, HUI
; APPLICANT: RICHARDS, DAMN
; APPLICANT: VALLEE, FRANCOIS
; APPLICANT: VIRAG, CRISTINA
; TITLE OF INVENTION: NOVEL PURIFIED POLYPEPTIDES FROM BACTERIA
; FILE REFERENCE: IPT-207.01
; CURRENT APPLICATION NUMBER: US/10/953,901
; PRIOR FILING DATE: 2004-09-29
; PRIOR APPLICATION NUMBER: PCT/CA03/00465
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 60/370,060
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 60/369,831
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 60/369,819
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 60/369,826
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 60/370,852
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: 60/370,681
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: 60/371,014
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/371,180
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/371,008
; PRIOR FILING DATE: 2002-04-09
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 901
; SOFTWARE: Patentin Ver. 3.3
; SEQ ID NO 593
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
```

```
US-10-953-901-593
```

```
Query Match      30.5%; Score 32; DB 5; Length 16;
Best Local Similarity 70.0%; Pred. NO. 8.2e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      10 GFIVEGEV 19
        |||||
Db      5 GDIVGEVGM 14
```

```
RESULT 22
US-10-661-156-170
; Sequence 170, Application US/10661156
; Publication No. US20050100963A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondaredidhar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR and VEGF/KDR Binding Peptides and
; FILE REFERENCE: D0617.70012US00
; CURRENT APPLICATION NUMBER: US/10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 617
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 170
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Library Isolate
; US-10-661-156-170

Query Match      30.5%; Score 32; DB 5; Length 20;
Best Local Similarity 50.0%; Pred. NO. 1e+03;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
```

```
Qy      8 PGFIVEGEV 19
        |||||
Db      2 PGFISYEQNAL 13

RESULT 23
US-10-307-956-25
; Sequence 25, Application US/10307956
; Publication No. US20030119072A1
; GENERAL INFORMATION:
; APPLICANT: Hoekstra, Merl F.
```

```

; APPLICANT: Xie, Weilin
; APPLICANT: Murray, Brian
; APPLICANT: Mercurio, Frank
; TITLE OF INVENTION: METHODS FOR MODULATING SIGNAL
; TITLE OF INVENTION: TRANSDUCTION MEDIATED BY TGF-BETA AND RELATED PROTEINS
; FILE REFERENCE: 860098.433
; CURRENT APPLICATION NUMBER: US/10/307,956
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: US/09/385,918
; PRIOR FILING DATE: 1999-08-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-307-956-25

```

```

Query Match      29.5% Score 31: DB 4: Length 14;
Best Local Similarity 38.5% Pred. No. 1e+03;
Matches 5: Conservative 4; Mismatches 4; Indels 0; Gaps 0;

```

```

QY      5 GMSPPGFVGEQ 17
      |||:|:|
Db      2 GLTRPPGYLSEEG 14

```

```

RESULT 24
US-10-211-088-356
; Sequence 356, Application US/10211088
; Publication No. US20030104479A1
; GENERAL INFORMATION:
; APPLICANT: Bright, Gary R.
; APPLICANT: Premkumar, D. David
; APPLICANT: Chen, Yih-Tai
; TITLE OF INVENTION: NO. US20030104479A1 Fusion Proteins And Assays For Molecular B
; FILE REFERENCE: 01-1022-US
; CURRENT APPLICATION NUMBER: US/10/211,088
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/309,395
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/341,589
; PRIOR FILING DATE: 2001-12-13
; NUMBER OF SEQ ID NOS: 366
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 356
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Post-translational modification site
US-10-211-088-356

```

```

Query Match      29.5% Score 31: DB 4: Length 15;
Best Local Similarity 55.6% Pred. No. 1.1e+03;
Matches 5: Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```

```

QY      2 PAKGMSPPG 10
      |||:|:|
Db      2 PGKGVKSPG 10

```

```

RESULT 25
US-10-950-163-8
; Sequence 8, Application US/10950163
; Publication No. US2005015291A1
; GENERAL INFORMATION:
; APPLICANT: Harby, Michele
; TITLE OF INVENTION: NOROVIRUS MONOCLONAL ANTIBODIES AND PEPTIDES
; FILE REFERENCE: 33576/US/2
; CURRENT APPLICATION NUMBER: US/10/950,163
; CURRENT FILING DATE: 2004-09-24
; PRIOR APPLICATION NUMBER: US 60/508,262

```

```

; PRIOR FILING DATE: 2003-09-24
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Grimsby virus
US-10-950-163-8

```

```

Query Match      29.5% Score 31: DB 5: Length 17;
Best Local Similarity 71.4% Pred. No. 1.2e+03;
Matches 5: Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      2 PAKGMSPP 8
      |||:|:|
Db      7 PAKGLSP 13

```

```

Search completed: January 26, 2006, 08:38:40
Job time : 66 secs

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OM protein - protein search, using sw model

Run on: January 26, 2006, 08:05:12 : Search time 3.7911 Seconds
(without alignments)
57.099 Million cell updates/sec

Title: US-09-662-293-13

Perfect score: 105
Sequence: 1 DPAKGMSPGFIVGEGVL 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 75621 seqs, 10829074 residues

Total number of hits satisfying chosen parameters: 37628

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database :

Published Applications AA New:
1: /cgn2_6/ptodata/1/pubpaa/us06_NEW_PUB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/us07_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/PTCT_NEW_PUB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	31.4	20	6	US-10-939-890-146
2	32	30.5	20	6	US-10-939-890-170
3	31	29.5	20	6	US-10-623-155-463
4	31	29.5	20	6	US-10-623-155-541
5	29	27.6	20	6	US-10-623-155-413
6	29	27.6	20	6	US-10-623-155-524
7	29	27.6	20	7	US-11-094-142-16
8	28	26.7	12	6	US-10-889-197-25
9	28	26.7	15	6	US-10-939-890-203
10	28	26.7	16	7	US-11-054-515-3003
11	28	26.7	20	6	US-10-893-584-212
12	28	26.7	21	7	US-11-058-735-60
13	27	25.7	11	7	US-11-145-661-78
14	27	25.7	14	7	US-11-143-984A-164
15	27	25.7	15	6	US-10-516-676-1
16	27	25.7	15	6	US-10-532-426-2
17	27	25.7	16	7	US-11-054-515-2153
18	27	25.7	16	7	US-11-054-515-2780
19	27	25.7	16	7	US-11-054-515-2783
20	27	25.7	20	6	US-11-053-100-18
21	26.5	25.2	20	6	US-10-485-788A-598
22	26	24.8	8	7	US-11-147-994-10
23	26	24.8	9	7	US-11-178-269-27
24	26	24.8	9	7	US-11-043-788-482
25	26	24.8	9	7	US-11-147-994-8

26	24.8	9	7	US-11-147-994-9	Sequence 9, Appli
27	24.8	10	7	US-11-147-994-7	Sequence 7, Appli
28	24.8	17	6	US-10-939-890-193	Sequence 193, App
29	24.8	15	6	US-10-893-584-240	Sequence 240, App
30	24.8	18	6	US-10-842-206-26	Sequence 26, Appli
31	24.8	18	6	US-10-980-459-12	Sequence 12, Appli
32	24.8	19	6	US-10-503-575-131	Sequence 131, App
33	24.8	20	6	US-10-997-201A-31	Sequence 31, Appli
34	24.8	20	6	US-10-623-155-532	Sequence 532, App
35	24.8	20	6	US-10-623-155-542	Sequence 542, App
36	24.8	20	6	US-10-623-155-545	Sequence 545, App
37	24.8	21	6	US-10-893-584-205	Sequence 205, Appli
38	24.8	21	6	US-10-880-238-47	Sequence 47, Appli
39	23.8	8	6	US-10-989-226-81	Sequence 81, Appli
40	23.8	8	7	US-11-066-967-133	Sequence 133, App
41	23.8	9	7	US-11-053-100-9	Sequence 9, Appli
42	23.8	11	7	US-11-045-024-1467	Sequence 1467, Ap
43	23.8	11	7	US-11-045-024-6285	Sequence 6285, Ap
44	23.8	14	7	US-11-116-144-285	Sequence 285, App
45	23.8	16	7	US-11-060-646-5	Sequence 5, Appli
46	23.8	17	7	US-11-193-512-47	Sequence 47, Appli
47	23.8	19	6	US-10-893-584-233	Sequence 233, App
48	23.8	20	6	US-10-623-155-414	Sequence 414, App
49	23.8	20	6	US-10-623-155-525	Sequence 525, App
50	23.3	11	7	US-11-105-708-11	Sequence 11, Appli
51	22.9	6	6	US-10-986-501-338	Sequence 338, App
52	22.9	9	7	US-11-045-024-1247	Sequence 1247, Ap
53	22.9	9	7	US-11-045-024-8847	Sequence 8847, Ap
54	22.9	10	6	US-10-919-492-35	Sequence 35, Appli
55	22.9	10	7	US-11-045-024-5221	Sequence 5221, Ap
56	22.9	10	7	US-11-129-104-61	Sequence 61, Appli
57	22.9	10	7	US-11-129-104-62	Sequence 62, Appli
58	22.9	12	7	US-11-145-861-371	Sequence 371, App
59	22.9	13	7	US-11-145-861-6	Sequence 6, Appli
60	22.9	14	7	US-11-129-104-7	Sequence 7, Appli
61	22.9	15	6	US-10-866-120-4	Sequence 4, Appli
62	22.9	15	6	US-10-919-492-6	Sequence 6, Appli
63	22.9	15	6	US-10-919-492-13	Sequence 13, Appli
64	22.9	19	6	US-10-503-575-119	Sequence 119, App
65	22.9	20	7	US-11-022-562-145	Sequence 145, App
66	22.9	20	7	US-11-022-562-146	Sequence 146, App
67	22.9	21	7	US-11-058-735-72	Sequence 72, Appli
68	21.9	6	6	US-10-485-788A-79	Sequence 79, Appli
69	21.9	8	6	US-10-485-788A-80	Sequence 80, Appli
70	21.9	8	6	US-10-945-674A-52	Sequence 52, Appli
71	21.9	9	6	US-10-850-635-26	Sequence 26, Appli
72	21.9	9	6	US-10-945-674A-29	Sequence 29, Appli
73	21.9	9	6	US-10-945-674A-40	Sequence 40, Appli
74	21.9	9	7	US-11-010-748A-51	Sequence 51, Appli
75	21.9	9	7	US-11-010-748A-617	Sequence 617, App
76	21.9	9	7	US-11-010-748A-618	Sequence 618, App
77	21.9	9	7	US-11-010-748A-620	Sequence 620, App
78	21.9	9	7	US-11-010-748A-621	Sequence 621, App
79	21.9	9	7	US-11-010-748A-625	Sequence 625, App
80	21.9	9	7	US-11-010-748A-635	Sequence 635, App
81	21.9	9	7	US-11-055-557-28	Sequence 28, Appli
82	21.9	11	7	US-11-033-365-12	Sequence 12, Appli
83	21.9	12	6	US-10-893-584-102	Sequence 102, App
84	21.9	13	6	US-10-893-584-198	Sequence 198, App
85	21.9	14	6	US-10-746-959C-5	Sequence 5, Appli
86	21.9	14	6	US-10-945-674A-87	Sequence 87, Appli
87	21.9	15	6	US-10-939-890-200	Sequence 200, App
88	21.9	15	6	US-10-939-890-202	Sequence 202, App
89	21.9	15	6	US-10-893-584-247	Sequence 247, App
90	21.9	15	7	US-11-187-558-4	Sequence 4, Appli
91	21.9	16	6	US-10-919-492-3	Sequence 3, Appli
92	21.9	16	6	US-10-919-492-10	Sequence 10, Appli
93	21.9	16	7	US-11-108-185-42	Sequence 42, Appli
94	21.9	17	6	US-10-880-238-107	Sequence 107, App
95	21.9	17	6	US-10-880-238-109	Sequence 109, App
96	21.9	17	6	US-10-945-674A-18	Sequence 18, Appli
97	21.9	17	6	US-10-945-674A-91	Sequence 91, Appli
98	21.9	17	7	US-11-010-748A-405	Sequence 405, App

QY 2 PAKGMSPP 9
DB 9 PTSGMPP 16

RESULT 4

US-10-623-155-541
Sequence 541, Application US/10623155
Publication No. US20050261166A1
GENERAL INFORMATION:
APPLICANT: Wang, Tonglong
APPLICANT: Peckham, David W.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.455C20
CURRENT APPLICATION NUMBER: US/10/623.155
CURRENT FILING DATE: 2003-07-17
NUMBER OF SEQ ID NOS: 560
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 541
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens
US-10-623-155-541

Query Match 29.5%; Score 31; DB 6; Length 20;
Best Local Similarity 62.5%; Pred. No. 39;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PAKGMSPP 9
DB 9 PTSGMPP 16

RESULT 5

US-10-623-155-413
Sequence 413, Application US/10623155
Publication No. US20050261166A1
GENERAL INFORMATION:
APPLICANT: Wang, Tonglong
APPLICANT: Peckham, David W.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.455C20
CURRENT APPLICATION NUMBER: US/10/623.155
CURRENT FILING DATE: 2003-07-17
NUMBER OF SEQ ID NOS: 560
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 413
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens
US-10-623-155-413

Query Match 27.6%; Score 29; DB 6; Length 20;
Best Local Similarity 62.5%; Pred. No. 79;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 10 GFIVGEEG 17
DB 9 GAIGKEG 16

RESULT 6
US-10-623-155-524
Sequence 524, Application US/10623155
Publication No. US20050261166A1
GENERAL INFORMATION:

APPLICANT: Wang, Tonglong
APPLICANT: Peckham, David W.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.455C20
CURRENT APPLICATION NUMBER: US/10/623.155
CURRENT FILING DATE: 2003-07-17
NUMBER OF SEQ ID NOS: 560
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 524
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens
US-10-623-155-524

Query Match 27.6%; Score 29; DB 6; Length 20;
Best Local Similarity 62.5%; Pred. No. 79;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 10 GFIVGEEG 17
DB 9 GAIGKEG 16

RESULT 7

US-11-094-142-16
Sequence 16, Application US/11094142
Publication No. US20050260770A1
GENERAL INFORMATION:
APPLICANT: Cohen, Irvin R.
APPLICANT: Quintana, Francisco Javier
APPLICANT: Doman, Eylan
APPLICANT: Elizur, Gad
APPLICANT: Hagedorn, Peter H.
TITLE OF INVENTION: ANTIGEN ARRAY AND DIAGNOSTIC USES THEREOF
FILE REFERENCE: 29462
CURRENT APPLICATION NUMBER: US/11/094.142
CURRENT FILING DATE: 2005-03-31
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PatentIn version 3.3
SEQ ID NO 16
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic peptide
US-11-094-142-16

Query Match 27.6%; Score 29; DB 7; Length 20;
Best Local Similarity 55.6%; Pred. No. 79;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 10 GFIVGEEG 18
DB 7 GAVFGEGL 15

RESULT 8

US-10-889-197-25
Sequence 25, Application US/10889197
Publication No. US20050271689A1
GENERAL INFORMATION:
APPLICANT: HUANG, CHUN-MING
APPLICANT: ZHANG, JIANPENG
APPLICANT: TANG, DE-CHU
TITLE OF INVENTION: NOVEL TARGETS AND COMPOSITIONS FOR USE IN
DECONTAMINATION, IMMUNOPROPHYLAXIS, AND POST-EXPOSURE
FILE REFERENCE: 858610-2006.1
CURRENT APPLICATION NUMBER: US/10/889.197
CURRENT FILING DATE: 2004-07-12

; PRIOR APPLICATION NUMBER: 60/486,369
 ; PRIOR FILING DATE: 2003-07-11
 ; NUMBER OF SEQ ID NOS: 44
 ; SOFTWARE: PatentIn Ver. 3.2
 ; SEQ ID NO 25
 ; LENGTH: 12
 ; TYPE: PRT
 ; ORGANISM: Bacillus anthracis
 US-10-889-197-25

Query Match 26.7%; Score 28; DB 6; Length 12;
 Best Local Similarity 55.6%; Pred. No. 63;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 8 PGFVIGEE 16
 Db 4 PAGFTFGFK 12

RESULT 9
 US-10-939-890-203
 ; Sequence 203, Application US/10939890
 ; Publication No. US20050250700A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sato, Aaron K.
 ; APPLICANT: Sexton, Daniel J.
 ; APPLICANT: Dransfield, Daniel T.
 ; APPLICANT: Ladhner, Robert C.
 ; APPLICANT: Arbogast, Christophe
 ; APPLICANT: Bussac, Philippe
 ; APPLICANT: Fan, Hong
 ; APPLICANT: Khurana, Sucha
 ; APPLICANT: Linder, Karen E.
 ; APPLICANT: Marinelli, Edmund R.
 ; APPLICANT: Nanjappan, Palanappa
 ; APPLICANT: Nunn, Adrian D.
 ; APPLICANT: Pillai, Radhakrishna
 ; APPLICANT: Pochon, Sibylle
 ; APPLICANT: Ramalingam, Kondareddiar
 ; APPLICANT: Shrivastava, Ajay
 ; APPLICANT: Song, Bo
 ; APPLICANT: Swenson, Rolf E.
 ; APPLICANT: Von Wronski, Mathew A.
 ; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
 ; FILE REFERENCE: D0617, 70014US00
 ; CURRENT APPLICATION NUMBER: US/10/939,890
 ; CURRENT FILING DATE: 2004-09-13
 ; PRIOR APPLICATION NUMBER: US 10/661,156
 ; PRIOR FILING DATE: 2003-09-11
 ; PRIOR APPLICATION NUMBER: US 10/382,082
 ; PRIOR FILING DATE: 2003-03-03
 ; PRIOR APPLICATION NUMBER: PC/US03/06731
 ; PRIOR FILING DATE: 2003-03-03
 ; PRIOR APPLICATION NUMBER: US 60/440,411
 ; PRIOR FILING DATE: 2003-01-15
 ; PRIOR APPLICATION NUMBER: US 60/360,851
 ; PRIOR FILING DATE: 2002-03-01
 ; NUMBER OF SEQ ID NOS: 883
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 203
 ; LENGTH: 15
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Library Isolate
 US-10-939-890-203

Query Match 26.7%; Score 28; DB 6; Length 15;
 Best Local Similarity 71.4%; Pred. No. 81;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 PAKGMSP 8
 Db 4 PAKGMSP 8

Db 3 PCKGMPLP 9

RESULT 10
 US-11-054-515-3003
 ; Sequence 3003, Application US/11054515
 ; Publication No. US20050255532A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Buys
 ; FILE REFERENCE: P8523P3
 ; CURRENT APPLICATION NUMBER: US/11/054,515
 ; CURRENT FILING DATE: 2005-02-10
 ; PRIOR APPLICATION NUMBER: 60/543,296
 ; PRIOR FILING DATE: 2004-02-11
 ; PRIOR APPLICATION NUMBER: 60/580,347
 ; PRIOR FILING DATE: 2004-06-18
 ; PRIOR APPLICATION NUMBER: 10/293,418
 ; PRIOR FILING DATE: 2002-11-14
 ; PRIOR APPLICATION NUMBER: 60/331,469
 ; PRIOR FILING DATE: 2001-11-16
 ; PRIOR APPLICATION NUMBER: 60/340,817
 ; PRIOR FILING DATE: 2001-12-19
 ; PRIOR APPLICATION NUMBER: 09/880,748
 ; PRIOR FILING DATE: 2001-06-15
 ; PRIOR APPLICATION NUMBER: 60/293,499
 ; PRIOR FILING DATE: 2001-05-25
 ; PRIOR APPLICATION NUMBER: 60/277,379
 ; PRIOR FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/276,248
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/240,816
 ; PRIOR FILING DATE: 2000-10-17
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 3247
 ; SEQ ID NO 3003
 ; LENGTH: 16
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-054-515-3003

Query Match 26.7%; Score 28; DB 7; Length 16;
 Best Local Similarity 54.5%; Pred. No. 87;
 Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 1 DPAKGMSPGF 11
 Db 4 DPLTGYSLDGF 14

RESULT 11
 US-10-893-584-212
 ; Sequence 212, Application US/10893584
 ; Publication No. US20050272048A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Borgford, Thor
 ; APPLICANT: Braun, Curtis
 ; APPLICANT: Putac, Admir
 ; APPLICANT: Scoll, Dominik
 ; TITLE OF INVENTION: Rictin-Like Toxin Variants for Treatment of Cancer,
 ; FILE REFERENCE: 10447-025
 ; CURRENT APPLICATION NUMBER: US/10/893,584
 ; CURRENT FILING DATE: 2004-07-19
 ; PRIOR APPLICATION NUMBER: US 09/551,151
 ; PRIOR FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: US 09/403,752
 ; PRIOR FILING DATE: 1999-10-29
 ; PRIOR APPLICATION NUMBER: US 10/089,058
 ; PRIOR FILING DATE: 2000-10-04
 ; NUMBER OF SEQ ID NOS: 274
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 212

LENGTH: 20
TYPE: PRT
ORGANISM: E. coli
US-10-893-584-212

Query Match 26.7%; Score 28; DB 6; Length 20;
Best Local Similarity 38.5%; Pred. No. 1.1e+02;
Matches 5; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 2 PAKGSPGPIVG 14
DB 2 PGRVVGPGRVVG 14

RESULT 12
US-11-058-735-60
Sequence 60, Application US/11058735
Publication No. US20050261475A1
GENERAL INFORMATION:
APPLICANT: TSENG, HUANG-CHUN
TITLE OF INVENTION: SOLID-PHASE CAPTURE-RELEASE-TAG METHODS FOR
FILE REFERENCE: HMV-094.01
CURRENT APPLICATION NUMBER: US/11/058,735
PRIOR FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,748
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 80
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO: 60
LENGTH: 21
TYPE: PRT
ORGANISM: Mus musculus
US-11-058-735-60

Query Match 26.7%; Score 28; DB 7; Length 21;
Best Local Similarity 62.5%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 PAKGSPG 9
DB 10 PPKGLSVP 17

RESULT 13
US-11-145-861-78
Sequence 78, Application US/11145861
Publication No. US20060014138A1
GENERAL INFORMATION:
APPLICANT: Chinaiyan, Arul
APPLICANT: Wang, Xiaoju
TITLE OF INVENTION: Phase Microarray Profiling of the Humoral Response to Disease
FILE REFERENCE: UM-09899
CURRENT APPLICATION NUMBER: US/11/145,861
PRIOR FILING DATE: 2005-06-06
NUMBER OF SEQ ID NOS: 464
SOFTWARE: PatentIn version 3.3
SEQ ID NO: 78
LENGTH: 11
TYPE: PRT
ORGANISM: Homo sapiens
US-11-145-861-78

Query Match 25.7%; Score 27; DB 7; Length 11;
Best Local Similarity 55.6%; Pred. No. 81;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 11 FIVEGEGVL 19
DB 3 FLEGEGQIL 11

RESULT 14
US-11-143-984A-164
Sequence 164, Application US/11143984A
Publication No. US20060014180A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL HUMAN PHOSPHATASES
FILE REFERENCE: D0072 DIV1
CURRENT APPLICATION NUMBER: US/11/143,984A
PRIOR FILING DATE: 2005-06-02
PRIOR APPLICATION NUMBER: US 60/256,868
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: US 60/280,186
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: US 60/287,735
PRIOR FILING DATE: 2001-05-01
PRIOR APPLICATION NUMBER: US 60/295,848
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/300,465
PRIOR FILING DATE: 2001-06-25
NUMBER OF SEQ ID NOS: 208
SOFTWARE: PatentIn version 3.2
SEQ ID NO: 164
LENGTH: 14
TYPE: PRT
ORGANISM: Homo sapiens
US-11-143-984A-164

Query Match 25.7%; Score 27; DB 7; Length 14;
Best Local Similarity 57.1%; Pred. No. 1.1e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 5 GMSPPGF 11
DB 1 GVCPPNF 7

RESULT 15
US-10-516-676-1
Sequence 1, Application US/10516676
Publication No. US20050244393A1
GENERAL INFORMATION:
APPLICANT: Philippart, Pierre
TITLE OF INVENTION: SEALANT OR TISSUE GENERATING PRODUCT
FILE REFERENCE: 232037
CURRENT APPLICATION NUMBER: US/10/516,676
PRIOR FILING DATE: 2004-12-03
PRIOR APPLICATION NUMBER: 10/1176,401
PRIOR FILING DATE: 2002-06-21
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn version 3.2
SEQ ID NO: 1
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthesized
US-10-516-676-1

Query Match 25.7%; Score 27; DB 6; Length 15;
Best Local Similarity 40.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

OY 5 GMSPPGPIVGEGVL 19
DB 1 GTPGPGIAGQGVV 15

RESULT 16
US-10-532-426-2

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; Sequence 2, Application US/10532426
; Publication No. US20060009516A1
; GENERAL INFORMATION:
; APPLICANT: Rosenberg, Lawrence
; TITLE OF INVENTION: USE OF IN GAP FOR REVERSING DIABETES
; FILE REFERENCE: 1912-0308PUS1
; CURRENT APPLICATION NUMBER: US/10/532,426
; PRIOR FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/420,677
; PRIOR FILING DATE: 2002-10-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: IN GAP peptide
US-10-532-426-2
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Query Match      25.7%; Score 27; DB 6; Length 15;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
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Oy      1 DPAKMSPPG 10
      ||| |||
Db      4 DPSHOTLPNG 13
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RESULT 17
US-11-054-515-2153
; Sequence 2153, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Buys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2153
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2153
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Query Match      25.7%; Score 27; DB 7; Length 16;
Best Local Similarity 54.5%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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Oy      1 DPAKMSPPGF 11
      ||| |||
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```
Db      4 DPLTGYSPDGF 14
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RESULT 18
US-11-054-515-2780
; Sequence 2780, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Buys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2780
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2780
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Query Match      25.7%; Score 27; DB 7; Length 16;
Best Local Similarity 54.5%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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Oy      1 DPAKMSPPGF 11
      ||| |||
Db      4 DPLTGYSPDGF 14
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RESULT 19
US-11-054-515-2783
; Sequence 2783, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Buys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
```

PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/2277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 2783
LENGTH: 16
TYPE: PRT
ORGANISM: Homo sapiens
US-11-054-515-2783

Query Match 25.7%; Score 27; DB 7; Length 16;
Best Local Similarity 54.5%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 DPAKMSPPGF 11
Db 4 DPLGYSPDGF 14

RESULT 20
US-11-053-100-18
Sequence 18, Application US/11053100
Publication No. US20050255554A1
GENERAL INFORMATION:
APPLICANT: CHIKOTI, Ashutosh
TITLE OF INVENTION: FUSION PEPTIDES ISOLATABLE BY PHASE TRANSITION
FILE REFERENCE: 4176-101 CIP
CURRENT APPLICATION NUMBER: US/11/053,100
CURRENT FILING DATE: 2005-02-08
PRIOR APPLICATION NUMBER: US 09/812,382
PRIOR FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: US 60/190,659
PRIOR FILING DATE: 2000-03-20
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PatentIn version 3.3
SEQ ID NO 18
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Synthetic Construct
NAME/KEY: REPEAT
LOCATION: (1)-(20)
OTHER INFORMATION: ELP1 [K1V2F1-4]
US-11-053-100-18

Query Match 25.7%; Score 27; DB 7; Length 20;
Best Local Similarity 52.9%; Pred. No. 1.6e+02;
Matches 9; Conservative 1; Mismatches 3; Indels 4; Gaps 2;

QY 2 PAKGMSPPGFVGEV 18
Db 2 PGKGV--PG--VGIVGV 14

RESULT 21
US-10-485-788A-598
Sequence 598, Application US/10485788A
Publication No. US20050282743A1
GENERAL INFORMATION:
APPLICANT: Lu, Peter S.
APPLICANT: Rabinowitz, Joshua D.
APPLICANT: Schweitzer, Johannes
APPLICANT: Carrick, Deanna Marie
APPLICANT: Arbor Vita Corporation
TITLE OF INVENTION: Molecular Interactions in Cells
FILE REFERENCE: 20054-003320US

CURRENT APPLICATION NUMBER: US/10/485,788A
CURRENT FILING DATE: 2004-02-03
PRIOR APPLICATION NUMBER: US 60/309,841
PRIOR FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: US 60/360,061
PRIOR FILING DATE: 2002-02-25
PRIOR APPLICATION NUMBER: WO PCT/US02/24655
PRIOR FILING DATE: 2002-08-02
NUMBER OF SEQ ID NOS: 841
SOFTWARE: PatentIn version 3.1
SEQ ID NO 598
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens
US-10-485-788A-598

Query Match 25.2%; Score 26.5; DB 6; Length 20;
Best Local Similarity 66.7%; Pred. No. 1.9e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 DPAKMSPP 9
Db 10 DPGF-MSP 17

RESULT 22
US-11-147-994-10
Sequence 10, Application US/11147994
Publication No. US20060013855A1
GENERAL INFORMATION:
APPLICANT: Medivac, LLC
APPLICANT: CARPENTER, Kenneth W.
APPLICANT: TURNELL, William G.
APPLICANT: DEFFE, Kristin M.
APPLICANT: GRAKO, Kathryn A.
TITLE OF INVENTION: BIOACTIVE STENTS FOR TYPE II DIABETICS AND METHODS FOR USE
FILE REFERENCE: MEDIV2030-3
CURRENT APPLICATION NUMBER: US/11/147,994
CURRENT FILING DATE: 2005-06-07
PRIOR APPLICATION NUMBER: US 11/098,891
PRIOR FILING DATE: 2004-04-04
PRIOR APPLICATION NUMBER: US 60/559,937
PRIOR FILING DATE: 2004-04-05
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.3
SEQ ID NO 10
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Small proteinaceous motif
US-11-147-994-10

Query Match 24.8%; Score 26; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.8e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PPGF 11
Db 2 PPGF 5

RESULT 23
US-11-178-269-27
Sequence 27, Application US/11178269
Publication No. US20050272661A1
GENERAL INFORMATION:
APPLICANT: Richelson, Elliott
APPLICANT: Cusack, Bernadette Marie
APPLICANT: Pang, Yuan-Ping
APPLICANT: McCormick, Daniel J.
APPLICANT: Faug, Abdul

; APPLICANT: Tyler, Beth Marie
; APPLICANT: Boules, Mona
; TITLE OF INVENTION: NEO-TRYPTOPHAN
; FILE REFERENCE: 07039/141001
; CURRENT APPLICATION NUMBER: US/11/178,269
; PRIOR FILING DATE: 2005-07-08
; PRIOR APPLICATION NUMBER: US/10/858,226
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US/10/265,099
; PRIOR FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: US/09/755,638
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 09/289,693
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/098,119
; PRIOR FILING DATE: 1998-08-27
; PRIOR APPLICATION NUMBER: US 60/092,195
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: US 60/081,356
; PRIOR FILING DATE: 1998-04-10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-11-178-269-27

Query Match 24.8%; Score 26; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.8e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 8 PPGR 11
|||
Db 2 PPGR 5

RESULT 24
US-11-043-788-482
; Sequence 482, Application US/11043788
; Publication No. US20060014166A1
; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
; TITLE OF INVENTION: THEREOF FOR DIAGNOSIS OF ENDOMETRIOSIS
; FILE REFERENCE: 1847.1006
; CURRENT APPLICATION NUMBER: US/11/043,788
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 506
; SEQ ID NO 482
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-043-788-482

Query Match 24.8%; Score 26; DB 7; Length 9;
Best Local Similarity 80.0%; Pred. No. 5.8e+04;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 MSPRG 10
:||||
Db 4 LSPRG 8

RESULT 25
US-11-147-994-8
; Sequence 8, Application US/11147994
; Publication No. US20060013855A1
; GENERAL INFORMATION:

; APPLICANT: Medivase, LLC
; APPLICANT: CARPENTER, Kenneth W.
; APPLICANT: TURNELL, William G.
; APPLICANT: DEFIFE, Kristin M.
; APPLICANT: GRAGO, Kathryn A.
; TITLE OF INVENTION: BIOACTIVE STENTS FOR TYPE II DIABETICS AND METHODS FOR USE
; FILE REFERENCE: MEDIV2030-3
; CURRENT APPLICATION NUMBER: US/11/147,994
; PRIOR FILING DATE: 2005-06-07
; PRIOR APPLICATION NUMBER: US 11/098,891
; PRIOR FILING DATE: 2004-04-04
; PRIOR APPLICATION NUMBER: US 60/559,937
; PRIOR FILING DATE: 2004-04-05
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Small proteinaceous motif
US-11-147-994-8

Query Match 24.8%; Score 26; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.8e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 8 PPGR 11
|||
Db 3 PPGR 6

Search completed: January 26, 2006, 08:39:07
Job time : 3.7931 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 26, 2006, 07:48:50 : Search time 10 Seconds

(without alignments)
192.434 Million cell updates/sec

Title: US-09-662-293-13

Perfect score: 105

Sequence: 1 DPAKMSPEGFVGEVLS 20

Scoring table: BLOSUM62

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 4071

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	32	30.5	15	2	F57789	galbladder stone
2	31	29.5	17	2	PH0082	neuroglian protein
3	28	26.7	10	2	S26506	collagen alpha 1(V
4	28	26.7	15	2	SS4712	zein Zp22/6 protei
5	28	26.7	20	2	B60801	acrosome stabilizi
6	28	26.7	21	2	PT0089	4-hydroxybenzoate
7	27	25.7	16	2	C49048	T-cell receptor be
8	27	25.7	16	2	PS0210	28k protein 4209 -
9	26	24.8	9	2	S65433	bradykinin - horn
10	26	24.8	9	2	A43065	hydroxyproline-3-b
11	26	24.8	9	2	B60246	ornitho-kinin - ch
12	26	24.8	9	2	A26744	bradykinin-like pe
13	26	24.8	9	2	A61057	Thr-6 bradykinin -
14	26	24.8	9	2	A60579	bradykinin-like pe
15	26	24.8	9	2	A61363	bradykinin - commo
16	26	24.8	9	2	A61358	bradykinin-like pe
17	26	24.8	11	2	S13279	ile-ser-bradykinin
18	26	24.8	11	2	B26744	megacoliakinin -
19	26	24.8	11	2	A61365	phyllokinin - Rohd
20	26	24.8	12	2	A61360	vespakinin M - hor
21	26	24.8	12	2	A61359	vespakinin X - hor
22	26	24.8	13	2	A61361	bradykinin-like pe
23	26	24.8	14	2	A61362	bradykinin-like pe
24	26	24.8	15	2	A36279	chemoattractant pr
25	26	24.8	17	1	A61339	vespakinin I - e
26	26	24.8	20	2	S39380	pectinesterase (EC
27	26	24.8	21	2	S69502	NFI/CAAT-binding c
28	25	23.8	10	2	A36454	tyrosin-modulating p
29	25	23.8	10	2	C60527	sperm-activating p

30	25	23.8	12	2	T46794	hypothetical prote
31	25	23.8	20	2	A33878	myosin light chain
32	25	23.8	20	2	A61576	insulin-like growt
33	25	23.8	20	2	A46644	temperature-labile
34	24	22.9	10	2	B60588	sperm-activating p
35	24	22.9	10	2	B60788	sperm-activating p
36	24	22.9	15	2	I65478	c-Ki-ras - hamster
37	24	22.9	15	2	PT0097	glutathione peroxi
38	24	22.9	17	2	S77834	DNA-directed RNA p
39	24	22.9	17	2	S57518	T cell receptor be
40	24	22.9	19	2	C37072	proteoglycan 65k c
41	24	22.9	19	2	S11611	ribosomal protein
42	24	22.9	20	2	P00688	photosystem I 14.0
43	24	22.9	20	2	P00687	photosystem I 14.1
44	23	21.9	9	2	S35538	ribosomal protein
45	23	21.9	10	2	C60588	sperm-activating p
46	23	21.9	10	2	B60527	sperm-activating p
47	23	21.9	10	2	I60588	sperm-activating p
48	23	21.9	12	2	C36201	1-aminocyclopropan
49	23	21.9	13	2	A59387	VCAM-1 5'UTR bindi
50	23	21.9	18	2	S13974	chlorophyll a/b-bi
51	23	21.9	19	2	S29766	cytochrome c (EDH)
52	23	21.9	19	2	B28457	proteoglycan II, b
53	23	21.9	20	2	B39108	lectin, galactose/
54	23	21.9	20	2	A31516	50k allergen - per
55	23	21.9	20	2	S38288	photosystem I chai
56	23	21.9	20	2	S06150	nephelitosenoxide -
57	23	21.9	21	2	A60696	malate dehydrogena
58	22	21.4	15	2	PA0040	protein Qa300033 -
59	22	21.0	9	2	PA0033	sperm-activating p
60	22	21.0	10	2	D60527	28k protein 4412 -
61	22	21.0	12	2	PS0213	histone H2B - huma
62	22	21.0	12	2	S65409	GTP-binding protei
63	22	21.0	14	2	A35377	20k protein 5503 -
64	22	21.0	15	2	PS0255	translation elonga
65	22	21.0	16	2	PA0110	alpha-conotoxin Ep
66	22	21.0	18	2	A59042	hypothetical prote
67	22	21.0	18	2	A36133	human leukocyte an
68	22	21.0	18	2	I59649	histone H2B (clone
69	22	21.0	20	2	S19240	histone H2B - huma
70	22	21.0	20	2	B33290	nitrophorin 3 - Rh
71	22	21.0	20	2	C56385	proteasome chain 7
72	22	21.0	21	2	S09088	T-cell receptor al
73	21	20.0	8	2	A35768	pev-cachykinin - p
74	21	20.0	9	2	PD0027	sperm-activating p
75	21	20.0	10	2	F60527	lysyl-bradykinin -
76	21	20.0	10	2	S39030	transgelin - sheep
77	21	20.0	11	2	A40693	cytochrome P450 UT
78	21	20.0	12	2	S39762	43.2k bile stone p
79	21	20.0	12	2	E58502	malate dehydrogena
80	21	20.0	14	2	B60683	hypothetical 1.5k
81	21	20.0	15	2	B39109	insulin-like growt
82	21	20.0	15	2	S05700	complement factor
83	21	20.0	16	2	PL0110	glutathione transf
84	21	20.0	16	2	S55307	pyruvate dehydroge
85	21	20.0	16	2	A31963	hypothetical prote
86	21	20.0	17	2	S01104	thyroid hormone re
87	21	20.0	17	2	I55612	myosin heavy chain
88	21	20.0	18	2	I51203	group III allergen
89	21	20.0	18	2	A39997	hypothetical prote
90	21	20.0	18	2	A35678	fibrinopeptide A -
91	21	20.0	19	2	B29501	phosphocARRIER p
92	21	20.0	19	2	A48400	vitronectin - shee
93	21	20.0	19	2	S22233	vitronectin - bovine
94	21	20.0	19	2	S02808	nicotin - goat
95	21	20.0	20	2	S22232	immunodeficiency v
96	21	20.0	20	2	B48400	chymotrypsin (EC 3
97	21	20.0	20	2	S65399	neurofilament heav
98	21	20.0	20	2	A61414	transitional endop
99	21	20.0	20	2	I53671	
100	21	20.0	21	2	S38273	

hypothetical prote
myosin light chain
insulin-like growt
temperature-labile
sperm-activating p
sperm-activating p
c-Ki-ras - hamster
glutathione peroxi
DNA-directed RNA p
T cell receptor be
proteoglycan 65k c
ribosomal protein
photosystem I 14.0
photosystem I 14.1
ribosomal protein
sperm-activating p
sperm-activating p
sperm-activating p
1-aminocyclopropan
VCAM-1 5'UTR bindi
chlorophyll a/b-bi
cytochrome c (EDH)
proteoglycan II, b
lipoprotein Acfd p
lectin, galactose/
50k allergen - per
photosystem I chai
nephelitosenoxide -
malate dehydrogena
protein Qa300033 -
sperm-activating p
28k protein 4412 -
histone H2B - huma
GTP-binding protei
20k protein 5503 -
translation elonga
alpha-conotoxin Ep
hypothetical prote
human leukocyte an
histone H2B (clone
histone H2B - huma
nitrophorin 3 - Rh
proteasome chain 7
T-cell receptor al
pev-cachykinin - p
sperm-activating p
lysyl-bradykinin -
transgelin - sheep
cytochrome P450 UT
43.2k bile stone p
malate dehydrogena
hypothetical 1.5k
insulin-like growt
complement factor
glutathione transf
pyruvate dehydroge
hypothetical prote
thyroid hormone re
myosin heavy chain
group III allergen
hypothetical prote
fibrinopeptide A -
phosphocARRIER p
vitronectin - shee
vitronectin - bovine
nicotin - goat
immunodeficiency v
chymotrypsin (EC 3
neurofilament heav
transitional endop

ALIGNMENTS

RESULT 1

F57789 galbladder stone matrix protein 2, 41K - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004
 C/Accession: F57789
 R/Brette, J.P.; Brette, M.B.
 submitted to the Protein Sequence Database, February 1996
 A/Description: The proteins of galbladder stones.
 A/Reference number: A57789
 A/Accession: F57789
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-15 <BIN>
 A/Cross-references: UNIPROT:Q7M4P9; UNIPARC:UPI000017C122
 A/Note: 9-Phe was also found

Query Match 30.5%; Score 32; DB 2; Length 15;
 Best Local Similarity 60.0%; Pred. No. 79;
 Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 8 PGFVGEEG 17
 ||| |
 Db 5 PDGFEQSSG 14

RESULT 2

PH0082 neuroglial protein, short form - fruit fly (Drosophila sp.) (fragment)
 C/Species: Drosophila sp.
 C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
 C/Accession: PH0082
 R/Hotisch, M.; Bieber, A.J.; Patel, N.H.; Goodman, C.S.
 Neuron 4, 697-709, 1990
 A/Title: Differential splicing generates a nervous system-specific form of Drosophila ne
 A/Reference number: PH0082; MUID:90262720; PMID:1693086
 A/Accession: PH0082
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-17 <HOR>
 A/Cross-references: UNIPARC:UPI000017BEEF

Query Match 29.5%; Score 31; DB 2; Length 17;
 Best Local Similarity 40.0%; Pred. No. 1.3e+02;
 Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

OY 5 GMSPPGFVGEV 19
 ||: ||: ||: ||
 Db 1 GMDGDFIGQTR 15

RESULT 3

S26506 collagen alpha 1(VI) chain - bovine (fragment)
 C/Species: Bos primigenius taurus (cattle)
 C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
 C/Accession: S26506
 R/Jander, R.; Rautenberg, J.; Gnanville, R.W.
 Eur. J. Biochem. 133, 39-46, 1983
 A/Title: Further characterization of the three polypeptide chains of bovine and human st
 A/Reference number: S26506; MUID:83209648; PMID:6852033
 A/Accession: S26506
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-10 <JAN>
 A/Cross-references: UNIPROT:Q7M2N0; UNIPARC:UPI000017C4E3
 C/Keywords: hydroxyproline
 F/9/Modified site: hydroxyproline (Pro) #status experimental
 Query Match 26.7%; Score 28; DB 2; Length 10;

Best Local Similarity 66.7%; Pred. No. 2.1e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

OY 2 PAKGMSPPG 10
 ||: ||: ||
 Db 4 PARQ--PPG 10

RESULT 4

S54712 zein Zp22/6 protein - maize
 C/Species: Zea mays (maize)
 C/Date: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
 C/Accession: S54712
 R/Chaudhuri, S.; Messing, J.
 Mol. Gen. Genet. 246, 707-715, 1995
 A/Title: RFLP mapping of the maize dzr1 locus, which regulates methionine-rich 10 kDa ze
 A/Reference number: S54712; MUID:95206245; PMID:7898438
 A/Accession: S54712
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-15 <CHA>
 A/Cross-references: UNIPROT:Q7M1F8; UNIPARC:UPI000017B16A

Query Match 26.7%; Score 28; DB 2; Length 15;
 Best Local Similarity 36.4%; Pred. No. 3.4e+02;
 Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 2 PAKGMSPPGF 12
 ||: ||: ||
 Db 4 PQGSLAPPAIL 14

RESULT 5

B60801 acrosome stabilizing factor small chain - rabbit (fragment)
 C/Species: Oryctolagus cuniculus (domestic rabbit)
 C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
 C/Accession: B60801
 R/Wilson, W.L.; Oliphant, G.
 Biol. Reprod. 37, 159-169, 1987
 A/Title: Isolation and biochemical characterization of the subunits of the rabbit sperm
 A/Reference number: A60801; MUID:88000873; PMID:3651543
 A/Accession: B60801
 A/Molecule type: protein
 A/Residues: 1-20 <WIL>
 A/Cross-references: UNIPARC:UPI000017C5B4
 C/Comment: spermatozoa must undergo capacitation and the acrosome reaction to become cap
 C/Keywords: glycoprotein; semen

Query Match 26.7%; Score 28; DB 2; Length 20;
 Best Local Similarity 50.0%; Pred. No. 4.7e+02;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 DPAKMSPPG 10
 ||: ||: ||
 Db 1 DTKKAEP 10

RESULT 6

PT0089 4-hydroxybenzoate 3-monoxygenase (EC 1.14.13.2) - Comamonas testosteroni (fragment)
 A/Alternate names: p-hydroxybenzoate 3-hydroxylase
 C/Species: Comamonas testosteroni
 C/Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004
 C/Accession: PT0089
 R/Taugita, A.
 submitted to JIPID, May 1996
 A/Description: Purification and characterization of p-hydroxybenzoate 3-hydroxylase from
 A/Reference number: PT0089
 A/Accession: PT0089
 A/Molecule type: protein
 A/Residues: 1-21 <CHR>

A:Cross-references: UNIPROT:Q7M1D8; UNIPARC:UPI0000175264
C:Superfamily: 4-hydroxybenzoate 3-monooxygenase
C:Keywords: PAD; homodimer; oxidoreductase

Query Match 26.7%; Score 28; DB 2; Length 21;
Best Local Similarity 35.4%; Pred. No. 5e+02;
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 5 GMSPPGFVGE 15
DB 9 GAGPSGLLGG 19

RESULT 7

C49048
T-cell receptor beta chain V region (CDR3 junction, clone Vbeta20.1) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 30-May-1997
C/Accession: C49048
R:Sloud, M.; Kjeldsen-Kragh, J.; Suleyman, S.; Vinje, O.; Natvig, J.B.; Forre, O.
Eur. J. Immunol. 22, 2413-2418, 1992

A:Title: Limited heterogeneity of T cell receptor variable region gene usage in juvenile
A:Reference number: A49048; MUID:92387250; PMID:1387614
A/Accession: C49048
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-16 <STO>
A:Cross-references: UNIPARC:UPI000017C3A9
A:Experimental source: patient EV, IL-2R+ synovial T-cells
A>Note: sequence extracted from NCBI backbone (NCBIP:113265)
C:Keywords: T-cell receptor

Query Match 25.7%; Score 27; DB 2; Length 16;
Best Local Similarity 57.1%; Pred. No. 5.2e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 8 PPGFVVG 14
DB 10 PPGVTFG 16

RESULT 8

PS0210
28K protein 4209 - rice (strain Nihonbare) (fragment)

C:Species: Oryza sativa (rice)
C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C/Accession: PS0210

R:Tugita, A.; Miyatake, N.
submitted to JIPID, April 1993
A/Reference number: PS0208

A/Accession: PS0210
A:Molecule type: protein
A:Residues: 1-16 <TSA>
A:Cross-references: UNIPROT:Q7M281; UNIPARC:UPI000017B0F9
A:Experimental source: germ. bran, strain Nihonbare
C:Comment: molecular weight 28k, pI 7.3.

Query Match 25.7%; Score 27; DB 2; Length 16;
Best Local Similarity 42.9%; Pred. No. 5.2e+02;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 9 PPGFVGE 15
DB 1 PGLVIGD 7

RESULT 9

S65433
bradykinin - horn fly (fragment)
C:Species: Haematobia irritans (horn fly)
C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C/Accession: S65433
R:Wijffels, G.; Fitzgerald, C.; Gough, J.; Ridding, G.; Elvin, C.; Kemp, D.; Willadsen, H.

Eur. J. Biochem. 237, 414-423, 1996
A:Title: Cloning and characterisation of angiotensin-converting enzyme from the dipter
A:Reference number: S65431; MUID:56215437; PMID:8647080

A/Accession: S65433
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <WIS>
A:Cross-references: UNIPARC:UPI000002CF4A
A>Note: the source is designated as Haematobia irritans exigua

Query Match 24.8%; Score 26; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 PPGF 11
DB 2 PPGF 5

RESULT 10

A43065
hydroxyproline-3-bradykinin - frog (Helleophryne purcelli)

C:Species: Helleophryne purcelli
C>Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C/Accession: A43065
R:Nakajima, T.; Yasuhara, T.; Erpamer, G.F.; Visser, J.
Experientia 35, 1133, 1979
A:Title: Occurrence of Hyp(3)-bradykinin in methanol extracts of the skin of the South
A:Reference number: A43065; MUID:80024576; PMID:488255
A/Accession: A43065

A:Molecule type: protein
A:Residues: 1-9 <NAK>
A:Cross-references: UNIPROT:Q7LZ17; UNIPARC:UPI000002CF4A
C:Keywords: bradykinin; hydroxyproline; skin
F:3/Modified site: hydroxyproline (Pro) #status experimental

Query Match 24.8%; Score 26; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 PPGF 11
DB 2 PPGF 5

RESULT 11

B60246
ornitho-kinin - chicken

C:Species: Gallus gallus (chicken)
C>Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 16-Aug-2004
C/Accession: B60246
R:Kimura, M.; Sueyoshi, T.; Morita, T.; Tanaka, K.; Iwanaga, S.
Adv. Exp. Med. Biol. 247A, 359-367, 1989
A:Title: Ornitho-kininogen and ornitho-kinin: isolation, characterization and chemical
A:Reference number: A60246; MUID:90102072; PMID:2603803
A/Accession: B60246

A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <KIM>
A:Cross-references: UNIPROT:Q7LZ50; UNIPARC:UPI000017A4F8

Query Match 24.8%; Score 26; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 PPGF 11
DB 2 PPGF 5

RESULT 12

A26744
bradykinin-like peptide - garden dagger wasp

N;Alternate names: Thr-6-bradykinin
C:Species: Megascollia flavifrons (garden dagger wasp)
C:Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 05-Oct-2004
C:Accession: A26744
R:Yasuhara, T.; Mantel, P.; Nakajima, T.; Piek, T.
R:Yasuhara, T.; Mantel, P.; Nakajima, T.; Piek, T.
A:Title: Two knins isolated from an extract of the venom reservoirs of the solitary wasp
A:Reference number: A94322; MUID:87293024; PMID:3617088
A:Accession: A26744
A:Molecule type: protein
A:Residues: 1-9 <YAS>
A:Cross-references: UNIPARC:UPI000012DF29

Query Match 24.8%; Score 26; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 PGPF 11
Db 2 PGPF 5

RESULT 13
A61057
Thr-6 bradykinin - scollid wasp (Colpa interrupta)
C:Species: Colpa interrupta
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 05-Oct-2004
C:Accession: A61057
R:Piek, T.; Hue, B.; Mantel, P.; Nakajima, T.; Pelhate, M.; Yasuhara, T.
Comp. Biochem. Physiol. C 96, 157-162, 1990
A:Title: Theocaine(6)-bradykinin in the venom of the wasp Colpa interrupta (F.) presynap
A:Reference number: A61057; MUID:91130217; PMID:1980872
A:Accession: A61057
A:Molecule type: protein
A:Residues: 1-9 <PIE>
A:Cross-references: UNIPARC:UPI000012DF29
C:Keywords: bradykinin; presynaptic neurotoxin; venom

Query Match 24.8%; Score 26; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 PGPF 11
Db 2 PGPF 5

RESULT 14
A60579
bradykinin-like peptide - slider turtle
C:Species: Pseudemys scripta (slider)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 05-Oct-2004
C:Accession: A60579
R:Conlon, J.M.; Hicke, J.W.; Smith, D.D.
Endocrinology 126, 985-991, 1990
A:Title: Isolation and biological activity of a novel kinin ((Thr(6))bradykinin) from th
A:Reference number: A60579; MUID:90126625; PMID:2298179
A:Accession: A60579
A:Molecule type: protein
A:Residues: 1-9 <CON>
A:Cross-references: UNIPARC:UPI000012DF29
C:Keywords: This peptide increases aortic blood flow but, unlike bradykinin in mammalian

Query Match 24.8%; Score 26; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 PGPF 11
Db 2 PGPF 5

RESULT 15
A61363
bradykinin - common frog
C:Species: Rana temporaria (common frog)
C:Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 05-Oct-2004
C:Accession: A61363
R:Anastasi, A.; Erspamer, V.; Bertaccini, G.
Comp. Biochem. Physiol. A 14, 43-52, 1965
A:Title: Occurrence of bradykinin in the skin of Rana temporaria.
A:Reference number: A61363
A:Accession: A61363
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <AMA>
A:Cross-references: UNIPROT:Q7LZJ8; UNIPARC:UPI00002CF4A
C:Keywords: skin

Query Match 24.8%; Score 26; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 PGPF 11
Db 2 PGPF 5

RESULT 16
A61358
bradykinin-like peptide I - Japanese pond frog
C:Species: Rana nigromaculata (Japanese pond frog)
C:Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 05-Oct-2004
C:Accession: A61358
R:Nakajima, T.
Chem. Pharm. Bull. 16, 769-770, 1968
A:Title: Occurrence of a new active peptide on smooth muscle and bradykinin in the skin
A:Reference number: A61358; MUID:68412013; PMID:5677638
A:Accession: A61358
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <NAK>
A:Cross-references: UNIPROT:Q7LZ54; UNIPARC:UPI000017A4F0
C:Keywords: skin

Query Match 24.8%; Score 26; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 PGPF 11
Db 2 PGPF 5

RESULT 17
S13279
Ile-Ser-bradykinin - human (fragment)
N;Alternate names: T-kinin
C:Species: Homo sapiens (man)
C:Date: 02-Dec-1993 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S13279
R:Wunderer, G.; Walter, I.; Eschenbacher, B.; Lang, M.; Kellermann, J.; Kindermann, G.
Biol. Chem. Hoppe-Seyler 371, 977-981, 1990
A:Title: Ile-Ser-bradykinin is an aberrant permeability factor in various human malignan
A:Reference number: S13279; MUID:91166748; PMID:2076202
A:Accession: S13279
A:Molecule type: protein
A:Residues: 1-11 <WUN>
A:Cross-references: UNIPROT:Q7M4P1; UNIPARC:UPI0000148EBE
C:Keywords: bradykinin

Query Match 24.8%; Score 26; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PGPF 11
|||
Db 4 PGPF 7

RESULT 18
B26744

megascoliaktin - garden dagger wasp
N:Alternate names: 6-Thr-bradykinin-Lys-Ala
C:Species: Megascollia flavifrons (garden dagger wasp)
C:Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 05-Oct-2004
C:Accession: B26744; A28609
R:Yashnara, T.; Mantel, P.; Nakajima, T.; Plek, T.
Toxicol 25, 527-535, 1987
A:Title: Two kinins isolated from an extract of the venom reservoirs of the solitary wasp
A:Reference number: A94322; MUID:87293024; PMID:3617088
A:Accession: B26744
A:Molecule type: protein
A:Residues: 1-11 <YAS>
A:Cross-references: UNIPROT:P12797; UNIPARC:UPI0000126AD6
R:Nakajima, T.; Plek, T.; Yashnara, T.; Mantel, P.
Toxicol 26, 34, 1988
A:Title: Two kinins isolated from the venom of Megascollia flavifrons.
A:Reference number: A28609
A:Accession: A28609
A:Molecule type: protein
A:Residues: 1-11 <NAK>
A:Cross-references: UNIPARC:UPI0000126AD6
C:Keywords: bradykinin; presynaptic neurotoxin; venom

Query Match 24.8%; Score 26; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PGPF 11
|||
Db 2 PGPF 5

RESULT 19
A61365

Phylloklinin - Rohde's leaf frog
N:Alternate names: bradykinin-1-isoleucyl-tyrosine-O-sulfate
C:Species: Phyllomedusa rohdei (Rohde's leaf frog)
C:Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 05-Oct-2004
C:Accession: A61365
R:Anastasi, A.; Bertaccini, G.; Erppamer, V.
Br. J. Pharmacol. 27, 479-485, 1966
A:Title: Pharmacological data on phylloklinin (bradykinin-1-isoleucyl-tyrosine-O-sulphate)
A:Reference number: A61365; MUID:67179312; PMID:5970899
A:Accession: A61365
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-11 <ANA>
A:Cross-references: UNIPROT:Q7LZ52; UNIPARC:UPI000017A4F2
C:Keywords: sulfoprotein
F:11/Binding site: sulfate (Tyr) (covalent) #status experimental

Query Match 24.8%; Score 26; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PGPF 11
|||
Db 2 PGPF 5

RESULT 20

A61360
vespakinin M - hornet (Vespa mandarinia)
C:Species: Vespa mandarinia
C:Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 05-Oct-2004
C:Accession: A61360

R:Kishimura, H.; Yasuhara, T.; Yoshida, H.; Nakajima, T.
Chem. Pharm. Bull. 24, 2896-2897, 1976
A:Title: Vespakinin-M, a novel bradykinin analogue containing hydroxyproline, in the ve
A:Reference number: A61360; MUID:77114342; PMID:1017116
A:Accession: A61360
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-12 <KIS>
A:Cross-references: UNIPROT:Q7M3T3; UNIPARC:UPI000017A4F3
C:Keywords: hydroxyproline; venom
F:4/Modified site: 4-hydroxyproline (Pro) #status experimental

Query Match 24.8%; Score 26; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PGPF 11
|||
Db 3 PGPF 6

RESULT 21

A61359
vespakinin X - hornet (Vespa xanthoptera)
C:Species: Vespa xanthoptera
C:Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 05-Oct-2004
C:Accession: A61359
R:Yashnara, T.; Yoshida, H.; Nakajima, T.
Chem. Pharm. Bull. 25, 936-941, 1977
A:Title: Chemical investigation of the hornet (Vespa xanthoptera Cameron) venom. The st
A:Reference number: A61359; MUID:87187853; PMID:264186
A:Accession: A61359
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-12 <YAS>
A:Cross-references: UNIPROT:Q7M3T2; UNIPARC:UPI000017A4F4
C:Keywords: venom

Query Match 24.8%; Score 26; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PGPF 11
|||
Db 3 PGPF 6

RESULT 22

A61361
bradykinin-like peptide - Bombina orientalis
C:Species: Bombina orientalis
C:Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 05-Oct-2004
C:Accession: A61361
R:Yashnara, T.; Hira, M.; Nakajima, T.; Yanahara, N.; Yanahara, C.; Hashimoto, T.; Sa
Chem. Pharm. Bull. 21, 1388-1391, 1973
A:Title: Active peptides on smooth muscle in the skin of Bombina orientalis Boulenger a
A:Reference number: A61361; MUID:73256822; PMID:4732297
A:Accession: A61361
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-13 <YAS>
A:Cross-references: UNIPROT:P83060; UNIPARC:UPI000017A4F5
C:Keywords: skin

Query Match 24.8%; Score 26; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PGPF 11
|||
Db 2 PGPF 5

RESULT 23

A61362
bradykinin-like peptide III - Japanese pond frog
C:Species: Rana nigromaculata (Japanese pond frog)
C>Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 05-Oct-2004
C:Accession: A61362
R:Nakajima, T.
Chem. Pharm. Bull. 16, 2088-2089, 1968
A:Title: On the third active peptide on smooth muscle in the skin of Rana nigromaculata
A:Reference number: A61362; MUID:65117202; PMID:5751736
A:Accession: A61362
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-14 <NAK>
A:Cross-references: UNIPROT:Q7LZ53; UNIPARC:UPI000017AAFI
C:Keywords: skin

Query Match 24.8%; Score 26; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PPGF 11
|||
Db 2 PPGF 5

RESULT 24

A36279
chemoattractant protein - earthworm (Lumbricus terrestris) (fragment)
C:Species: Lumbricus terrestris (common earthworm)
C>Date: 18-Jan-1991 #sequence_revision 18-Jan-1991 #text_change 09-Jul-2004
C:Accession: A36279
R:Jiang, X.C.; Inouchi, J.; Wang, D.; Halpern, M.
J. Biol. Chem. 265, 8736-8744, 1990
A:Title: Purification and characterization of a chemoattractant from electric shock-induced snakes.
A:Reference number: A36279; MUID:90256800; PMID:2160465
A:Accession: A36279
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <JIA>
A:Cross-references: UNIPROT:O44335; UNIPARC:UPI000017BD77

Query Match 24.8%; Score 26; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PPGF 11
|||
Db 5 PPGF 8

RESULT 25

A61339
vespulinin 1 - eastern yellowjacket
N:Contains: vespulinin 2
C:Species: Vespula maculifrons (eastern yellowjacket)
C>Date: 17-Jul-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C:Accession: A61339
R:Yoshida, H.; Geller, R.G.; Pisano, J.J.
Biochemistry 15, 61-64, 1976
A:Title: Vespulinin: new carbohydrate-containing bradykinin derivatives.
A:Reference number: A61339; MUID:76114777; PMID:1247511
A:Accession: A61339
A:Molecule type: protein
A:Residues: 1-17 <YOS>
A:Cross-references: UNIPROT:P57672; UNIPARC:UPI0000138459
C:Superfamily: vespulinin
C:Keywords: antihypertensive; bradykinin; glycoprotein; venom
F1-17/Product: vespulinin 1 #status experimental <MAT1>
F3-17/Product: vespulinin 2 #status experimental <MAT2>
F9-17/Region: bradykinin-like
F3,4/Binding site: carbohydrate (Thr) (covalent) #status experimental

Query Match 24.8%; Score 26; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PPGF 11
|||
Db 10 PPGF 13

Search completed: January 26, 2006, 08:05:06
Job time : 11 secs

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OM protein - protein search, using sw model

Run on: January 26, 2006, 07:47:56 ; Search time 59,4828 Seconds
(without alignments)
237.221 Million cell updates/sec

Title: US-09-662-293-13

Perfect score: 105

Sequence: 1 DPAKMSPPGPIVCEGVLS 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 15779

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%

Database : Listing first 100 summaries

Uniprot 05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	30.5	15	2	Q7M4P9_HUMAN
2	30	28.6	17	2	Q6N6S9_VITVI
3	30	28.6	18	2	Q6NFB4_HUMAN
4	28	26.7	10	2	Q7M2N0_BOVIN
5	28	26.7	15	2	Q7M1F8_MAIZE
6	28	26.7	16	2	Q7SM54_DELA
7	28	26.7	20	2	Q71HRS_LACDU
8	28	26.7	20	2	Q79CFO_RHILE
9	28	26.7	21	2	Q7M1D8_COMTE
10	27	25.7	16	2	Q7M2B1_ORYSA
11	27	25.7	16	2	Q9T2Q4_BRANA
12	27	25.7	19	2	Q9N195_BOVIN
13	27	25.7	21	2	Q9S554_MOUSE
14	26	24.8	9	1	BRK1_RANNI
15	26	24.8	9	1	KNL3_BOMVA
16	26	24.8	9	1	KNL3_CYPDO
17	26	24.8	9	2	P84497_TRASC
18	26	24.8	9	2	Q7L250_CHICK
19	26	24.8	9	2	Q7L2J8_CHICK
20	26	24.8	9	2	Q7L2T7_SNEOB
21	26	24.8	11	1	BRKP_PHYRO
22	26	24.8	11	1	BRK_MEGFL
23	26	24.8	11	2	Q7S811_HUMAN
24	26	24.8	11	2	Q7M4P1_HUMAN
25	26	24.8	12	1	VESP_VESMA
26	26	24.8	12	1	VESP_VESXA
27	26	24.8	13	1	BRK_PARID
28	26	24.8	13	1	SCX2_TITDI
29	26	24.8	14	1	BRK3_RANNI
30	26	24.8	15	2	Q9R5T1_9FLAO
31	26	24.8	17	1	TL09_SPIOL

32	26	24.8	17	1	VESP_VESMC	P57672 vespuia mac
33	26	24.8	18	2	Q16053_HUMAN	Q16053 homo sapien
34	25.5	24.3	18	2	Q763U4_USEUD	Q763U4 naravelia l
35	25.5	24.3	18	2	Q763U5_CLEVI	Q763U5 clematis vi
36	25.5	24.3	20	2	Q763W5_USEUD	Q763W5 clematis ja
37	25.5	24.3	21	2	Q763T7_USEUD	Q763T7 knowltonia
38	25.5	24.3	21	2	Q763T9_USEUD	Q763T9 pulsatilla
39	25.5	24.3	21	2	Q763U0_USEUD	Q763U0 anemone fla
40	25.5	24.3	21	2	Q763U1_USEUD	Q763U1 clematis vi
41	25.5	24.3	21	2	Q763U2_USEUD	Q763U2 clematis ge
42	25.5	24.3	21	2	Q763U3_USEUD	Q763U3 clematis ei
43	25.5	24.3	21	2	Q763U6_USEUD	Q763U6 clematis no
44	25.5	24.3	21	2	Q763U7_USEUD	Q763U7 clematis se
45	25.5	24.3	21	2	Q763U8_USEUD	Q763U8 clematis fr
46	25.5	24.3	21	2	Q763U9_USEUD	Q763U9 clematis ba
47	25.5	24.3	21	2	Q763V0_USEUD	Q763V0 clematis de
48	25.5	24.3	21	2	Q763V3_USEUD	Q763V3 clematis an
49	25.5	24.3	21	2	Q763V4_USEUD	Q763V4 clematis po
50	25.5	24.3	21	2	Q763V5_USEUD	Q763V5 clematis te
51	25.5	24.3	21	2	Q763V6_USEUD	Q763V6 clematis or
52	25.5	24.3	21	2	Q763V7_USEUD	Q763V7 clematis ca
53	25.5	24.3	21	2	Q763V8_USEUD	Q763V8 clematis cr
54	25.5	24.3	21	2	Q763V9_USEUD	Q763V9 clematis af
55	25.5	24.3	21	2	Q763W0_USEUD	Q763W0 clematis ta
56	25.5	24.3	21	2	Q763W1_USEUD	Q763W1 clematis pi
57	25.5	24.3	21	2	Q763W2_USEUD	Q763W2 clematis al
58	25.5	24.3	21	2	Q763W3_USEUD	Q763W3 clematis un
59	25.5	24.3	21	2	Q763W4_USEUD	Q763W4 clematis st
60	25.5	24.3	21	2	Q763W7_USEUD	Q763W7 clematis la
61	25.5	24.3	21	2	Q763W8_USEUD	Q763W8 clematis pa
62	25.5	24.3	21	2	Q763X0_USEUD	Q763X0 clematis oc
63	25.5	24.3	21	2	Q763X1_USEUD	Q763X1 clematis wi
64	25.5	24.3	21	2	Q763X2_USEUD	Q763X2 clematis ap
65	25.5	24.3	21	2	Q763X3_CLELI	Q763X3 clematis fu
66	25.5	24.3	21	2	Q763V1_CLELI	Q763V1 clematis li
67	25.5	24.3	21	2	Q763W9_CLEFE	Q763W9 clematis le
68	25.5	24.3	21	2	Q763V2_CLELA	Q763V2 clematis la
69	25.5	24.3	21	2	Q763W6_CLEFL	Q763W6 clematis fl
70	25	23.8	10	1	TM0F_AEDAE	P19425 aedes aegypt
71	25	23.8	10	2	Q7M3T6_TRIGR	Q7M3T6 tritipneustes
72	25	23.8	12	2	Q4W620_9CALI	Q4W620 norovirus n
73	25	23.8	12	2	Q84268_9PAPI	Q84268 human papil
74	25	23.8	13	1	FARB_ASCSU	P33173 ascaris suu
75	25	23.8	13	2	Q16007_HUMAN	Q16007 homo sapien
76	25	23.8	18	2	Q9Z190_MOUSE	Q9Z190 mus musculu
77	25	23.8	19	1	TRP3_LEDMA	P81735 leucophaea
78	25	23.8	20	1	PYRX_PSEFL	P65586 pseudomonas
79	25	23.8	20	2	Q90V63_MURCI	Q90V63 rattus sp.
80	25	23.8	20	2	Q7L2H3_MELCA	Q7L2H3 meleagris g
81	25	23.8	21	2	Q5HCHE_HUMAN	Q5HCHE homo sapien
82	25	23.8	21	2	Q9UC26_HUMAN	Q9UC26 homo sapien
83	24	22.9	10	2	Q7M4B6_STRNU	Q7M4B6 strongyloce
84	24	22.9	11	2	Q7M4D4_PSEDP	Q7M4D4 pseudocentr
85	24	22.9	11	2	P82436_TOBAC	P82436 nicotiana t
86	24	22.9	15	2	Q80XQ4_TMESAU	Q80XQ4 mesocricetu
87	24	22.9	17	2	Q9HE01_PARER	Q9HE01 paracoccidi
88	24	22.9	17	2	Q9HE02_AJEBE	Q9HE02 ajelloyces
89	24	22.9	17	2	Q9HE03_AJEBE	Q9HE03 ajelloyces
90	24	22.9	17	2	Q49077_MYCCA	Q49077 mycoplasma
91	24	22.9	19	2	Q7MS46_HALBA	Q7MS46 halobacteri
92	24	22.9	19	2	Q77S06_GCTIC	Q77S06 porcine cir
93	24	22.9	19	2	Q9Y1T3_GCTIC	Q9Y1T3 bovine circ
94	24	22.9	20	2	Q9T2I8_NICSY	Q9T2I8 nicotiana s
95	24	22.9	20	2	Q9T2I9_NICSY	Q9T2I9 nicotiana s
96	24	22.9	21	2	Q9MBH5_9CAUD	Q9MBH5 streptococc
97	23.5	22.4	12	2	Q5ISY4_9CALI	Q5ISY4 norovirus t
98	23.5	22.4	12	2	Q5ISY5_9CALI	Q5ISY5 norovirus t
99	23.5	22.4	16	2	Q506K8_9CALI	Q506K8 norovirus h
100	23.5	22.4	18	2	Q88290_9CALI	Q88290 small round

ALIGNMENTS

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RESULT 1
Q7M4P9_HUMAN PRELIMINARY; PRT; 15 AA.
ID Q7M4P9_HUMAN PRELIMINARY; PRT; 15 AA.
AC Q7M4P9;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DE 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Galbladder stone matrix protein 2, 41k (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1];
RP PROTEIN SEQUENCE.
RA Binette J.P., Binette M.B.;
RL Submitted (FEB-1996) to the PIR data bank.
DR PIR; F57789; F57789.
FT NON_TER 1 1
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1539 MW; DD8774ED4B7A4786 CRC64;

Query Match 30.5%; Score 32; DB 2; Length 15;
Best Local Similarity 60.0%; Pred. No. 8.3e+02;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 8 PPGFIVEEG 17
DB 5 PDGFIEGSSG 14

RESULT 2
Q6N69_VITVI PRELIMINARY; PRT; 17 AA.
ID Q6N69_VITVI PRELIMINARY; PRT; 17 AA.
AC Q6N69;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE 20S proteasome beta subunit (Fragment).
OS Vitis vinifera (Grape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Vitaceae; Vitis.
OX NCBI_TaxID=29760;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RA TISSUE-Leaf;
RA Carvalho M.B., Caeiro A.S., Price C.B., Teixeira A.R., Ferreira R.B.;
RL Submitted (JUL-2004) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY684130; AAU04834.1.; mRNA.
DR GO; GO:0005829; C:cytosol; IEA.
KW Proteasome.
FT NON_TER 1 1
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 1808 MW; C19F776A03A8BD9F CRC64;

Query Match 28.6%; Score 30; DB 2; Length 17;
Best Local Similarity 50.0%; Pred. No. 1.9e+03;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 2 PAKGMSPPGIVE 15
DB 3 PAKGTTTIAFLFKE 16

RESULT 3
Q8NFB4_HUMAN PRELIMINARY; PRT; 18 AA.
ID Q8NFB4_HUMAN PRELIMINARY; PRT; 18 AA.
AC Q8NFB4;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)

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DE Mutant enamelrin (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22294456; PubMed=12407086;
RA Kida M., Ariga T., Shirakawa T., Oguchi H., Sakiyama Y.;
RT "Autosomal-dominant hypoplastic form of amelogenesis imperfecta caused
RT by an enamelrin gene mutation at the exon-intron boundary.";
RL J. Dent. Res. 81:738-742(2002).
DR EMBL; AF530444; AAM97323.1.; Genomic_DNA.
FT NON_TER 1 1
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 1893 MW; 492D282E3B8BE512 CRC64;

Query Match 28.6%; Score 30; DB 2; Length 18;
Best Local Similarity 43.8%; Pred. No. 2.1e+03;
Matches 7; Conservative 2; Mismatches 3; Indels 4; Gaps 1;

QY 6 MSPPGF---IVGEEG 17
DB 2 LPPPGYGRPPISNEEG 17

RESULT 4
Q7M2N0_BOVIN PRELIMINARY; PRT; 10 AA.
ID Q7M2N0_BOVIN PRELIMINARY; PRT; 10 AA.
AC Q7M2N0;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Collagen alpha 1(VI) chain (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1];
RP PROTEIN SEQUENCE.
RX PubMed=6852033;
RA Jander R., Rautenberg J., Glanville R.W.;
RT "Further characterization of the three polypeptide chains of bovine
RT and human short-chain collagen (intima collagen).";
RL Eur. J. Biochem. 133:39-46(1983).
DR PIR; S26506; S26506.
FT NON_TER 1 1
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 965 MW; CAA96668640DC776 CRC64;

Query Match 26.7%; Score 28; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 2.3e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY 2 PAKGMSPPG 10
DB 4 PARG--PPG 10

RESULT 5
Q7M1F8_MAIZE PRELIMINARY; PRT; 15 AA.
ID Q7M1F8_MAIZE PRELIMINARY; PRT; 15 AA.
AC Q7M1F8;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Zein Zp22/6 protein.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.

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OK NCBI_TaxID=4577;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=95206245; PubMed=7898438; DOI=10.1007/BF00290716;
 RA Chaudhuri S., Messing J.,
 RT "RFLP mapping of the maize dzrl locus, which regulates methionine-rich
 RL 10 kDa zein accumulation.";
 DR Mol. Gen. Genet. 246:707-715(1995).
 PIR: S54712; S54712.
 SQ SEQUENCE 15 AA; 1605 MW; 5DFB414D8D001609 CRC64;

Query Match 26.7%; Score 28; DB 2; Length 15;
 Best Local Similarity 36.4%; Pred. No. 3.5e+03;
 Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 PAKMSPPGFI 12
 DB 4 PQOSLAPPAII 14

RESULT 6

ID Q7SM54_9DELA PRELIMINARY; PRT; 16 AA.
 AC Q7SM54;
 DT 01-OCT-2003 (TReMBLrel. 25; Created)
 DT 01-OCT-2003 (TReMBLrel. 25; Last sequence update)
 DE tax protein (Fragment).
 OS Human T-lymphotropic virus 1.
 OC Viruses; Retroviroidea; Retroviridae; Deltaretrovirus.
 NC NCBI_TaxID=11908;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Gonzalez Perez M.P., Garcia Sainz A.,
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF529562; AAP87693.1; -; Genomic_DNA.
 FT NON TER 1
 SQ SEQUENCE 16 AA; 1782 MW; 9CDDDFE4146E2F CRC64;

Query Match 26.7%; Score 28; DB 2; Length 16;
 Best Local Similarity 66.7%; Pred. No. 3.7e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 GMSPPG 10
 DB 2 GLEPPG 7

RESULT 7

ID Q71HR5_LACDL PRELIMINARY; PRT; 20 AA.
 AC Q71HR5;
 DT 05-JUL-2004 (TReMBLrel. 27; Created)
 DT 05-JUL-2004 (TReMBLrel. 27; Last sequence update)
 DT 05-JUL-2004 (TReMBLrel. 27; Last annotation update)
 DE histidyl-tRNA synthetase (EC 6.1.1.21) (Fragment).
 OS Lactobacillus delbrueckii (subsp. lactis).
 OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 OC Lactobacillus.
 NC NCBI_TaxID=29397;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Langenheim J.F., Ulrich R.L.,
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF96531; AAC07223.1; -; Genomic_DNA.
 DR GO; GO:0004821; F:histidine-tRNA ligase activity; IEA.
 KW Aminoacyl-tRNA synthetase; Ligase.
 FT NON TER 1
 SQ SEQUENCE 20 AA; 2123 MW; 43ABC93211F8210C CRC64;

Query Match 26.7%; Score 28; DB 2; Length 20;
 Best Local Similarity 50.0%; Pred. No. 4.7e+03;
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 10 GFIVGEEGVL 19
 DB 11 GFGIGEEELM 20

RESULT 8

ID Q79CF0_RHILE PRELIMINARY; PRT; 20 AA.
 AC Q79CF0;
 DT 05-JUL-2004 (TReMBLrel. 27; Created)
 DT 05-JUL-2004 (TReMBLrel. 27; Last sequence update)
 DT 05-JUL-2004 (TReMBLrel. 27; Last annotation update)
 DE 4-hydroxybenzoate hydroxylase (EC 1.14.13.2) (Fragment).
 GN Name=poba.
 OS Rhizobium leguminosarum.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
 NC NCBI_TaxID=384;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA STRAIN=B155;
 RC Wong C.M., Dilworth M.J., Glenn A.R.,
 RT "4-Hydroxybenzoate hydroxylase (poba) is positively regulated by pobR
 RL in Rhizobium leguminosarum bv. viciael.";
 RL FEWS Microbiol. Lett. 0:0-0(1995).
 DR EMBL; U40388; AAA83007.1; -; Genomic_DNA.
 DR HSSP; P20586; 1K01
 DR GO; GO:0018659; F:4-hydroxybenzoate 3-monooxygenase activity; IEA.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR InterPro; IPR002938; MoxY_FAD_binding.
 DR Pfam; PF01494; FAD_binding_3; 1.
 KW Oxidoreductase.
 FT NON TER 20
 SQ SEQUENCE 20 AA; 2011 MW; 378D1B9CB7605522 CRC64;

Query Match 26.7%; Score 28; DB 2; Length 20;
 Best Local Similarity 36.4%; Pred. No. 4.7e+03;
 Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 5 GMSPPGFI 15
 DB 9 GSGSPGILGQ 19

RESULT 9

ID Q7MID8_COMTE PRELIMINARY; PRT; 21 AA.
 AC Q7MID8;
 DT 01-MAR-2004 (TReMBLrel. 26; Created)
 DT 01-MAR-2004 (TReMBLrel. 26; Last sequence update)
 DT 01-MAR-2004 (TReMBLrel. 26; Last annotation update)
 DE 4-hydroxybenzoate 3-monooxygenase (EC 1.14.13.2) (Fragment).
 OS Comamonas testosteroni (Pseudomonas testosteroni).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Comamonadaceae; Comamonas.
 NC NCBI_TaxID=285;
 RN [1]
 RP PROTEIN SEQUENCE.
 RA Taugita A.,
 RL Submitted (MAY-1996) to the PIR data bank.
 DR PIR; P10089; P10089.
 DR HSSP; P20586; 11UT.
 DR GO; GO:0018659; F:4-hydroxybenzoate 3-monooxygenase activity; IEA.
 DR InterPro; IPR002938; MoxY_FAD_binding.
 DR Pfam; PF01494; FAD_binding_3; 1.
 FT NON TER 21
 SQ SEQUENCE 21 AA; 2109 MW; 52178D0D46B76055 CRC64;

Query Match 26.7%; Score 28; DB 2; Length 21;

Query Match	Score 27:	DB 2: length
FT NON_TER	1	1
FT NON_TER	21	21
SQ SEQUENCE	21 AA;	2366 MW; 103EC45620595224 CRC64

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Best Local Similarity 40.0%; Pred. No. 7.1e+03;
Matches 8; Conservative 2; Mismatches 4; Indels 6; Gaps 1;

Qy 1 DPAKMSPPRIVEEGVLS 20
Db 5 DPARLQP-----ERGLS 18

RESULT 14

BRK1_RANNT

ID BRK1_RANNT STANDARD; PRT; 9 AA.

AC Q7L254;

DT 05-JUL-2004 (Rel. 44, Created)

DT 05-JUL-2004 (Rel. 44, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE Bradykinin-like peptide 1.

OS Rana nigromaculata (Japanese pond frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana;

OC Pelophylax.

OX NCBI_TaxID=8409;

RN [1]

RP PROTEIN SEQUENCE.

RX MEDLINE=68412013; PubMed=5677638;

RA Nakajima T.;

RT "Occurrence of a new active peptide on smooth muscle and bradykinin in the skin of Rana nigromaculata hallowell.",

RL Chem. Pharm. Bull. 16:769-770(1968).

CC -1- FUNCTION: Induces smooth muscle contraction.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- SIMILARITY: Belongs to the bradykinin family.

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DR PIR; A61358; A61358.

KW Bradykinin; Direct protein sequencing; Vasoactive; Vasodilator.

SQ SEQUENCE 9 AA; 1017 MW; 3687D771A9C86777 CRC64;

Query Match 24.8%; Score 26; DB 1; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.2e+06;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PGPF 11

Db 2 PGPF 5

RESULT 15

KNL3_BOMVA

ID KNL3_BOMVA STANDARD; PRT; 9 AA.

AC P83058;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE [Thr6]bradykinin.

OS Bombina variegata (Yellow-bellied toad).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Archaeobatrachia; Bombinatoridae; Bombina.

OX NCBI_TaxID=8348;

RN [1]

RP PROTEIN SEQUENCE, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.

RX MEDLINE=22217713; PubMed=12230583;

RA Chen T., Orr D.F., Bjournson A.J., McClean S., O'Rourke M., Hirst D.G., Rao P., Shaw C.;

RT "Novel bradykinins and their precursor cDNAs from European yellow-bellied toad (Bombina variegata) skin.",

RL Eur. J. Biochem. 269:4693-4700(2002).

CC -1- FUNCTION: Produces in vitro relaxation of rat arterial smooth muscle and constriction of intestinal smooth muscle.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: Expressed by the skin glands.

CC -1- SIMILARITY: Belongs to the bradykinin family.

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OY 8 PGPF 11
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 DB 2 PGPF 5

RESULT 17

ID P84497 TRASC PRELIMINARY; PRT; 9 AA.
 AC P84497;
 DT 10-MAY-2005 (TREMBLrel. 30, Created)
 DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)
 DE [Thr6]bradykinin.
 OS Trachemys scripta (Red-eared slider turtle) (Pseudemys scripta).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Testudines; Cryptodira; Testudinoidae; Emydidae; Trachemys.
 OX NCBI_TaxID=34903;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX PubMed=2298179;
 RA Conlon J.M., Hicks J.W., Smith D.D.;
 RT "Isolation and biological activity of a novel kinin
 (Thr(6)bradykinin) from the turtle, Pseudemys scripta.";
 RL Endocrinology 126:985-991(1990).
 KW Direct protein sequencing.
 SQ SEQUENCE 9 AA; 1074 MW; 3393D771A9C86777 CRC64;

Query Match 24.8%; Score 26; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 PGPF 11
 ||||
 DB 2 PGPF 5

RESULT 18

ID Q7LZ50 CHICK PRELIMINARY; PRT; 9 AA.
 AC Q7LZ50;
 DT 01-MAR-2004 (TREMBLrel. 26, Created)
 DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Ornitho-kinin.
 OS Gallus gallus (Chicken).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=90102072; PubMed=2603803;
 RA Kimura M., Sueyoshi T., Morita T., Tanaka K., Iwanaga S.;
 RT "Ornitho-kininogen and ornitho-kinin: isolation, characterization and
 chemical structure.";
 RL Adv. Exp. Med. Biol. 247A:359-367(1989).
 DR PIR; B60246; B60246.
 SQ SEQUENCE 9 AA; 1040 MW; 339D3771A9C86777 CRC64;

Query Match 24.8%; Score 26; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 PGPF 11
 ||||
 DB 2 PGPF 5

RESULT 19
 Q7LZJ8 RANTE
 ID Q7LZJ8 RANTE PRELIMINARY; PRT; 9 AA.
 AC Q7LZJ8;

DT 01-MAR-2004 (TREMBLrel. 26, Created)
 DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Bradykinin.
 OS Rana temporaria (European common frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana;
 CC Rana.
 OX NCBI_TaxID=8407;
 RN [1]
 RP PROTEIN SEQUENCE.
 RA Anastasi A., Erspamer V., Bertaccini G.;
 RT "Occurrence of bradykinin in the skin of Rana temporaria.";
 RL Comp. Biochem. Physiol. 14:43-52(1965).
 DR PIR; A61363; A61363.
 SQ SEQUENCE 9 AA; 1060 MW; 3393D775B9C86777 CRC64;

Query Match 24.8%; Score 26; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 20

ID Q7LZ17 9NEOB PRELIMINARY; PRT; 9 AA.
 AC Q7LZ17;
 DT 01-MAR-2004 (TREMBLrel. 26, Created)
 DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Hydroxyproline-3-bradykinin.
 OS Heliophryne purcellii (Cape ghost frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Heliophrynidae;
 OC Heliophryne.
 OX NCBI_TaxID=31911;
 RN [1]
 RP PROTEIN SEQUENCE.
 RA Nakajima T., Yasuhara T., Erspamer G.F., Visser J.;
 RT "Occurrence of Hyp(3)-bradykinin in methanol extracts of the skin of
 the South African leptodactylid frog Heliophryne purcellii.";
 RL Experientia 35:1133-1133(1979).
 RN [2]
 RP PROTEIN SEQUENCE.
 RX PubMed=488255;
 RA Nakajima T., Yasuhara T., Erspamer G.F., Visser J.;
 RT "Occurrence of Hyp3-bradykinin in methanol extracts of the skin of the
 South African leptodactylid frog Heliophryne purcellii.";
 RL Experientia 35:1133-0(1979).
 DR PIR; A43065; A43065.
 SQ SEQUENCE 9 AA; 1060 MW; 3393D775B9C86777 CRC64;

Query Match 24.8%; Score 26; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 PGPF 11
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 DB 2 PGPF 5

RESULT 21

BRKP_PHYRO
 ID BRKP_PHYRO STANDARD; PRT; 11 AA.
 AC Q7LZ52;
 DT 05-JUL-2004 (Rel. 44, Created)
 DT 05-JUL-2004 (Rel. 44, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Phyllokinin (Bradykinin)-isoleucyl-tyrosine O-sulfate).
 OS Phylomedusa rohdei (Rohde's leaf frog).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;
 CC Phyllomedusinae; Phyllomedusa.
 CC NCBI_TaxID=8394;
 CC [1]
 CC PROTEIN SEQUENCE AND SULFATION OF TYR-11.
 CC MEDLINE=67179312; PubMed=5970899;
 CC RA Anastasi A., Bertaccini G., Erspamer V.;
 CC RT "Pharmacological data on phyllokinin (bradykinin-1-isoleucyl-tyrosine O-
 CC sulphate) and bradykinin-1-isoleucyl-tyrosine";
 CC Br. J. Pharmacol. 27:479-485(1966).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the bradykinin family.
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC
 CC DR PIR: A61365.
 CC KM Bradykinin; Direct protein sequencing; Sulfation; Vasoactive;
 CC Vasoconstrictor.
 CC FT MOD_RES 11 Sulfotyrosine.
 CC SQ SEQUENCE 11 AA; 1337 MW; 25051393D75B9C8 CRC64;
 CC
 CC Query Match 24.8%; Score 26; DB 1; Length 11;
 CC Best Local Similarity 100.0%; Pred. No. 5.1e+03;
 CC Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 8 PGPF 11
 CC [1]
 CC [1]
 CC [1]
 CC Db 2 PGPF 5

RESULT 22
 BRK_MEGFL STANDARD; PRT; 11 AA.
 AC P12797;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Megascollakinin ([Thr6]bradykinin-Lys-Ala) [Contains: Bradykinin-like
 DE peptide ([Thr6]bradykinin)].
 OS Megascollia flavifrons (Garden dagger wasp) (Solitary wasp).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
 OC Scolidae; Megascollia.
 CC NCBI_TaxID=7437;
 CC RN [1]
 CC RP PROTEIN SEQUENCE.
 CC RC TISSUE=Venom;
 CC MEDLINE=87233024; PubMed=3617088; DOI=10.1016/0041-0101(87)90288-1;
 CC RA Yasuhara T., Mantel P., Nakajima T., Plek T.;
 CC RT "Two kinds isolated from an extract of the venom reservoirs of the
 CC solitary wasp Megascollia flavifrons";
 CC Toxicon 25:527-535(1987).
 CC [2]
 CC PROTEIN SEQUENCE.
 CC RC TISSUE=Venom;
 CC RA Nakajima T., Plek T., Yasuhara T., Mantel P.;
 CC RT "Two kinds isolated from the venom of Megascollia flavifrons";
 CC Toxicon 26:34-34(1988).
 CC -1- FUNCTION: Both proteins have bradykinin-like, although lower
 CC activities (e.g. smooth muscle contraction).
 CC -1- SUBCELLULAR LOCATION: Secreted; venom reservoirs.
 CC -1- SIMILARITY: Belongs to the bradykinin family.
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 CC removed.

CC
 CC DR PIR: A26744; A26744.
 CC DR PIR: B26744; B26744.
 CC DR GO: GO:0005615; C:extracellular space; IDA.
 CC DR GO: GO:0045776; P:negative regulation of blood pressure; ISS.
 CC DR GO: GO:0045987; P:positive regulation of smooth muscle contra. TAS.
 CC KM Bradykinin; Direct protein sequencing; Vasoactive; Vasoconstrictor.
 CC FT PEPTIDE 11
 CC FT PEPTIDE 1 9 Bradykinin-like peptide.
 CC SQ SEQUENCE 11 AA; 1274 MW; 33867393D771A9C8 CRC64;
 CC
 CC Query Match 24.8%; Score 26; DB 1; Length 11;
 CC Best Local Similarity 100.0%; Pred. No. 5.1e+03;
 CC Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 8 PGPF 11
 CC [1]
 CC [1]
 CC [1]
 CC Db 2 PGPF 5

RESULT 23
 075811_HUMAN PRELIMINARY; PRT; 11 AA.
 ID 075811_HUMAN PRELIMINARY;
 AC 075811;
 DT 01-NOV-1998 (TRENBLUREL. 08, Created)
 DT 01-NOV-1998 (TRENBLUREL. 08, Last sequence update)
 DT 01-NOV-1998 (TRENBLUREL. 08, Last annotation update)
 DE E2B-3 R2 (Fragment).
 OS Homo sapiens (Human).
 CC Name=c-erbB-3;
 CC NCBI_TaxID=9606;
 CC RN [1]
 CC RP NUCLEOTIDE SEQUENCE.
 CC RC TISSUE=Ovarian carcinoma;
 CC MEDLINE=98345147; PubMed=9681822; DOI=10.1038/sj.onc.1201866;
 CC RA Lee H., Mainle N.J.;
 CC RT "Isolation and characterization of four alternate c-erbB3 transcripts
 CC expressed in ovarian carcinoma-derived cell lines and normal human
 CC tissues";
 CC Oncogene 16:3243-3252(1998).
 CC DR EMBL, U88358; AAC39858.1; mRNA.
 CC FT NON_CODING 1
 CC SQ SEQUENCE 11 AA; 1017 MW; 21B23636EB72878 CRC64;
 CC
 CC Query Match 24.8%; Score 26; DB 2; Length 11;
 CC Best Local Similarity 40.0%; Pred. No. 5.1e+03;
 CC Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 CC
 CC QY 1 DPAKMSPPG 10
 CC [1]
 CC [1]
 CC [1]
 CC Db 1 EPCGGLCPKG 10

RESULT 24
 07M4P1_HUMAN PRELIMINARY; PRT; 11 AA.
 ID 07M4P1_HUMAN PRELIMINARY;
 AC 07M4P1;
 DT 01-MAR-2004 (TRENBLUREL. 26, Created)
 DT 01-MAR-2004 (TRENBLUREL. 26, Last sequence update)
 DT 01-MAR-2004 (TRENBLUREL. 26, Last annotation update)
 DE Ile-Ser-Bradykinin (Fragment).
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 CC Homo.
 CC NCBI_TaxID=9606;
 CC RN [1]
 CC RP PROTEIN SEQUENCE.
 CC RC TISSUE=Venom;
 CC MEDLINE=91166748; PubMed=2076202;
 CC RA Wunderer G., Walter I., Eschenbacher B., Lang M., Kellermann J.,

RA Kindermann G.;
RT "Ile-ser-bradykinin is an aberrant permeability factor in various
RL human malignant effusions.";
DR Biol. Chem. Hoppe-Seyler 371:977-981(1990).
FT PIR; S13279; S13279.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1260 MW; 33D55258B9C6777 CRC64;

Query Match 24.8%; Score 26; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 PGPF 11
|||
Db 4 PGPF 7

RESULT 25

VESP_VESMA STANDARD; PRT; 12 AA.
ID_VESP_VESMA
AC Q7M3T3;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Vespakinin M.
OS Vespakinin M.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Vespinae; Vespa.
OX NCBI_TaxID=7446;
RN [1]
RP PROTEIN SEQUENCE, AND HYDROXYLATION.
RC TISSUE=Venom;
RX MEDLINE=77114342; PubMed=1017116;
RA Kishimura H., Yasuhara T., Yoshida H., Nakajima T.;
RT "Vespakinin-M, a novel bradykinin analogue containing hydroxyproline,
in the venom of Vespa mandarina Smith.";
RL Chem. Pharm. Bull. 24:2896-2897(1976).
CC -! FUNCTION: Bradykinins are a potent but short-lived agent of
arteriolar dilation and increased capillary permeability (By
similarity).
CC -! SUBCELLULAR LOCATION: Secreted; venom reservoirs.
CC -! SIMILARITY: Belongs to the bradykinin family.
CC -----
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CC removed.
CC -----
CC PIR; A61360; A61360.
KW Bradykinin; Direct protein sequencing; Hydroxylation; Vasoactive;
KW Vasodilator.
FT MOD_RES 4 4 4-hydroxyproline.
SQ SEQUENCE 12 AA; 1346 MW; 34F513C44C75B9C8 CRC64;

Query Match 24.8%; Score 26; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 PGPF 11
|||
Db 3 PGPF 6

Search completed: January 26, 2006, 08:04:04
Job time : 61.4828 secs